



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 19, 2023 – 08:08 PM EDT

PDB ID : 2G3M
Title : Crystal structure of the Sulfolobus solfataricus alpha-glucosidase MalA
Authors : Ernst, H.A.; Lo Leggio, L.; Willemoes, M.; Leonard, G.; Blum, P.; Larsen, S.
Deposited on : 2006-02-20
Resolution : 2.55 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.35
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35

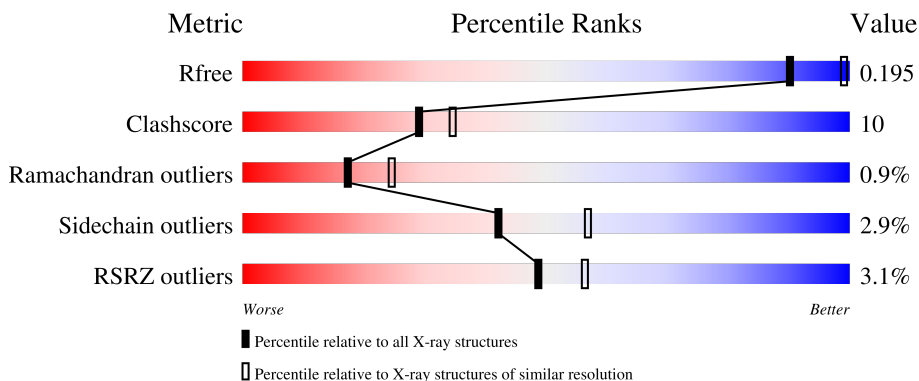
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



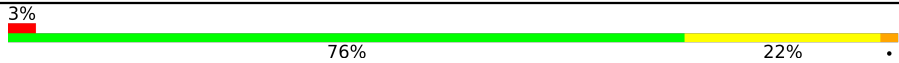
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	693	 3% 76% 23%
1	B	693	 2% 76% 23%
1	C	693	 4% 75% 24%
1	D	693	 3% 75% 24%
1	E	693	 2% 78% 20%

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Mol	Chain	Length	Quality of chain
1	F	693	 <p>A horizontal bar chart representing the quality of the chain. The bar is divided into three segments: a small red segment on the left labeled '3%', a large green segment in the middle labeled '76%', and a yellow segment on the right labeled '22%'. A small black dot is visible at the far right end of the bar.</p>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 35378 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Alpha-glucosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	691	5684	3703	919	1047	15	0	1	0
1	B	691	5684	3703	919	1047	15	0	1	0
1	C	691	5684	3703	919	1047	15	0	1	0
1	D	691	5684	3703	919	1047	15	0	1	0
1	E	691	5684	3703	919	1047	15	0	1	0
1	F	692	5695	3709	923	1048	15	0	1	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	cloning artifact	UNP O59645
A	2	ARG	-	cloning artifact	UNP O59645
A	3	ILE	-	cloning artifact	UNP O59645
A	4	LEU	-	cloning artifact	UNP O59645
B	1	MET	-	cloning artifact	UNP O59645
B	2	ARG	-	cloning artifact	UNP O59645
B	3	ILE	-	cloning artifact	UNP O59645
B	4	LEU	-	cloning artifact	UNP O59645
C	1	MET	-	cloning artifact	UNP O59645
C	2	ARG	-	cloning artifact	UNP O59645
C	3	ILE	-	cloning artifact	UNP O59645
C	4	LEU	-	cloning artifact	UNP O59645
D	1	MET	-	cloning artifact	UNP O59645
D	2	ARG	-	cloning artifact	UNP O59645
D	3	ILE	-	cloning artifact	UNP O59645
D	4	LEU	-	cloning artifact	UNP O59645
E	1	MET	-	cloning artifact	UNP O59645

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Chain	Residue	Modelled	Actual	Comment	Reference
E	2	ARG	-	cloning artifact	UNP O59645
E	3	ILE	-	cloning artifact	UNP O59645
E	4	LEU	-	cloning artifact	UNP O59645
F	1	MET	-	cloning artifact	UNP O59645
F	2	ARG	-	cloning artifact	UNP O59645
F	3	ILE	-	cloning artifact	UNP O59645
F	4	LEU	-	cloning artifact	UNP O59645

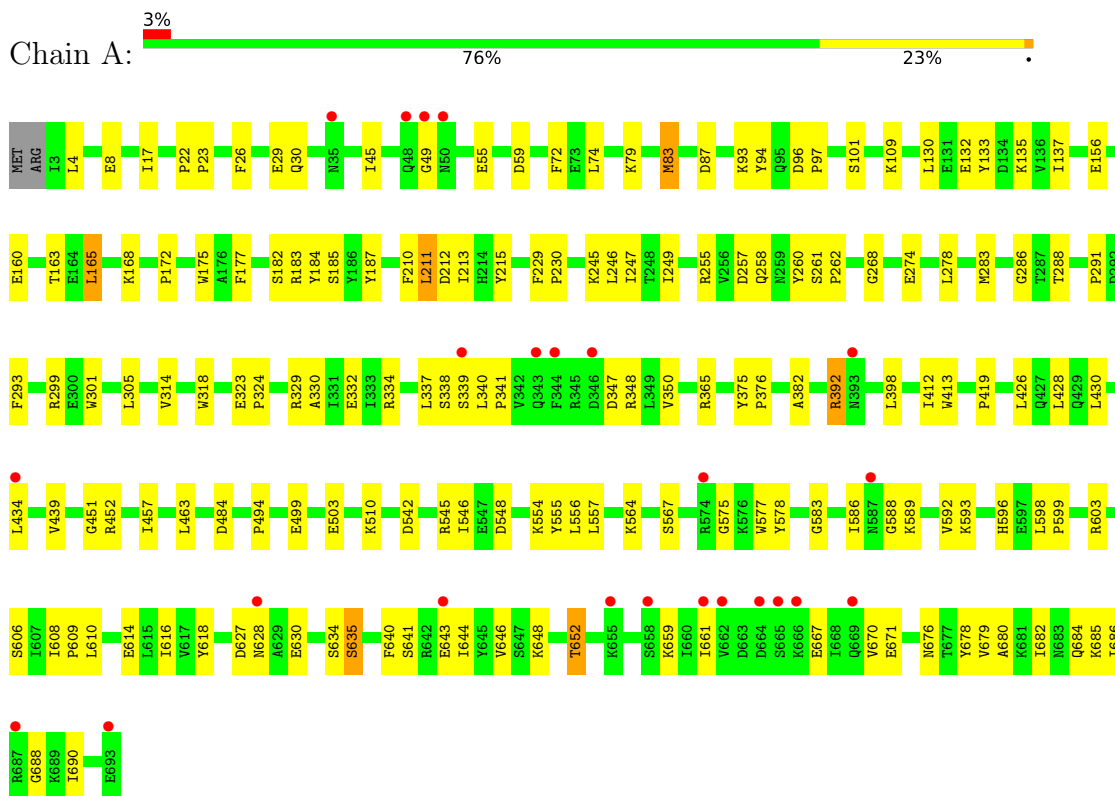
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	213	Total O 213 213	0	0
2	B	210	Total O 210 210	0	0
2	C	178	Total O 178 178	0	0
2	D	221	Total O 221 221	0	0
2	E	249	Total O 249 249	0	0
2	F	192	Total O 192 192	0	0

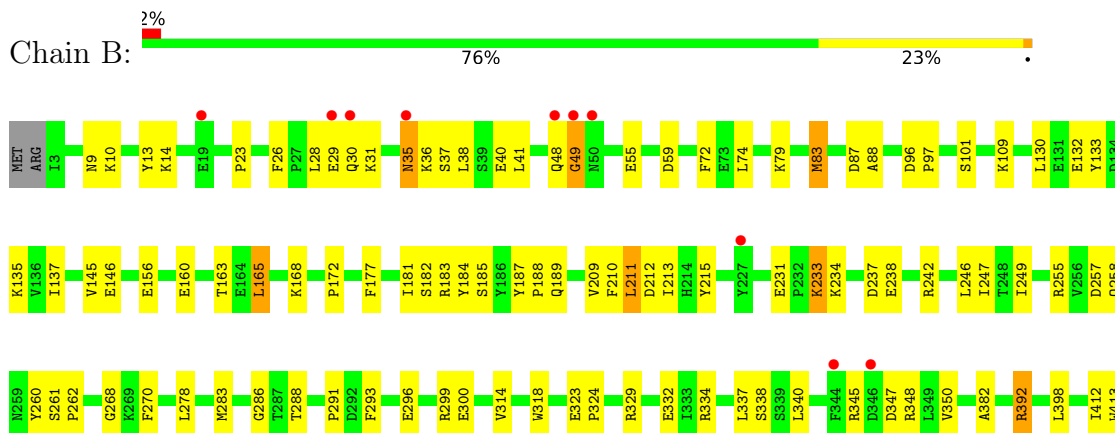
3 Residue-property plots [i](#)

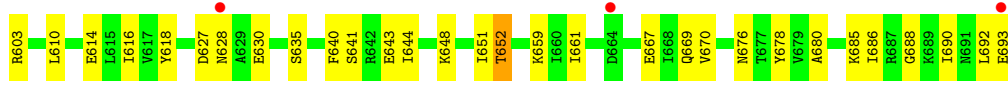
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Alpha-glucosidase

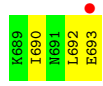
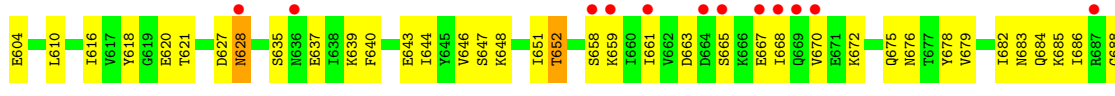
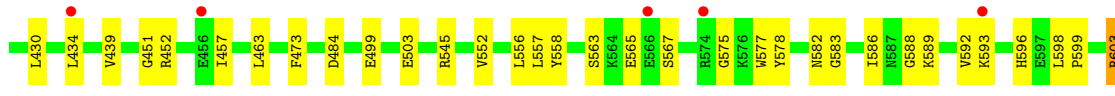
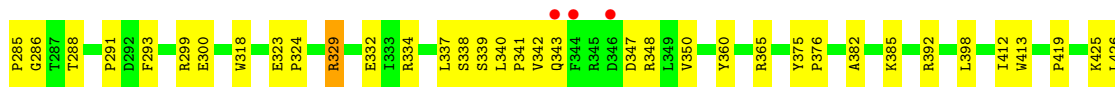
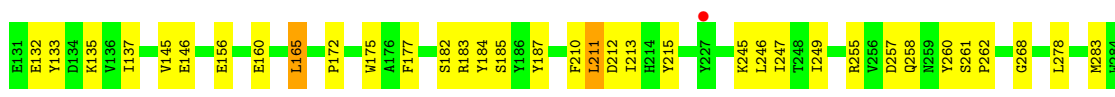
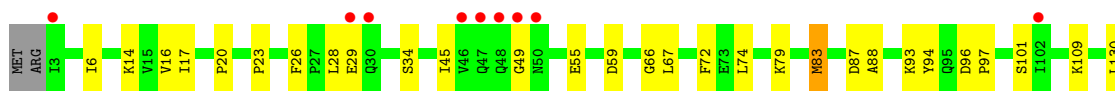
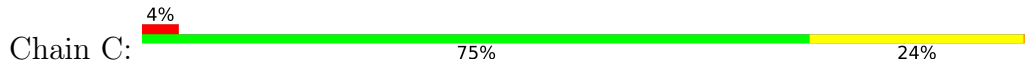


• Molecule 1: Alpha-glucosidase

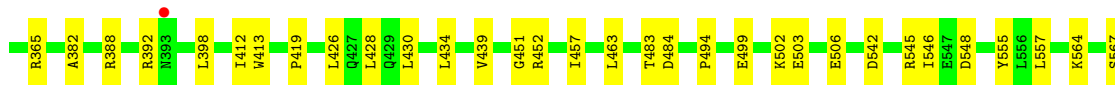
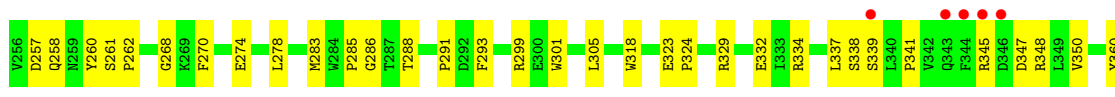
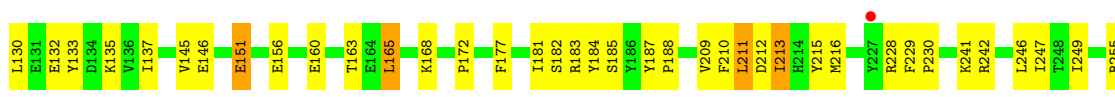
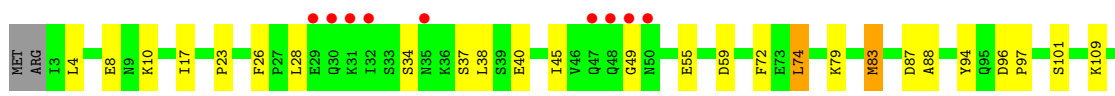
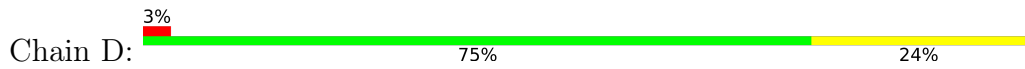




● Molecule 1: Alpha-glucosidase



● Molecule 1: Alpha-glucosidase



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	103.17Å 173.56Å 154.08Å 90.00° 108.00° 90.00°	Depositor
Resolution (Å)	34.25 – 2.55 34.25 – 2.55	Depositor EDS
% Data completeness (in resolution range)	99.9 (34.25-2.55) 100.0 (34.25-2.55)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.95 (at 2.54Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.170 , 0.195 0.171 , 0.195	Depositor DCC
R_{free} test set	8380 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	33.7	Xtrriage
Anisotropy	0.344	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 41.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.018 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	35378	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.64% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.36	0/5838	0.61	0/7902
1	B	0.36	0/5838	0.61	0/7902
1	C	0.36	0/5838	0.60	0/7902
1	D	0.37	0/5838	0.61	0/7902
1	E	0.37	0/5838	0.62	0/7902
1	F	0.36	0/5849	0.61	0/7916
All	All	0.36	0/35039	0.61	0/47426

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5684	0	5651	109	0
1	B	5684	0	5651	115	0
1	C	5684	0	5651	125	0
1	D	5684	0	5651	127	0
1	E	5684	0	5651	111	0
1	F	5695	0	5664	123	0
2	A	213	0	0	2	0
2	B	210	0	0	3	0
2	C	178	0	0	2	0
2	D	221	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	249	0	0	4	0
2	F	192	0	0	4	0
All	All	35378	0	33919	651	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (651) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:661:ILE:HG12	1:D:667:GLU:HG2	1.41	1.02
1:A:258:GLN:HG3	1:E:278:LEU:HD21	1.51	0.93
1:D:564:LYS:H	1:D:564:LYS:HD2	1.31	0.91
1:B:564:LYS:H	1:B:564:LYS:HD2	1.37	0.88
1:B:35:ASN:H	1:B:35:ASN:HD22	1.23	0.85
1:B:258:GLN:HG3	1:D:278:LEU:HD21	1.58	0.85
1:E:163:THR:HG22	1:E:168:LYS:HD3	1.57	0.83
1:C:686:ILE:HD13	1:C:690:ILE:HD11	1.57	0.83
1:C:278:LEU:HD21	1:F:258:GLN:HG3	1.58	0.83
1:C:299:ARG:HG3	1:C:382:ALA:HB2	1.60	0.82
1:C:596:HIS:HD2	1:C:598:LEU:H	1.26	0.82
1:C:332:GLU:HG3	1:F:332:GLU:HG3	1.60	0.81
1:A:686:ILE:HD13	1:A:690:ILE:HD11	1.63	0.81
1:D:341:PRO:HA	1:F:345:ARG:NH1	1.97	0.80
1:B:278:LEU:HD21	1:D:258:GLN:HG3	1.61	0.79
1:E:577:TRP:CZ3	1:E:603:ARG:HB3	2.16	0.79
1:A:670:VAL:CG1	1:A:678:TYR:HB3	2.11	0.79
1:D:651:ILE:HD13	1:D:692:LEU:HD21	1.65	0.78
1:C:299:ARG:CG	1:C:382:ALA:HB2	2.14	0.78
1:D:299:ARG:HG3	1:D:382:ALA:HB2	1.66	0.78
1:A:610:LEU:HD11	1:A:616:ILE:HD11	1.66	0.77
1:A:163:THR:HG22	1:A:168:LYS:HD3	1.67	0.77
1:B:564:LYS:HD2	1:B:564:LYS:N	1.98	0.77
1:E:299:ARG:HG3	1:E:382:ALA:HB2	1.66	0.77
1:F:163:THR:HG22	1:F:168:LYS:HD3	1.68	0.76
1:C:596:HIS:CD2	1:C:598:LEU:H	2.02	0.76
1:D:618:TYR:HB2	1:D:652:THR:HG23	1.66	0.76
1:F:8:GLU:HB2	1:F:34:SER:HB2	1.68	0.75
1:D:163:THR:HG22	1:D:168:LYS:HD3	1.69	0.75
1:D:564:LYS:HD2	1:D:564:LYS:N	2.02	0.75
1:E:163:THR:CG2	1:E:168:LYS:HD3	2.17	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:596:HIS:HD2	1:F:598:LEU:H	1.35	0.74
1:B:314:VAL:O	1:B:392:ARG:NH2	2.20	0.74
1:B:35:ASN:H	1:B:35:ASN:ND2	1.86	0.73
1:B:347:ASP:O	1:B:350:VAL:HG12	1.89	0.73
1:B:299:ARG:HG2	1:B:382:ALA:HB2	1.70	0.73
1:C:567:SER:OG	1:C:593:LYS:HE3	1.89	0.73
1:F:37:SER:OG	1:F:40:GLU:HG3	1.88	0.73
1:B:299:ARG:CG	1:B:382:ALA:HB2	2.19	0.72
1:B:37:SER:OG	1:B:40:GLU:HG3	1.89	0.72
1:E:596:HIS:HD2	1:E:598:LEU:H	1.37	0.72
1:E:299:ARG:CG	1:E:382:ALA:HB2	2.18	0.72
1:E:38:LEU:HD21	1:E:45:ILE:HD12	1.71	0.72
1:B:651:ILE:HD13	1:B:692:LEU:HD21	1.72	0.72
1:F:596:HIS:CD2	1:F:598:LEU:H	2.08	0.72
1:B:596:HIS:HD2	1:B:598:LEU:H	1.36	0.71
1:A:686:ILE:CD1	1:A:690:ILE:HD11	2.20	0.71
1:B:36:LYS:HE3	2:B:896:HOH:O	1.89	0.71
1:D:686:ILE:HD13	1:D:690:ILE:HD11	1.72	0.71
1:C:618:TYR:HB2	1:C:652:THR:HG23	1.71	0.70
1:A:258:GLN:CG	1:E:278:LEU:HD21	2.19	0.70
1:C:258:GLN:HG3	1:F:278:LEU:HD21	1.71	0.70
1:B:686:ILE:HD13	1:B:690:ILE:HD11	1.72	0.70
1:A:670:VAL:HG11	1:A:678:TYR:HB3	1.71	0.70
1:C:425:LYS:HG3	2:C:832:HOH:O	1.92	0.70
1:D:299:ARG:CG	1:D:382:ALA:HB2	2.22	0.69
1:A:286:GLY:O	1:A:288:THR:HG23	1.93	0.69
1:A:8:GLU:O	1:A:30:GLN:HG3	1.93	0.69
1:C:17:ILE:HD11	1:C:45:ILE:HD13	1.74	0.69
1:E:13:TYR:CE2	1:E:36:LYS:HG3	2.27	0.69
1:B:268:GLY:H	1:D:258:GLN:HG2	1.59	0.68
1:C:286:GLY:O	1:C:288:THR:HG23	1.94	0.68
1:A:630:GLU:HB2	1:A:641:SER:HB3	1.76	0.68
1:F:299:ARG:CG	1:F:382:ALA:HB2	2.24	0.68
1:F:610:LEU:HD11	1:F:616:ILE:HD11	1.74	0.67
1:A:314:VAL:O	1:A:392:ARG:NH2	2.28	0.67
1:B:233:LYS:HE3	1:B:237:ASP:OD2	1.94	0.67
1:B:286:GLY:O	1:B:288:THR:HG23	1.94	0.67
1:C:278:LEU:HD21	1:F:258:GLN:CG	2.25	0.67
1:A:278:LEU:HD21	1:E:258:GLN:HG3	1.76	0.67
1:B:14:LYS:HD2	1:B:28:LEU:HD12	1.76	0.67
1:B:185:SER:OG	1:B:212:ASP:HB3	1.95	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:646:VAL:HG21	1:C:686:ILE:HD12	1.77	0.67
1:D:286:GLY:O	1:D:288:THR:HG23	1.95	0.67
1:A:567:SER:OG	1:A:593:LYS:HE3	1.95	0.66
1:C:563:SER:OG	1:C:565:GLU:HG2	1.95	0.66
1:E:286:GLY:O	1:E:288:THR:HG23	1.95	0.66
1:B:258:GLN:HG2	1:D:268:GLY:H	1.60	0.66
1:B:258:GLN:CG	1:D:278:LEU:HD21	2.23	0.66
1:F:38:LEU:HD21	1:F:45:ILE:HD12	1.76	0.66
1:E:314:VAL:O	1:E:392:ARG:NH2	2.29	0.66
1:F:286:GLY:O	1:F:288:THR:HG23	1.96	0.66
1:D:577:TRP:CZ3	1:D:603:ARG:HB3	2.31	0.66
1:C:337:LEU:HD21	1:F:337:LEU:HD21	1.76	0.65
1:F:686:ILE:CD1	1:F:690:ILE:HD11	2.27	0.65
1:C:185:SER:OG	1:C:212:ASP:HB3	1.95	0.65
1:A:185:SER:OG	1:A:212:ASP:HB3	1.96	0.65
1:B:278:LEU:HD21	1:D:258:GLN:CG	2.27	0.65
1:A:452:ARG:HD3	1:A:484:ASP:O	1.97	0.65
1:E:185:SER:OG	1:E:212:ASP:HB3	1.97	0.65
1:F:185:SER:OG	1:F:212:ASP:HB3	1.97	0.65
1:E:30:GLN:O	1:E:32:ILE:HG22	1.97	0.65
1:F:651:ILE:HD13	1:F:692:LEU:HD21	1.78	0.65
1:A:163:THR:CG2	1:A:168:LYS:HD3	2.26	0.64
1:D:564:LYS:H	1:D:564:LYS:CD	2.08	0.64
1:D:185:SER:OG	1:D:212:ASP:HB3	1.96	0.64
1:F:682:ILE:HG22	1:F:684:GLN:HG2	1.80	0.64
1:B:334:ARG:O	1:B:338:SER:HB2	1.98	0.64
1:B:337:LEU:HD21	1:D:337:LEU:HD21	1.79	0.64
1:F:23:PRO:HG3	2:F:722:HOH:O	1.97	0.63
1:B:564:LYS:H	1:B:564:LYS:CD	2.11	0.63
1:C:258:GLN:HG2	1:F:268:GLY:H	1.63	0.63
1:C:23:PRO:HG3	2:C:722:HOH:O	1.98	0.63
1:B:452:ARG:HD3	1:B:484:ASP:O	1.99	0.63
1:C:332:GLU:CG	1:F:332:GLU:HG3	2.28	0.63
1:E:452:ARG:HD3	1:E:484:ASP:O	1.99	0.63
1:F:452:ARG:HD3	1:F:484:ASP:O	1.98	0.63
1:F:567:SER:OG	1:F:593:LYS:HE3	1.98	0.63
1:E:554:LYS:O	1:E:603:ARG:HD3	1.99	0.63
1:A:577:TRP:CZ3	1:A:603:ARG:HB3	2.33	0.63
1:B:23:PRO:HG3	2:B:722:HOH:O	1.99	0.63
1:D:452:ARG:HD3	1:D:484:ASP:O	1.97	0.63
1:B:574:ARG:HD3	2:B:876:HOH:O	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:577:TRP:CZ3	1:B:603:ARG:HB3	2.34	0.63
1:F:610:LEU:HB2	1:F:614:GLU:HB3	1.79	0.63
1:A:596:HIS:HD2	1:A:598:LEU:H	1.46	0.62
1:F:575:GLY:O	1:F:588:GLY:N	2.33	0.62
1:F:618:TYR:HB2	1:F:652:THR:HG23	1.80	0.62
1:C:339:SER:HB3	1:D:339:SER:CB	2.29	0.62
1:A:261:SER:HB3	1:A:262:PRO:HD3	1.81	0.62
1:C:452:ARG:HD3	1:C:484:ASP:O	1.99	0.62
1:D:87:ASP:O	1:D:348:ARG:HD3	2.00	0.62
1:B:87:ASP:O	1:B:348:ARG:HD3	2.00	0.62
1:D:323:GLU:N	1:D:324:PRO:HA	2.15	0.62
1:F:686:ILE:HD13	1:F:690:ILE:HD11	1.82	0.62
1:B:163:THR:HG22	1:B:168:LYS:HD3	1.82	0.61
1:A:299:ARG:CG	1:A:382:ALA:HB2	2.29	0.61
1:E:574:ARG:HD3	2:E:893:HOH:O	2.00	0.61
1:F:87:ASP:O	1:F:348:ARG:HD3	2.00	0.61
1:F:299:ARG:HG2	1:F:382:ALA:HB2	1.81	0.61
1:C:683:ASN:HD22	1:C:683:ASN:H	1.47	0.61
1:D:23:PRO:HG3	2:D:721:HOH:O	2.00	0.61
1:F:17:ILE:HD11	1:F:45:ILE:HD13	1.83	0.61
1:B:596:HIS:CD2	1:B:598:LEU:H	2.17	0.61
1:F:261:SER:HB3	1:F:262:PRO:HD3	1.82	0.61
1:B:55:GLU:HG2	1:B:137:ILE:HG12	1.82	0.61
1:C:261:SER:HB3	1:C:262:PRO:HD3	1.83	0.61
1:C:627:ASP:O	1:C:628:ASN:HB3	1.99	0.61
1:A:661:ILE:HG12	1:A:667:GLU:HG2	1.83	0.60
1:B:261:SER:HB3	1:B:262:PRO:HD3	1.82	0.60
1:C:26:PHE:HB3	1:C:165:LEU:HD22	1.83	0.60
1:B:9:ASN:ND2	1:B:10:LYS:HG3	2.15	0.60
1:B:578:TYR:CE1	1:B:583:GLY:HA2	2.36	0.60
1:C:668:ILE:HD13	1:C:682:ILE:HA	1.83	0.60
1:D:261:SER:HB3	1:D:262:PRO:HD3	1.83	0.60
1:E:323:GLU:N	1:E:324:PRO:HA	2.16	0.60
1:F:340:LEU:HB3	1:F:342:VAL:HG12	1.83	0.60
1:E:23:PRO:HG3	2:E:723:HOH:O	2.01	0.60
1:E:575:GLY:O	1:E:588:GLY:N	2.34	0.60
1:C:618:TYR:HB2	1:C:652:THR:CG2	2.31	0.60
1:D:575:GLY:O	1:D:588:GLY:N	2.33	0.60
1:F:347:ASP:O	1:F:350:VAL:HG12	2.02	0.60
1:A:330:ALA:O	1:A:334:ARG:HG2	2.02	0.60
1:F:323:GLU:N	1:F:324:PRO:HA	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:PRO:HG3	2:A:720:HOH:O	2.01	0.60
1:C:683:ASN:HD22	1:C:683:ASN:N	1.98	0.60
1:A:596:HIS:CD2	1:A:598:LEU:H	2.20	0.60
1:B:575:GLY:O	1:B:588:GLY:N	2.35	0.60
1:B:323:GLU:N	1:B:324:PRO:HA	2.17	0.59
1:C:575:GLY:O	1:C:588:GLY:N	2.33	0.59
1:A:17:ILE:HD11	1:A:45:ILE:HD13	1.84	0.59
1:C:268:GLY:H	1:F:258:GLN:HG2	1.67	0.59
1:B:26:PHE:HB3	1:B:165:LEU:HD22	1.83	0.59
1:A:323:GLU:N	1:A:324:PRO:HA	2.17	0.59
1:D:607:ILE:C	1:D:608:ILE:HD12	2.23	0.59
1:E:596:HIS:CD2	1:E:598:LEU:H	2.20	0.59
1:C:334:ARG:O	1:C:338:SER:HB2	2.02	0.59
1:E:55:GLU:HG2	1:E:137:ILE:HG12	1.85	0.59
1:C:323:GLU:N	1:C:324:PRO:HA	2.17	0.59
1:F:577:TRP:CZ3	1:F:603:ARG:HB3	2.38	0.59
1:A:575:GLY:O	1:A:588:GLY:N	2.34	0.58
1:D:132:GLU:HG3	2:D:832:HOH:O	2.03	0.58
1:E:618:TYR:HB2	1:E:652:THR:HG23	1.86	0.58
1:A:339:SER:HB2	1:F:339:SER:HB3	1.84	0.58
1:B:643:GLU:OE2	1:B:685:LYS:HD3	2.03	0.58
1:C:557:LEU:C	1:C:557:LEU:HD23	2.23	0.58
1:B:268:GLY:N	1:D:258:GLN:HG2	2.19	0.58
1:F:557:LEU:HD23	1:F:558:TYR:N	2.17	0.58
1:B:340:LEU:HD11	1:E:340:LEU:HD13	1.85	0.58
1:C:686:ILE:CD1	1:C:690:ILE:HD11	2.29	0.58
1:D:614:GLU:HG2	1:D:648:LYS:HB3	1.83	0.58
1:A:87:ASP:O	1:A:348:ARG:HD3	2.04	0.58
1:D:55:GLU:HG2	1:D:137:ILE:HG12	1.86	0.58
1:E:261:SER:HB3	1:E:262:PRO:HD3	1.86	0.58
1:B:618:TYR:HB2	1:B:652:THR:HG23	1.84	0.58
1:A:419:PRO:HG2	1:A:457:ILE:HG23	1.85	0.58
1:D:499:GLU:O	1:D:503:GLU:HG3	2.04	0.58
1:F:55:GLU:HG2	1:F:137:ILE:HG12	1.86	0.57
1:F:412:ILE:HD12	1:F:439:VAL:HG11	1.87	0.57
1:B:35:ASN:HD22	1:B:35:ASN:N	1.91	0.57
1:C:87:ASP:O	1:C:348:ARG:HD3	2.04	0.57
1:E:419:PRO:HG2	1:E:457:ILE:HG23	1.87	0.57
1:E:8:GLU:O	1:E:32:ILE:HG23	2.04	0.57
1:A:337:LEU:HD21	1:E:337:LEU:HD21	1.87	0.57
1:B:499:GLU:O	1:B:503:GLU:HG3	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:26:PHE:HB3	1:D:165:LEU:HD22	1.87	0.57
1:A:55:GLU:HG2	1:A:137:ILE:HG12	1.86	0.57
1:D:686:ILE:CD1	1:D:690:ILE:HD11	2.35	0.57
1:E:661:ILE:CD1	1:E:693:GLU:HG3	2.35	0.57
1:C:258:GLN:HG2	1:F:268:GLY:N	2.19	0.57
1:F:618:TYR:HB2	1:F:652:THR:CG2	2.35	0.57
1:C:14:LYS:HD2	1:C:28:LEU:HD12	1.87	0.56
1:D:360:TYR:CZ	1:D:365:ARG:HD2	2.40	0.56
1:D:659:LYS:NZ	1:D:659:LYS:HB3	2.20	0.56
1:B:255:ARG:HG2	1:B:257:ASP:HB2	1.87	0.56
1:B:258:GLN:HG2	1:D:268:GLY:N	2.20	0.56
1:A:255:ARG:HG2	1:A:257:ASP:HB2	1.87	0.56
1:C:156:GLU:O	1:C:160:GLU:HG3	2.05	0.56
1:F:293:PHE:O	1:F:299:ARG:HD3	2.05	0.56
1:C:55:GLU:HG2	1:C:137:ILE:HG12	1.86	0.56
1:C:347:ASP:O	1:C:350:VAL:HG12	2.05	0.56
1:A:412:ILE:HD12	1:A:439:VAL:HG11	1.87	0.56
1:E:59:ASP:OD2	1:E:109:LYS:HD2	2.06	0.56
1:F:156:GLU:O	1:F:160:GLU:HG3	2.06	0.56
1:C:419:PRO:HG2	1:C:457:ILE:HG23	1.88	0.55
1:D:255:ARG:HG2	1:D:257:ASP:HB2	1.88	0.55
1:E:342:VAL:CG1	1:F:342:VAL:HG23	2.36	0.55
1:E:610:LEU:HD11	1:E:616:ILE:HD11	1.88	0.55
1:F:342:VAL:HG22	1:F:343:GLN:N	2.21	0.55
1:E:156:GLU:O	1:E:160:GLU:HG3	2.06	0.55
1:F:255:ARG:HG2	1:F:257:ASP:HB2	1.88	0.55
1:F:499:GLU:O	1:F:503:GLU:HG3	2.07	0.55
1:A:643:GLU:OE2	1:A:685:LYS:HD2	2.06	0.55
1:B:59:ASP:OD2	1:B:109:LYS:HD2	2.06	0.55
1:B:412:ILE:HD12	1:B:439:VAL:HG11	1.88	0.55
1:D:618:TYR:HB2	1:D:652:THR:CG2	2.34	0.55
1:F:419:PRO:HG2	1:F:457:ILE:HG23	1.88	0.55
1:D:163:THR:CG2	1:D:168:LYS:HD3	2.37	0.55
1:D:419:PRO:HG2	1:D:457:ILE:HG23	1.87	0.55
1:C:255:ARG:HG2	1:C:257:ASP:HB2	1.87	0.55
1:A:156:GLU:O	1:A:160:GLU:HG3	2.06	0.55
1:D:578:TYR:CE1	1:D:583:GLY:HA2	2.42	0.55
1:D:334:ARG:O	1:D:338:SER:HB2	2.07	0.55
1:B:614:GLU:HG2	1:B:648:LYS:HB3	1.87	0.55
1:C:651:ILE:HD13	1:C:692:LEU:HD21	1.89	0.55
1:D:156:GLU:O	1:D:160:GLU:HG3	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:234:LYS:O	1:E:238:GLU:HG3	2.07	0.55
1:D:637:GLU:OE2	1:D:639:LYS:HE3	2.08	0.54
1:B:661:ILE:HG12	1:B:667:GLU:HG2	1.88	0.54
1:B:419:PRO:HG2	1:B:457:ILE:HG23	1.88	0.54
1:C:59:ASP:OD2	1:C:109:LYS:HD2	2.07	0.54
1:C:299:ARG:HG2	1:C:382:ALA:HB2	1.90	0.54
1:F:334:ARG:O	1:F:338:SER:HB3	2.06	0.54
1:D:59:ASP:OD2	1:D:109:LYS:HD2	2.07	0.54
1:E:87:ASP:O	1:E:348:ARG:HD3	2.08	0.54
1:F:59:ASP:OD2	1:F:109:LYS:HD2	2.07	0.54
1:F:675:GLN:HG2	1:F:676:ASN:ND2	2.23	0.54
1:E:412:ILE:HD12	1:E:439:VAL:HG11	1.89	0.54
1:F:132:GLU:HG3	2:F:826:HOH:O	2.07	0.54
1:A:618:TYR:HB2	1:A:652:THR:HG23	1.90	0.54
1:C:577:TRP:CZ3	1:C:603:ARG:HB3	2.42	0.54
1:E:342:VAL:HG11	1:F:342:VAL:HG23	1.89	0.54
1:E:342:VAL:HG12	1:E:343:GLN:N	2.22	0.54
1:E:578:TYR:CE1	1:E:583:GLY:HA2	2.43	0.54
1:F:163:THR:CG2	1:F:168:LYS:HD3	2.35	0.54
1:A:299:ARG:HG3	1:A:382:ALA:HB2	1.90	0.54
1:E:255:ARG:HG2	1:E:257:ASP:HB2	1.89	0.53
1:D:652:THR:HA	1:D:676:ASN:O	2.08	0.53
1:E:682:ILE:HG22	1:E:684:GLN:HG2	1.91	0.53
1:C:682:ILE:HG22	1:C:684:GLN:HG2	1.91	0.53
1:E:577:TRP:CH2	1:E:603:ARG:HB3	2.43	0.53
1:B:651:ILE:HD13	1:B:692:LEU:CD2	2.38	0.53
1:E:659:LYS:HD2	1:E:667:GLU:HG3	1.90	0.53
1:A:652:THR:HA	1:A:676:ASN:O	2.09	0.53
1:A:59:ASP:OD2	1:A:109:LYS:HD2	2.08	0.53
1:C:499:GLU:O	1:C:503:GLU:HG3	2.08	0.53
1:D:83:MET:HG3	1:D:101:SER:HB3	1.91	0.53
1:D:412:ILE:HD12	1:D:439:VAL:HG11	1.89	0.53
1:A:268:GLY:H	1:E:258:GLN:HG2	1.74	0.53
1:B:299:ARG:HG3	1:B:382:ALA:HB2	1.91	0.53
1:B:652:THR:HA	1:B:676:ASN:O	2.09	0.53
1:C:182:SER:HB2	1:C:210:PHE:HB2	1.91	0.52
1:B:234:LYS:O	1:B:238:GLU:HG3	2.09	0.52
1:A:334:ARG:O	1:A:338:SER:HB3	2.09	0.52
1:B:156:GLU:O	1:B:160:GLU:HG3	2.09	0.52
1:C:412:ILE:HD12	1:C:439:VAL:HG11	1.89	0.52
1:D:596:HIS:CD2	1:D:598:LEU:H	2.27	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:182:SER:HB2	1:F:210:PHE:HB2	1.92	0.52
1:C:578:TYR:CE1	1:C:583:GLY:HA2	2.44	0.52
1:C:652:THR:HA	1:C:676:ASN:O	2.10	0.52
1:D:388:ARG:HD3	2:D:850:HOH:O	2.08	0.52
1:D:10:LYS:HG2	1:D:10:LYS:O	2.10	0.52
1:D:651:ILE:HD13	1:D:692:LEU:CD2	2.38	0.52
1:C:17:ILE:HD11	1:C:45:ILE:CD1	2.39	0.52
1:F:234:LYS:O	1:F:238:GLU:HG3	2.09	0.52
1:A:274:GLU:O	1:A:365:ARG:NH2	2.43	0.52
1:E:342:VAL:CG1	1:E:343:GLN:N	2.73	0.52
1:F:299:ARG:HG3	1:F:382:ALA:HB2	1.90	0.52
1:A:586:ILE:HD13	1:A:592:VAL:HG11	1.92	0.51
1:C:258:GLN:CG	1:F:278:LEU:HD21	2.38	0.51
1:A:268:GLY:N	1:E:258:GLN:HG2	2.25	0.51
1:A:557:LEU:HD23	1:A:557:LEU:C	2.30	0.51
1:D:293:PHE:O	1:D:299:ARG:HD3	2.10	0.51
1:A:554:LYS:O	1:A:603:ARG:HD3	2.11	0.51
1:B:163:THR:CG2	1:B:168:LYS:HD3	2.41	0.51
1:B:35:ASN:ND2	1:B:35:ASN:N	2.51	0.51
1:E:274:GLU:O	1:E:365:ARG:NH2	2.38	0.51
1:B:340:LEU:CD1	1:E:340:LEU:HD13	2.41	0.51
1:C:6:ILE:HG22	1:C:34:SER:HB2	1.92	0.51
1:A:499:GLU:O	1:A:503:GLU:HG3	2.11	0.51
1:A:679:VAL:HG12	1:A:680:ALA:N	2.26	0.51
1:D:586:ILE:HD13	1:D:592:VAL:HG11	1.93	0.51
1:E:652:THR:HA	1:E:676:ASN:O	2.11	0.51
1:A:299:ARG:HG2	1:A:382:ALA:HB2	1.91	0.51
1:A:132:GLU:HG3	2:A:835:HOH:O	2.11	0.50
1:A:578:TYR:CE1	1:A:583:GLY:HA2	2.46	0.50
1:B:72:PHE:CZ	1:B:79:LYS:HE2	2.46	0.50
1:B:172:PRO:HG2	1:B:177:PHE:CE1	2.46	0.50
1:C:268:GLY:N	1:F:258:GLN:HG2	2.26	0.50
1:E:182:SER:HB2	1:E:210:PHE:HB2	1.93	0.50
1:C:675:GLN:HG2	1:C:676:ASN:ND2	2.26	0.50
1:E:640:PHE:CE2	1:E:644:ILE:HD11	2.46	0.50
1:D:72:PHE:CZ	1:D:79:LYS:HE2	2.47	0.50
1:A:132:GLU:HB3	1:A:135:LYS:HB2	1.93	0.50
1:C:291:PRO:HG2	1:C:293:PHE:CE2	2.46	0.50
1:F:586:ILE:HD13	1:F:592:VAL:HG11	1.94	0.50
1:A:293:PHE:O	1:A:299:ARG:HD3	2.11	0.50
1:D:341:PRO:HA	1:F:345:ARG:HH12	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:659:LYS:HA	1:A:670:VAL:HG23	1.93	0.50
1:B:686:ILE:CD1	1:B:690:ILE:HD11	2.39	0.50
1:B:692:LEU:N	1:B:692:LEU:HD12	2.27	0.50
1:D:172:PRO:HG2	1:D:177:PHE:CE1	2.47	0.50
1:D:229:PHE:N	1:D:230:PRO:HD3	2.25	0.50
1:D:682:ILE:HG22	1:D:684:GLN:HG2	1.94	0.50
1:E:347:ASP:O	1:E:350:VAL:HG12	2.11	0.50
1:F:291:PRO:HG2	1:F:293:PHE:CE2	2.47	0.50
1:A:172:PRO:HG2	1:A:177:PHE:CE1	2.46	0.50
1:A:211:LEU:HD22	1:A:246:LEU:HD11	1.93	0.50
1:B:586:ILE:HD13	1:B:592:VAL:HG11	1.94	0.50
1:C:211:LEU:HD22	1:C:246:LEU:HD11	1.94	0.50
1:E:72:PHE:CZ	1:E:79:LYS:HE2	2.47	0.50
1:E:229:PHE:N	1:E:230:PRO:HD3	2.26	0.50
1:E:564:LYS:HD2	1:E:564:LYS:N	2.27	0.50
1:A:339:SER:HB2	1:F:339:SER:CB	2.41	0.50
1:A:83:MET:HG3	1:A:101:SER:HB3	1.93	0.49
1:B:293:PHE:O	1:B:299:ARG:HD3	2.12	0.49
1:B:627:ASP:O	1:B:628:ASN:CG	2.51	0.49
1:D:181:ILE:CG1	1:D:209:VAL:HG12	2.41	0.49
1:C:586:ILE:HD13	1:C:592:VAL:HG11	1.94	0.49
1:A:72:PHE:CZ	1:A:79:LYS:HE2	2.48	0.49
1:A:291:PRO:HG2	1:A:293:PHE:CE2	2.47	0.49
1:A:682:ILE:HG22	1:A:684:GLN:HG2	1.94	0.49
1:C:648:LYS:HD2	1:C:679:VAL:HG11	1.94	0.49
1:F:257:ASP:HB3	1:F:260:TYR:CB	2.42	0.49
1:C:72:PHE:CZ	1:C:79:LYS:HE2	2.48	0.49
1:C:172:PRO:HG2	1:C:177:PHE:CE1	2.48	0.49
1:C:451:GLY:O	1:C:452:ARG:HG3	2.12	0.49
1:B:554:LYS:O	1:B:603:ARG:HD3	2.13	0.49
1:E:586:ILE:HD13	1:E:592:VAL:HG11	1.94	0.49
1:C:83:MET:HG3	1:C:101:SER:HB3	1.94	0.49
1:C:683:ASN:N	1:C:683:ASN:ND2	2.60	0.49
1:E:291:PRO:HG2	1:E:293:PHE:CE2	2.48	0.49
1:F:72:PHE:CZ	1:F:79:LYS:HE2	2.47	0.49
1:F:132:GLU:HB3	1:F:135:LYS:HB2	1.95	0.49
1:F:610:LEU:HD11	1:F:616:ILE:CD1	2.43	0.49
1:D:257:ASP:HB3	1:D:260:TYR:CB	2.43	0.49
1:B:610:LEU:HD11	1:B:616:ILE:HD11	1.95	0.48
1:E:132:GLU:HB3	1:E:135:LYS:HB2	1.95	0.48
1:B:257:ASP:HB3	1:B:260:TYR:CB	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:291:PRO:HG2	1:B:293:PHE:CE2	2.47	0.48
1:D:291:PRO:HG2	1:D:293:PHE:CE2	2.47	0.48
1:E:659:LYS:HD2	1:E:667:GLU:CG	2.43	0.48
1:D:133:TYR:HB3	1:E:187:TYR:O	2.12	0.48
1:D:301:TRP:CZ2	1:D:305:LEU:HD11	2.48	0.48
1:E:392:ARG:NH1	2:E:905:HOH:O	2.46	0.48
1:E:564:LYS:HD2	1:E:564:LYS:H	1.77	0.48
1:A:556:LEU:HD23	1:A:557:LEU:N	2.28	0.48
1:E:312:GLN:HG2	2:E:929:HOH:O	2.12	0.48
1:B:211:LEU:HD22	1:B:246:LEU:HD11	1.95	0.48
1:C:300:GLU:HG2	1:C:385:LYS:NZ	2.29	0.48
1:A:589:LYS:HD2	1:A:589:LYS:HA	1.67	0.48
1:B:567:SER:OG	1:B:593:LYS:HE3	2.12	0.48
1:D:545:ARG:HB2	1:E:494:PRO:HG3	1.96	0.48
1:E:172:PRO:HG2	1:E:177:PHE:CE1	2.49	0.48
1:B:181:ILE:CG1	1:B:209:VAL:HG12	2.43	0.48
1:E:83:MET:HG3	1:E:101:SER:HB3	1.94	0.48
1:E:499:GLU:O	1:E:503:GLU:HG3	2.13	0.48
1:F:17:ILE:HD11	1:F:45:ILE:CD1	2.43	0.48
1:B:13:TYR:OH	1:B:36:LYS:HD2	2.13	0.48
1:E:211:LEU:HD22	1:E:246:LEU:HD11	1.95	0.48
1:E:247:ILE:HD12	1:E:247:ILE:N	2.29	0.48
1:F:172:PRO:HG2	1:F:177:PHE:CE1	2.48	0.48
1:F:189:GLN:HE22	1:F:231:GLU:HB2	1.78	0.48
1:C:659:LYS:HA	1:C:670:VAL:HG23	1.96	0.48
1:B:630:GLU:HB2	1:B:641:SER:HB3	1.95	0.48
1:E:661:ILE:HD13	1:E:693:GLU:HG3	1.96	0.48
1:F:31:LYS:O	1:F:31:LYS:HG3	2.13	0.48
1:F:211:LEU:HD22	1:F:246:LEU:HD11	1.96	0.48
1:A:257:ASP:HB3	1:A:260:TYR:CB	2.44	0.47
1:A:182:SER:HB2	1:A:210:PHE:HB2	1.96	0.47
1:A:494:PRO:HG3	1:C:545:ARG:HB2	1.96	0.47
1:A:347:ASP:O	1:A:350:VAL:HG12	2.13	0.47
1:C:339:SER:HB3	1:D:339:SER:HB3	1.96	0.47
1:E:17:ILE:HD11	1:E:45:ILE:HD13	1.95	0.47
1:B:132:GLU:HB3	1:B:135:LYS:HB2	1.95	0.47
1:F:645:TYR:HA	1:F:685:LYS:HA	1.97	0.47
1:A:133:TYR:HB3	1:B:187:TYR:O	2.13	0.47
1:A:247:ILE:HD12	1:A:247:ILE:N	2.29	0.47
1:B:182:SER:HB2	1:B:210:PHE:HB2	1.96	0.47
1:B:189:GLN:HE22	1:B:231:GLU:HB2	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:672:LYS:HD2	1:C:678:TYR:CE1	2.49	0.47
1:F:83:MET:HG3	1:F:101:SER:HB3	1.96	0.47
1:A:278:LEU:HD21	1:E:258:GLN:CG	2.45	0.47
1:B:83:MET:HG3	1:B:101:SER:HB3	1.95	0.47
1:B:670:VAL:HG22	1:B:680:ALA:HB2	1.97	0.47
1:D:451:GLY:O	1:D:452:ARG:HG3	2.14	0.47
1:A:17:ILE:HD11	1:A:45:ILE:CD1	2.45	0.47
1:B:247:ILE:N	1:B:247:ILE:HD12	2.30	0.47
1:C:132:GLU:HB3	1:C:135:LYS:HB2	1.97	0.47
1:C:257:ASP:HB3	1:C:260:TYR:CB	2.44	0.47
1:C:640:PHE:CE2	1:C:644:ILE:HD11	2.49	0.47
1:D:132:GLU:HB3	1:D:135:LYS:HB2	1.97	0.47
1:D:610:LEU:HD11	1:D:616:ILE:HD11	1.97	0.47
1:B:296:GLU:O	1:B:300:GLU:HG3	2.15	0.47
1:D:181:ILE:HG13	1:D:209:VAL:HG12	1.97	0.47
1:F:26:PHE:HB3	1:F:165:LEU:HD22	1.95	0.47
1:F:388:ARG:HD3	2:F:840:HOH:O	2.15	0.47
1:A:332:GLU:HG2	1:E:332:GLU:HG3	1.97	0.46
1:A:451:GLY:O	1:A:452:ARG:HG3	2.14	0.46
1:E:293:PHE:O	1:E:299:ARG:HD3	2.15	0.46
1:C:661:ILE:HD11	1:C:693:GLU:CD	2.35	0.46
1:D:37:SER:OG	1:D:40:GLU:HG3	2.14	0.46
1:D:345:ARG:O	1:D:345:ARG:HG3	2.15	0.46
1:E:299:ARG:HG2	1:E:382:ALA:HB2	1.95	0.46
1:C:183:ARG:HG2	1:C:184:TYR:N	2.31	0.46
1:C:643:GLU:CD	1:C:685:LYS:HD3	2.35	0.46
1:D:247:ILE:N	1:D:247:ILE:HD12	2.29	0.46
1:E:257:ASP:HB3	1:E:260:TYR:CB	2.44	0.46
1:E:555:TYR:HB3	1:E:606:SER:HB3	1.96	0.46
1:B:659:LYS:HE3	1:B:693:GLU:HG3	1.98	0.46
1:D:187:TYR:O	1:F:133:TYR:HB3	2.16	0.46
1:E:342:VAL:HG11	1:F:342:VAL:CG2	2.45	0.46
1:D:211:LEU:HD22	1:D:246:LEU:HD11	1.97	0.46
1:E:175:TRP:CE3	1:E:245:LYS:HG3	2.50	0.46
1:A:682:ILE:CG2	1:A:684:GLN:HG2	2.46	0.46
1:B:640:PHE:CE2	1:B:644:ILE:HD11	2.51	0.46
1:C:16:VAL:HG13	1:C:20:PRO:HG2	1.97	0.46
1:F:2:ARG:HG2	1:F:47:GLN:OE1	2.16	0.46
1:F:183:ARG:HG2	1:F:184:TYR:N	2.30	0.46
1:C:247:ILE:HD12	1:C:247:ILE:N	2.30	0.46
1:A:187:TYR:O	1:C:133:TYR:HB3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:670:VAL:CG1	1:B:678:TYR:HB3	2.46	0.46
1:D:608:ILE:HD12	1:D:608:ILE:N	2.31	0.46
1:C:596:HIS:HD2	1:C:598:LEU:N	2.05	0.46
1:C:692:LEU:N	1:C:692:LEU:HD12	2.31	0.46
1:D:228:ARG:C	1:D:230:PRO:HD3	2.37	0.46
1:A:183:ARG:HG2	1:A:184:TYR:N	2.31	0.45
1:B:183:ARG:HG2	1:B:184:TYR:N	2.31	0.45
1:C:360:TYR:CE2	1:C:365:ARG:HD2	2.51	0.45
1:F:3:ILE:HB	1:F:18:GLY:HA2	1.98	0.45
1:A:26:PHE:HB3	1:A:165:LEU:HD22	1.99	0.45
1:D:88:ALA:C	1:D:348:ARG:HD2	2.37	0.45
1:C:183:ARG:O	1:C:185:SER:HA	2.16	0.45
1:C:360:TYR:CZ	1:C:365:ARG:HD2	2.51	0.45
1:D:182:SER:HB2	1:D:210:PHE:HB2	1.97	0.45
1:E:183:ARG:HG2	1:E:184:TYR:N	2.31	0.45
1:C:557:LEU:HD23	1:C:558:TYR:N	2.31	0.45
1:D:589:LYS:HD2	1:D:589:LYS:HA	1.66	0.45
1:F:242:ARG:HG3	1:F:242:ARG:HH11	1.82	0.45
1:F:247:ILE:N	1:F:247:ILE:HD12	2.31	0.45
1:A:229:PHE:N	1:A:230:PRO:HD3	2.30	0.45
1:D:8:GLU:HB2	1:D:34:SER:HB2	1.98	0.45
1:D:609:PRO:HG2	1:D:623:PHE:HE2	1.82	0.45
1:D:687:ARG:HB3	1:D:687:ARG:NH1	2.32	0.45
1:A:258:GLN:CD	1:E:278:LEU:HD21	2.37	0.45
1:A:258:GLN:HG2	1:E:268:GLY:H	1.80	0.45
1:A:646:VAL:HG21	1:A:686:ILE:HD12	1.99	0.45
1:F:451:GLY:O	1:F:452:ARG:HG3	2.17	0.45
1:A:340:LEU:HD13	1:F:340:LEU:HD13	1.99	0.45
1:B:618:TYR:HB2	1:B:652:THR:CG2	2.45	0.45
1:E:183:ARG:O	1:E:185:SER:HA	2.16	0.45
1:E:451:GLY:O	1:E:452:ARG:HG3	2.15	0.45
1:B:451:GLY:O	1:B:452:ARG:HG3	2.17	0.45
1:F:670:VAL:CG1	1:F:678:TYR:HB3	2.47	0.45
1:A:564:LYS:N	1:A:564:LYS:HD3	2.32	0.44
1:B:249:ILE:HA	1:B:318:TRP:HB3	2.00	0.44
1:A:249:ILE:HA	1:A:318:TRP:HB3	2.00	0.44
1:C:620:GLU:O	1:C:621:THR:HB	2.18	0.44
1:C:658:SER:HB2	1:C:693:GLU:O	2.17	0.44
1:D:183:ARG:HG2	1:D:184:TYR:N	2.32	0.44
1:D:360:TYR:CE2	1:D:365:ARG:HD2	2.52	0.44
1:E:9:ASN:OD1	1:E:29:GLU:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:17:ILE:CD1	1:F:45:ILE:HD13	2.47	0.44
1:F:38:LEU:HD21	1:F:45:ILE:CD1	2.46	0.44
1:A:640:PHE:CE2	1:A:644:ILE:HD11	2.53	0.44
1:A:670:VAL:HG12	1:A:671:GLU:N	2.32	0.44
1:B:242:ARG:HH11	1:B:242:ARG:HG3	1.82	0.44
1:B:270:PHE:N	1:D:258:GLN:OE1	2.38	0.44
1:C:96:ASP:OD1	1:C:97:PRO:HA	2.18	0.44
1:D:151:GLU:OE1	1:D:151:GLU:HA	2.16	0.44
1:D:241:LYS:CE	1:D:242:ARG:HH12	2.30	0.44
1:F:175:TRP:CE3	1:F:245:LYS:HG3	2.53	0.44
1:F:557:LEU:HD23	1:F:557:LEU:C	2.38	0.44
1:E:340:LEU:HD12	1:E:341:PRO:HD2	2.00	0.44
1:F:651:ILE:HD13	1:F:692:LEU:CD2	2.45	0.44
1:E:28:LEU:O	1:E:29:GLU:C	2.55	0.43
1:F:640:PHE:CD2	1:F:644:ILE:HD11	2.53	0.43
1:A:22:PRO:HA	1:A:23:PRO:HD3	1.89	0.43
1:B:332:GLU:CG	1:D:332:GLU:HG3	2.47	0.43
1:C:285:PRO:HD2	1:C:288:THR:HG21	2.00	0.43
1:C:342:VAL:HG22	1:C:343:GLN:H	1.83	0.43
1:C:663:ASP:C	1:C:665:SER:H	2.22	0.43
1:A:172:PRO:HG2	1:A:177:PHE:HE1	1.83	0.43
1:B:183:ARG:O	1:B:185:SER:HA	2.19	0.43
1:C:610:LEU:HD11	1:C:616:ILE:HD11	1.98	0.43
1:B:669:GLN:OE1	1:B:669:GLN:HA	2.19	0.43
1:C:473:PHE:CG	1:C:552:VAL:HG21	2.53	0.43
1:C:637:GLU:OE1	1:C:639:LYS:HE3	2.18	0.43
1:B:88:ALA:O	1:B:348:ARG:HD2	2.19	0.43
1:E:249:ILE:HA	1:E:318:TRP:HB3	2.01	0.43
1:F:229:PHE:N	1:F:230:PRO:HD3	2.33	0.43
1:F:627:ASP:O	1:F:628:ASN:HB3	2.18	0.43
1:F:634:SER:O	1:F:635:SER:C	2.56	0.43
1:F:640:PHE:CE2	1:F:644:ILE:HD11	2.54	0.43
1:B:133:TYR:HB3	1:C:187:TYR:O	2.18	0.43
1:C:300:GLU:HG2	1:C:385:LYS:HZ1	1.82	0.43
1:C:672:LYS:HD2	1:C:678:TYR:HE1	1.81	0.43
1:F:9:ASN:OD1	1:F:30:GLN:HB2	2.19	0.43
1:F:314:VAL:O	1:F:392:ARG:NH2	2.51	0.43
1:F:652:THR:HA	1:F:676:ASN:O	2.19	0.43
1:B:145:VAL:HG22	1:B:146:GLU:N	2.34	0.43
1:B:257:ASP:HB3	1:B:260:TYR:HB3	2.00	0.43
1:C:340:LEU:HA	1:C:340:LEU:HD12	1.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:347:ASP:O	1:D:350:VAL:HG12	2.19	0.43
1:F:257:ASP:HB3	1:F:260:TYR:HB2	2.01	0.43
1:F:257:ASP:HB3	1:F:260:TYR:HB3	2.00	0.43
1:D:183:ARG:O	1:D:185:SER:HA	2.18	0.43
1:D:215:TYR:CD1	1:D:215:TYR:C	2.92	0.43
1:E:13:TYR:HE2	1:E:36:LYS:HG3	1.79	0.43
1:E:215:TYR:CD1	1:E:215:TYR:C	2.92	0.43
1:C:329:ARG:HB3	1:C:350:VAL:HG22	2.00	0.43
1:C:556:LEU:HD23	1:C:557:LEU:N	2.34	0.43
1:D:299:ARG:HG2	1:D:382:ALA:HB2	2.01	0.43
1:D:567:SER:OG	1:D:593:LYS:HE3	2.18	0.43
1:E:228:ARG:C	1:E:230:PRO:HD3	2.39	0.43
1:F:183:ARG:O	1:F:185:SER:HA	2.19	0.43
1:B:31:LYS:O	1:B:31:LYS:HG3	2.19	0.42
1:C:556:LEU:HD23	1:C:556:LEU:C	2.40	0.42
1:F:215:TYR:CD1	1:F:215:TYR:C	2.93	0.42
1:A:686:ILE:HD13	1:A:690:ILE:CD1	2.43	0.42
1:A:183:ARG:O	1:A:185:SER:HA	2.19	0.42
1:B:172:PRO:HG2	1:B:177:PHE:HE1	1.83	0.42
1:D:96:ASP:OD1	1:D:97:PRO:HA	2.19	0.42
1:B:258:GLN:OE1	1:D:270:PHE:N	2.38	0.42
1:C:342:VAL:HG22	1:C:343:GLN:N	2.34	0.42
1:E:285:PRO:HD2	1:E:288:THR:HG21	2.02	0.42
1:C:257:ASP:HB3	1:C:260:TYR:HB2	2.02	0.42
1:D:257:ASP:HB3	1:D:260:TYR:HB3	2.02	0.42
1:A:93:LYS:O	1:A:94:TYR:HB2	2.19	0.42
1:A:555:TYR:HB3	1:A:606:SER:HB3	2.01	0.42
1:B:473:PHE:CG	1:B:552:VAL:HG21	2.54	0.42
1:C:604:GLU:HA	1:C:618:TYR:CE2	2.55	0.42
1:D:609:PRO:CG	1:D:623:PHE:HE2	2.32	0.42
1:E:661:ILE:N	1:E:661:ILE:HD12	2.34	0.42
1:B:258:GLN:CD	1:D:278:LEU:HD21	2.40	0.42
1:C:249:ILE:HA	1:C:318:TRP:HB3	2.02	0.42
1:C:589:LYS:HA	1:C:589:LYS:HD2	1.68	0.42
1:F:145:VAL:HG22	1:F:146:GLU:N	2.35	0.42
1:D:257:ASP:HB3	1:D:260:TYR:HB2	2.01	0.42
1:E:647:SER:OG	1:E:648:LYS:N	2.52	0.42
1:F:249:ILE:HA	1:F:318:TRP:HB3	2.01	0.42
1:A:215:TYR:CD1	1:A:215:TYR:C	2.94	0.42
1:A:375:TYR:N	1:A:376:PRO:HD2	2.35	0.42
1:A:428:LEU:HD23	1:A:548:ASP:HA	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:94:TYR:CZ	1:E:452:ARG:HG2	2.55	0.42
1:D:241:LYS:CE	1:D:242:ARG:NH1	2.83	0.42
1:F:340:LEU:C	1:F:342:VAL:H	2.23	0.42
1:B:502:LYS:O	1:B:506:GLU:HG3	2.20	0.41
1:C:659:LYS:HD2	1:C:667:GLU:OE2	2.20	0.41
1:B:257:ASP:HB3	1:B:260:TYR:HB2	2.01	0.41
1:D:241:LYS:HE3	1:D:242:ARG:NH1	2.36	0.41
1:E:257:ASP:HB3	1:E:260:TYR:HB2	2.02	0.41
1:F:589:LYS:HD2	1:F:589:LYS:HA	1.68	0.41
1:A:257:ASP:HB3	1:A:260:TYR:HB2	2.01	0.41
1:C:215:TYR:CD1	1:C:215:TYR:C	2.93	0.41
1:C:582:ASN:C	1:C:582:ASN:OD1	2.59	0.41
1:D:28:LEU:HD23	1:D:28:LEU:HA	1.90	0.41
1:F:578:TYR:CE1	1:F:583:GLY:HA2	2.55	0.41
1:D:555:TYR:HB3	1:D:606:SER:OG	2.20	0.41
1:A:340:LEU:HD12	1:A:341:PRO:HD2	2.01	0.41
1:A:545:ARG:HB2	1:B:494:PRO:HG3	2.02	0.41
1:A:627:ASP:O	1:A:628:ASN:CG	2.59	0.41
1:C:66:GLY:O	1:C:67:LEU:HB2	2.20	0.41
1:D:213:ILE:HG22	1:D:216:MET:HE3	2.03	0.41
1:D:658:SER:N	1:D:693:GLU:O	2.49	0.41
1:E:22:PRO:HA	1:E:23:PRO:HD3	1.89	0.41
1:E:340:LEU:O	1:E:342:VAL:N	2.45	0.41
1:E:589:LYS:HA	1:E:589:LYS:HD2	1.68	0.41
1:B:215:TYR:CD1	1:B:215:TYR:C	2.94	0.41
1:F:74:LEU:HD12	1:F:74:LEU:HA	1.86	0.41
1:F:172:PRO:HG2	1:F:177:PHE:HE1	1.86	0.41
1:A:510:LYS:HE2	1:A:610:LEU:HD13	2.03	0.41
1:A:542:ASP:O	1:A:546:ILE:HD13	2.20	0.41
1:A:634:SER:O	1:A:635:SER:C	2.59	0.41
1:C:575:GLY:O	1:C:588:GLY:CA	2.68	0.41
1:D:249:ILE:HA	1:D:318:TRP:HB3	2.01	0.41
1:D:428:LEU:HD23	1:D:548:ASP:HA	2.03	0.41
1:D:483:THR:HG22	1:F:130:LEU:HD22	2.03	0.41
1:F:175:TRP:CD2	1:F:245:LYS:HG3	2.56	0.41
1:F:564:LYS:HG3	2:F:867:HOH:O	2.20	0.41
1:A:608:ILE:HA	1:A:609:PRO:HD3	1.89	0.41
1:B:96:ASP:OD1	1:B:97:PRO:HA	2.21	0.41
1:B:187:TYR:HB2	1:B:188:PRO:HA	2.03	0.41
1:C:575:GLY:O	1:C:588:GLY:HA3	2.21	0.41
1:E:510:LYS:HE2	1:E:610:LEU:HD13	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:682:ILE:HG21	1:E:686:ILE:HD11	2.02	0.41
1:F:345:ARG:O	1:F:345:ARG:HG3	2.21	0.41
1:F:579:ASN:HB3	1:F:582:ASN:OD1	2.21	0.41
1:B:38:LEU:HD12	1:B:38:LEU:HA	1.93	0.41
1:C:257:ASP:HB3	1:C:260:TYR:HB3	2.03	0.41
1:C:375:TYR:N	1:C:376:PRO:HD2	2.35	0.41
1:D:274:GLU:O	1:D:365:ARG:NH2	2.54	0.41
1:D:557:LEU:HD23	1:D:557:LEU:C	2.42	0.41
1:E:340:LEU:HD12	1:E:340:LEU:HA	1.88	0.41
1:E:632:THR:O	1:E:638:ILE:HA	2.20	0.41
1:F:608:ILE:HA	1:F:609:PRO:HD3	1.80	0.41
1:A:175:TRP:CE3	1:A:245:LYS:HG3	2.54	0.41
1:A:614:GLU:HG2	1:A:648:LYS:HB3	2.03	0.41
1:C:88:ALA:C	1:C:348:ARG:HD2	2.41	0.41
1:C:145:VAL:HG22	1:C:146:GLU:N	2.36	0.41
1:C:175:TRP:CE3	1:C:245:LYS:HG3	2.55	0.41
1:D:502:LYS:O	1:D:506:GLU:HG3	2.21	0.41
1:E:257:ASP:HB3	1:E:260:TYR:HB3	2.03	0.41
1:E:428:LEU:HD23	1:E:548:ASP:HA	2.02	0.41
1:E:627:ASP:O	1:E:628:ASN:HB3	2.21	0.41
1:C:182:SER:CB	1:C:210:PHE:HB2	2.51	0.40
1:C:183:ARG:C	1:C:185:SER:HA	2.41	0.40
1:D:285:PRO:HD2	1:D:288:THR:HG21	2.03	0.40
1:D:596:HIS:HD2	1:D:598:LEU:H	1.69	0.40
1:D:604:GLU:HA	1:D:618:TYR:CE2	2.56	0.40
1:F:575:GLY:O	1:F:588:GLY:CA	2.69	0.40
1:B:48:GLN:HB3	1:B:49:GLY:H	1.65	0.40
1:C:172:PRO:HG2	1:C:177:PHE:HE1	1.86	0.40
1:D:17:ILE:HD11	1:D:45:ILE:HD13	2.02	0.40
1:D:74:LEU:HD12	1:D:74:LEU:HA	1.86	0.40
1:D:494:PRO:HG3	1:F:545:ARG:HB2	2.02	0.40
1:A:96:ASP:OD1	1:A:97:PRO:HA	2.21	0.40
1:A:301:TRP:CZ2	1:A:305:LEU:HD11	2.57	0.40
1:C:93:LYS:O	1:C:94:TYR:HB2	2.21	0.40
1:D:4:LEU:HD21	1:D:38:LEU:HD13	2.03	0.40
1:D:145:VAL:HG22	1:D:146:GLU:N	2.36	0.40
1:D:187:TYR:HB2	1:D:188:PRO:HA	2.03	0.40
1:E:145:VAL:HG22	1:E:146:GLU:N	2.36	0.40
1:E:545:ARG:HB2	1:F:494:PRO:HG3	2.03	0.40
1:E:575:GLY:O	1:E:588:GLY:CA	2.69	0.40
1:F:366:VAL:HG12	1:F:367:LYS:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:345:ARG:HE	1:C:341:PRO:HA	1.86	0.40
1:E:555:TYR:HB3	1:E:606:SER:CB	2.52	0.40
1:D:542:ASP:O	1:D:546:ILE:HD13	2.21	0.40
1:D:620:GLU:HG2	1:D:634:SER:HA	2.04	0.40
1:F:663:ASP:C	1:F:665:SER:H	2.25	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	690/693 (100%)	651 (94%)	33 (5%)	6 (1%)	17	24
1	B	690/693 (100%)	653 (95%)	31 (4%)	6 (1%)	17	24
1	C	690/693 (100%)	648 (94%)	35 (5%)	7 (1%)	15	22
1	D	690/693 (100%)	652 (94%)	34 (5%)	4 (1%)	25	34
1	E	690/693 (100%)	649 (94%)	35 (5%)	6 (1%)	17	24
1	F	691/693 (100%)	649 (94%)	34 (5%)	8 (1%)	13	17
All	All	4141/4158 (100%)	3902 (94%)	202 (5%)	37 (1%)	17	24

All (37) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	29	GLU
1	C	29	GLU
1	E	29	GLU
1	F	635	SER
1	C	635	SER
1	F	29	GLU
1	A	29	GLU

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Mol	Chain	Res	Type
1	A	635	SER
1	A	688	GLY
1	D	688	GLY
1	F	664	ASP
1	B	635	SER
1	C	688	GLY
1	D	599	PRO
1	E	338	SER
1	E	341	PRO
1	E	688	GLY
1	A	599	PRO
1	C	599	PRO
1	C	647	SER
1	F	30	GLN
1	B	688	GLY
1	F	599	PRO
1	A	49	GLY
1	B	49	GLY
1	C	49	GLY
1	D	49	GLY
1	D	213	ILE
1	E	49	GLY
1	F	49	GLY
1	F	688	GLY
1	A	213	ILE
1	B	213	ILE
1	B	599	PRO
1	C	213	ILE
1	E	213	ILE
1	F	213	ILE

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	623/624 (100%)	607 (97%)	16 (3%)	46 61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	623/624 (100%)	604 (97%)	19 (3%)	41	55
1	C	623/624 (100%)	606 (97%)	17 (3%)	44	59
1	D	623/624 (100%)	604 (97%)	19 (3%)	41	55
1	E	623/624 (100%)	602 (97%)	21 (3%)	37	50
1	F	624/624 (100%)	606 (97%)	18 (3%)	42	57
All	All	3739/3744 (100%)	3629 (97%)	110 (3%)	42	57

All (110) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	74	LEU
1	A	83	MET
1	A	130	LEU
1	A	165	LEU
1	A	211	LEU
1	A	283	MET
1	A	329	ARG
1	A	392	ARG
1	A	398	LEU
1	A	413	TRP
1	A	426	LEU
1	A	430	LEU
1	A	434	LEU
1	A	463	LEU
1	A	652	THR
1	B	30	GLN
1	B	35	ASN
1	B	41	LEU
1	B	74	LEU
1	B	83	MET
1	B	130	LEU
1	B	165	LEU
1	B	211	LEU
1	B	233	LYS
1	B	283	MET
1	B	329	ARG
1	B	392	ARG
1	B	398	LEU
1	B	413	TRP

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Mol	Chain	Res	Type
1	B	426	LEU
1	B	430	LEU
1	B	434	LEU
1	B	463	LEU
1	B	652	THR
1	C	74	LEU
1	C	83	MET
1	C	130	LEU
1	C	165	LEU
1	C	211	LEU
1	C	283	MET
1	C	329	ARG
1	C	392	ARG
1	C	398	LEU
1	C	413	TRP
1	C	426	LEU
1	C	430	LEU
1	C	434	LEU
1	C	463	LEU
1	C	603	ARG
1	C	628	ASN
1	C	652	THR
1	D	74	LEU
1	D	83	MET
1	D	130	LEU
1	D	151	GLU
1	D	165	LEU
1	D	211	LEU
1	D	283	MET
1	D	329	ARG
1	D	392	ARG
1	D	398	LEU
1	D	413	TRP
1	D	426	LEU
1	D	430	LEU
1	D	434	LEU
1	D	463	LEU
1	D	628	ASN
1	D	652	THR
1	D	659	LYS
1	D	665	SER
1	E	28	LEU

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Mol	Chain	Res	Type
1	E	32	ILE
1	E	41	LEU
1	E	74	LEU
1	E	83	MET
1	E	130	LEU
1	E	165	LEU
1	E	211	LEU
1	E	233	LYS
1	E	283	MET
1	E	329	ARG
1	E	392	ARG
1	E	398	LEU
1	E	413	TRP
1	E	426	LEU
1	E	430	LEU
1	E	434	LEU
1	E	463	LEU
1	E	628	ASN
1	E	630	GLU
1	E	652	THR
1	F	41	LEU
1	F	74	LEU
1	F	83	MET
1	F	130	LEU
1	F	165	LEU
1	F	211	LEU
1	F	231	GLU
1	F	283	MET
1	F	329	ARG
1	F	392	ARG
1	F	398	LEU
1	F	413	TRP
1	F	426	LEU
1	F	430	LEU
1	F	434	LEU
1	F	463	LEU
1	F	628	ASN
1	F	652	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	ASN
1	A	48	GLN
1	A	343	GLN
1	A	596	HIS
1	B	9	ASN
1	B	30	GLN
1	B	35	ASN
1	B	48	GLN
1	B	343	GLN
1	B	596	HIS
1	C	48	GLN
1	C	343	GLN
1	C	596	HIS
1	C	675	GLN
1	C	676	ASN
1	C	683	ASN
1	D	9	ASN
1	D	48	GLN
1	D	243	ASN
1	D	343	GLN
1	D	596	HIS
1	E	48	GLN
1	E	243	ASN
1	E	343	GLN
1	E	596	HIS
1	E	669	GLN
1	F	48	GLN
1	F	343	GLN
1	F	596	HIS
1	F	675	GLN
1	F	676	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	691/693 (99%)	-0.11	24 (3%) 44 51	21, 31, 60, 74	0
1	B	691/693 (99%)	-0.11	15 (2%) 62 68	21, 32, 59, 78	0
1	C	691/693 (99%)	-0.04	31 (4%) 33 40	22, 32, 66, 84	0
1	D	691/693 (99%)	-0.14	20 (2%) 51 59	20, 30, 54, 78	0
1	E	691/693 (99%)	-0.18	13 (1%) 66 73	18, 30, 50, 80	0
1	F	692/693 (99%)	-0.09	24 (3%) 44 51	19, 31, 63, 83	0
All	All	4147/4158 (99%)	-0.11	127 (3%) 49 56	18, 31, 60, 84	0

All (127) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	49	GLY	7.0
1	B	30	GLN	5.0
1	D	49	GLY	4.7
1	E	30	GLN	4.6
1	A	693	GLU	4.6
1	F	693	GLU	4.4
1	C	687	ARG	4.1
1	C	628	ASN	4.0
1	C	50	ASN	3.8
1	F	29	GLU	3.8
1	C	667	GLU	3.7
1	F	661	ILE	3.7
1	E	29	GLU	3.7
1	C	661	ILE	3.7
1	C	693	GLU	3.7
1	C	49	GLY	3.6
1	E	49	GLY	3.6
1	E	50	ASN	3.6
1	D	35	ASN	3.6

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Mol	Chain	Res	Type	RSRZ
1	F	30	GLN	3.6
1	F	48	GLN	3.5
1	B	344	PHE	3.5
1	D	50	ASN	3.4
1	C	668	ILE	3.4
1	F	664	ASP	3.4
1	B	29	GLU	3.3
1	C	29	GLU	3.3
1	D	30	GLN	3.3
1	D	346	ASP	3.3
1	D	48	GLN	3.3
1	B	49	GLY	3.2
1	B	346	ASP	3.2
1	A	664	ASP	3.1
1	D	343	GLN	3.1
1	D	669	GLN	3.1
1	F	346	ASP	3.1
1	C	574	ARG	3.1
1	A	662	VAL	3.0
1	F	574	ARG	3.0
1	A	346	ASP	3.0
1	B	50	ASN	3.0
1	C	669	GLN	2.9
1	B	664	ASP	2.9
1	A	339	SER	2.9
1	D	29	GLU	2.9
1	C	658	SER	2.8
1	D	345	ARG	2.8
1	A	35	ASN	2.8
1	A	48	GLN	2.8
1	B	227	TYR	2.8
1	C	346	ASP	2.7
1	E	344	PHE	2.7
1	F	343	GLN	2.7
1	C	48	GLN	2.7
1	A	393	ASN	2.7
1	F	35	ASN	2.7
1	F	50	ASN	2.6
1	E	345	ARG	2.6
1	B	628	ASN	2.6
1	E	343	GLN	2.6
1	C	659	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	31	LYS	2.6
1	D	635	SER	2.6
1	A	665	SER	2.5
1	F	687	ARG	2.5
1	A	49	GLY	2.5
1	E	35	ASN	2.5
1	D	344	PHE	2.5
1	A	343	GLN	2.5
1	C	664	ASP	2.5
1	E	628	ASN	2.5
1	A	666	LYS	2.4
1	A	661	ILE	2.4
1	D	47	GLN	2.4
1	A	669	GLN	2.4
1	C	593	LYS	2.4
1	A	628	ASN	2.4
1	C	3	ILE	2.4
1	C	344	PHE	2.4
1	C	636	ASN	2.4
1	C	665	SER	2.4
1	F	665	SER	2.4
1	F	692	LEU	2.4
1	C	670	VAL	2.3
1	B	574	ARG	2.3
1	E	346	ASP	2.3
1	B	48	GLN	2.3
1	D	693	GLU	2.3
1	C	47	GLN	2.3
1	F	662	VAL	2.3
1	E	339	SER	2.3
1	F	669	GLN	2.3
1	C	30	GLN	2.3
1	A	574	ARG	2.2
1	A	655	LYS	2.2
1	B	35	ASN	2.2
1	A	643	GLU	2.2
1	B	19	GLU	2.2
1	A	687	ARG	2.2
1	C	102	ILE	2.2
1	E	32	ILE	2.2
1	F	32	ILE	2.2
1	A	587	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	227	TYR	2.2
1	B	566	GLU	2.2
1	E	48	GLN	2.2
1	C	434	LEU	2.2
1	C	566	GLU	2.2
1	A	50	ASN	2.1
1	C	343	GLN	2.1
1	F	344	PHE	2.1
1	F	666	LYS	2.1
1	F	658	SER	2.1
1	C	456	GLU	2.1
1	A	344	PHE	2.1
1	D	393	ASN	2.1
1	C	227	TYR	2.1
1	D	339	SER	2.1
1	F	391	HIS	2.0
1	B	693	GLU	2.0
1	D	32	ILE	2.0
1	A	658	SER	2.0
1	D	628	ASN	2.0
1	F	636	ASN	2.0
1	F	667	GLU	2.0
1	C	46	VAL	2.0
1	A	434	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.