Full wwPDB X-ray Structure Validation Report (i)

Oct 22, 2023 – 03:57 PM EDT

PDB ID	:	3DNM
Title	:	Crystal Structure Hormone-Sensitive Lipase from a Metagenome Library
Authors	:	Hwang, K.Y.; Nam, K.H.
Deposited on	:	2008-07-02
Resolution	:	2.80 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 (i) 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 (1)) were used in the production of this report:

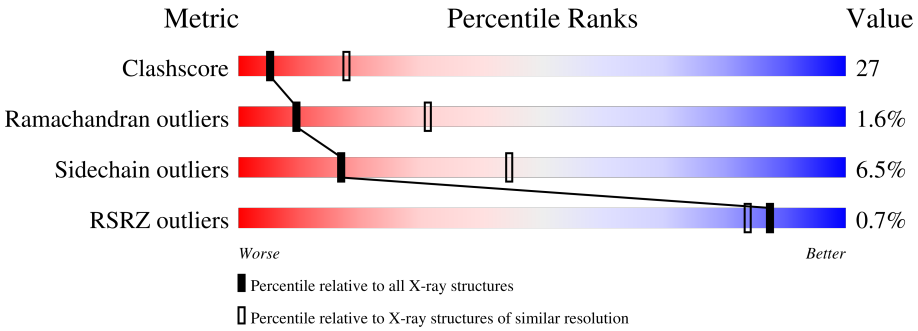
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.80 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))
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 <=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	336	51% 34% · 12%
1	B	336	% 50% 34% · 12%
1	C	336	% 43% 40% · 13%
1	D	336	45% 39% · 13%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	BME	C	325	-	-	-	X
2	BME	D	326	-	-	X	X
3	SO4	B	329	-	-	-	X

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9129 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 Esterase/lipase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	297	Total	C	N	O	S	0	0	0
			2235	1411	378	433	13			
1	B	296	Total	C	N	O	S	0	0	0
			2229	1408	377	431	13			
1	C	291	Total	C	N	O	S	0	0	0
			2187	1383	370	421	13			
1	D	291	Total	C	N	O	S	0	0	0
			2188	1385	370	420	13			

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	expression tag	UNP Q0GMU1
A	-12	ALA	-	expression tag	UNP Q0GMU1
A	-11	SER	-	expression tag	UNP Q0GMU1
A	-10	MET	-	expression tag	UNP Q0GMU1
A	-9	THR	-	expression tag	UNP Q0GMU1
A	-8	GLY	-	expression tag	UNP Q0GMU1
A	-7	GLY	-	expression tag	UNP Q0GMU1
A	-6	ASN	-	expression tag	UNP Q0GMU1
A	-5	ASN	-	expression tag	UNP Q0GMU1
A	-4	MET	-	expression tag	UNP Q0GMU1
A	-3	GLY	-	expression tag	UNP Q0GMU1
A	-2	ARG	-	expression tag	UNP Q0GMU1
A	-1	GLY	-	expression tag	UNP Q0GMU1
A	0	SER	-	expression tag	UNP Q0GMU1
A	310	LYS	-	expression tag	UNP Q0GMU1
A	311	LEU	-	expression tag	UNP Q0GMU1
A	312	ALA	-	expression tag	UNP Q0GMU1
A	313	ALA	-	expression tag	UNP Q0GMU1
A	314	ALA	-	expression tag	UNP Q0GMU1
A	315	LEU	-	expression tag	UNP Q0GMU1
A	316	GLU	-	expression tag	UNP Q0GMU1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	317	HIS	-	expression tag	UNP Q0GMU1
A	318	HIS	-	expression tag	UNP Q0GMU1
A	319	HIS	-	expression tag	UNP Q0GMU1
A	320	HIS	-	expression tag	UNP Q0GMU1
A	321	HIS	-	expression tag	UNP Q0GMU1
A	322	HIS	-	expression tag	UNP Q0GMU1
B	-13	MET	-	expression tag	UNP Q0GMU1
B	-12	ALA	-	expression tag	UNP Q0GMU1
B	-11	SER	-	expression tag	UNP Q0GMU1
B	-10	MET	-	expression tag	UNP Q0GMU1
B	-9	THR	-	expression tag	UNP Q0GMU1
B	-8	GLY	-	expression tag	UNP Q0GMU1
B	-7	GLY	-	expression tag	UNP Q0GMU1
B	-6	ASN	-	expression tag	UNP Q0GMU1
B	-5	ASN	-	expression tag	UNP Q0GMU1
B	-4	MET	-	expression tag	UNP Q0GMU1
B	-3	GLY	-	expression tag	UNP Q0GMU1
B	-2	ARG	-	expression tag	UNP Q0GMU1
B	-1	GLY	-	expression tag	UNP Q0GMU1
B	0	SER	-	expression tag	UNP Q0GMU1
B	310	LYS	-	expression tag	UNP Q0GMU1
B	311	LEU	-	expression tag	UNP Q0GMU1
B	312	ALA	-	expression tag	UNP Q0GMU1
B	313	ALA	-	expression tag	UNP Q0GMU1
B	314	ALA	-	expression tag	UNP Q0GMU1
B	315	LEU	-	expression tag	UNP Q0GMU1
B	316	GLU	-	expression tag	UNP Q0GMU1
B	317	HIS	-	expression tag	UNP Q0GMU1
B	318	HIS	-	expression tag	UNP Q0GMU1
B	319	HIS	-	expression tag	UNP Q0GMU1
B	320	HIS	-	expression tag	UNP Q0GMU1
B	321	HIS	-	expression tag	UNP Q0GMU1
B	322	HIS	-	expression tag	UNP Q0GMU1
C	-13	MET	-	expression tag	UNP Q0GMU1
C	-12	ALA	-	expression tag	UNP Q0GMU1
C	-11	SER	-	expression tag	UNP Q0GMU1
C	-10	MET	-	expression tag	UNP Q0GMU1
C	-9	THR	-	expression tag	UNP Q0GMU1
C	-8	GLY	-	expression tag	UNP Q0GMU1
C	-7	GLY	-	expression tag	UNP Q0GMU1
C	-6	ASN	-	expression tag	UNP Q0GMU1
C	-5	ASN	-	expression tag	UNP Q0GMU1

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	MET	-	expression tag	UNP Q0GMU1
C	-3	GLY	-	expression tag	UNP Q0GMU1
C	-2	ARG	-	expression tag	UNP Q0GMU1
C	-1	GLY	-	expression tag	UNP Q0GMU1
C	0	SER	-	expression tag	UNP Q0GMU1
C	310	LYS	-	expression tag	UNP Q0GMU1
C	311	LEU	-	expression tag	UNP Q0GMU1
C	312	ALA	-	expression tag	UNP Q0GMU1
C	313	ALA	-	expression tag	UNP Q0GMU1
C	314	ALA	-	expression tag	UNP Q0GMU1
C	315	LEU	-	expression tag	UNP Q0GMU1
C	316	GLU	-	expression tag	UNP Q0GMU1
C	317	HIS	-	expression tag	UNP Q0GMU1
C	318	HIS	-	expression tag	UNP Q0GMU1
C	319	HIS	-	expression tag	UNP Q0GMU1
C	320	HIS	-	expression tag	UNP Q0GMU1
C	321	HIS	-	expression tag	UNP Q0GMU1
C	322	HIS	-	expression tag	UNP Q0GMU1
D	-13	MET	-	expression tag	UNP Q0GMU1
D	-12	ALA	-	expression tag	UNP Q0GMU1
D	-11	SER	-	expression tag	UNP Q0GMU1
D	-10	MET	-	expression tag	UNP Q0GMU1
D	-9	THR	-	expression tag	UNP Q0GMU1
D	-8	GLY	-	expression tag	UNP Q0GMU1
D	-7	GLY	-	expression tag	UNP Q0GMU1
D	-6	ASN	-	expression tag	UNP Q0GMU1
D	-5	ASN	-	expression tag	UNP Q0GMU1
D	-4	MET	-	expression tag	UNP Q0GMU1
D	-3	GLY	-	expression tag	UNP Q0GMU1
D	-2	ARG	-	expression tag	UNP Q0GMU1
D	-1	GLY	-	expression tag	UNP Q0GMU1
D	0	SER	-	expression tag	UNP Q0GMU1
D	310	LYS	-	expression tag	UNP Q0GMU1
D	311	LEU	-	expression tag	UNP Q0GMU1
D	312	ALA	-	expression tag	UNP Q0GMU1
D	313	ALA	-	expression tag	UNP Q0GMU1
D	314	ALA	-	expression tag	UNP Q0GMU1
D	315	LEU	-	expression tag	UNP Q0GMU1
D	316	GLU	-	expression tag	UNP Q0GMU1
D	317	HIS	-	expression tag	UNP Q0GMU1
D	318	HIS	-	expression tag	UNP Q0GMU1
D	319	HIS	-	expression tag	UNP Q0GMU1

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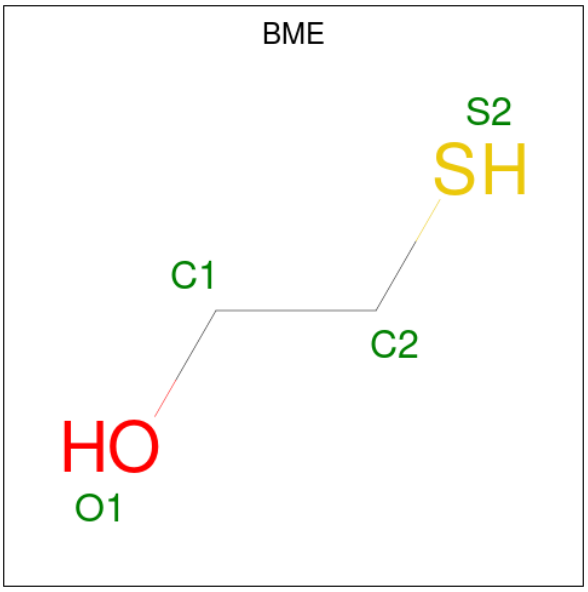
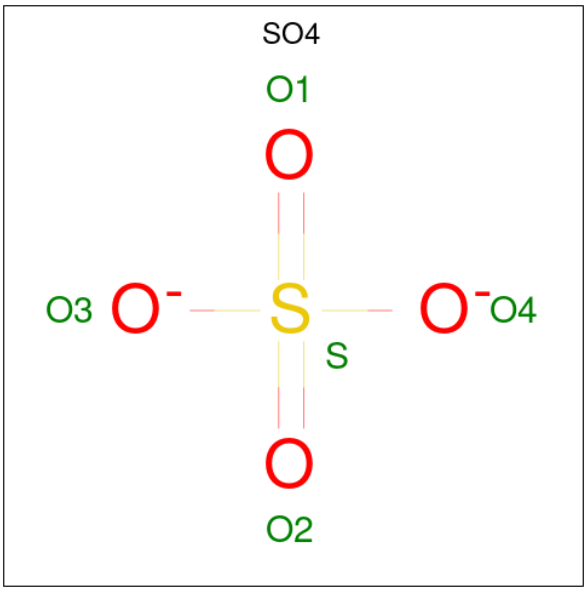
Chain	Residue	Modelled	Actual	Comment	Reference
D	320	HIS	-	expression tag	UNP Q0GMU1
D	321	HIS	-	expression tag	UNP Q0GMU1
D	322	HIS	-	expression tag	UNP Q0GMU1

- Molecule 2 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C_2H_6OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	S	0	0
			4	2	1	1		
2	B	1	Total	C	O	S	0	0
			4	2	1	1		
2	C	1	Total	C	O	S	0	0
			4	2	1	1		
2	D	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0

- Molecule 4 is water.

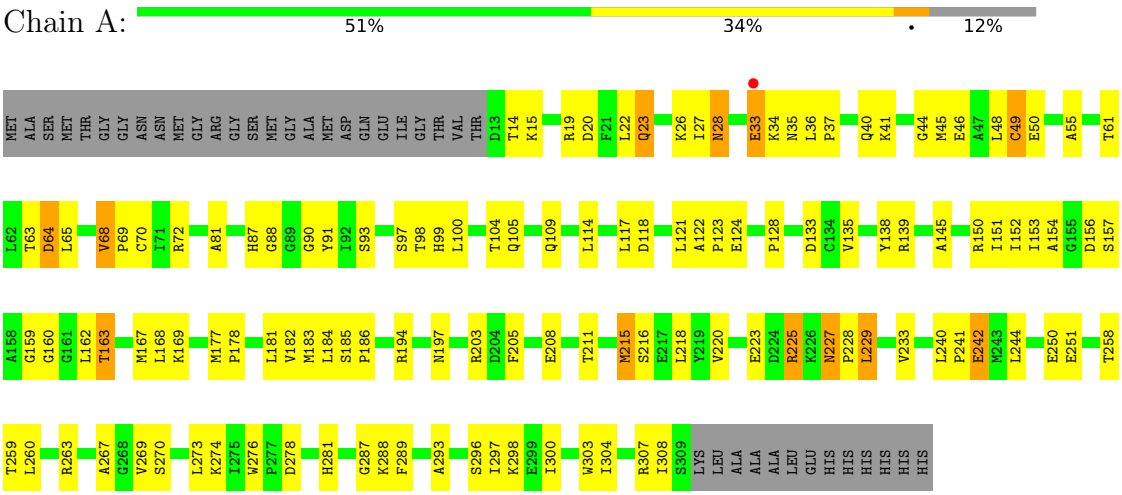
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	63	Total O 63 63	0	0
4	B	56	Total O 56 56	0	0
4	C	49	Total O 49 49	0	0
4	D	36	Total O 36 36	0	0

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.

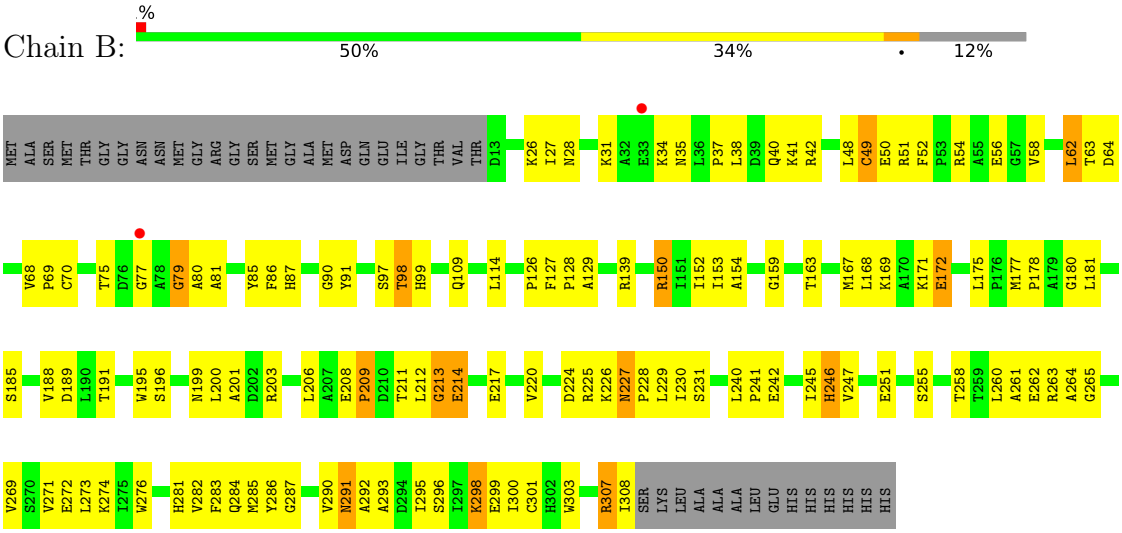
• Molecule 1: Esterase/lipase

Chain A:



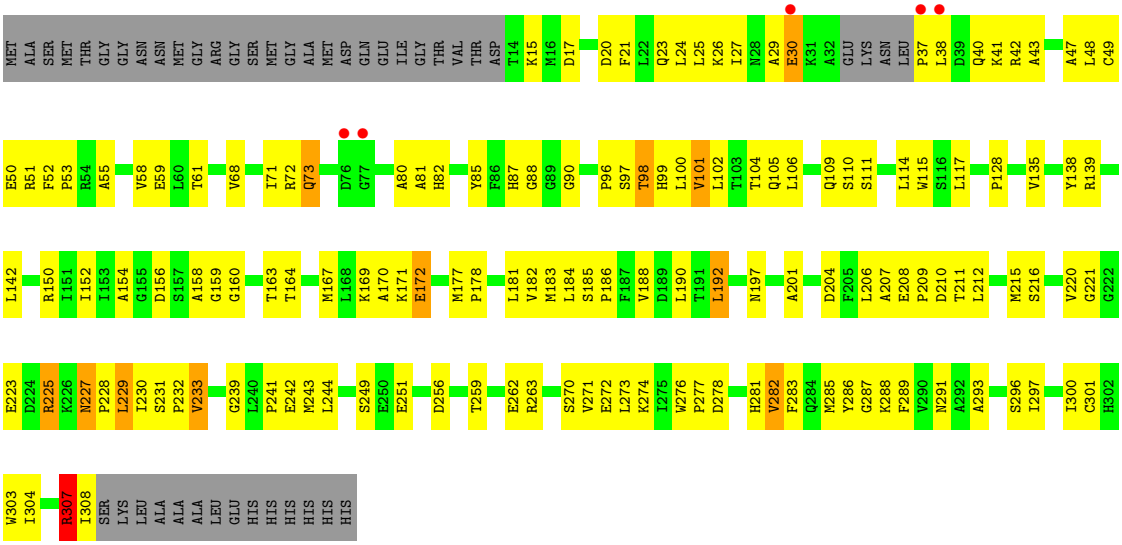
• Molecule 1: Esterase/lipase

Chain B:



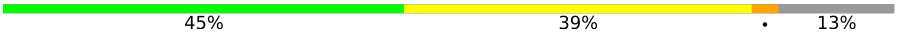
• Molecule 1: Esterase/lipase

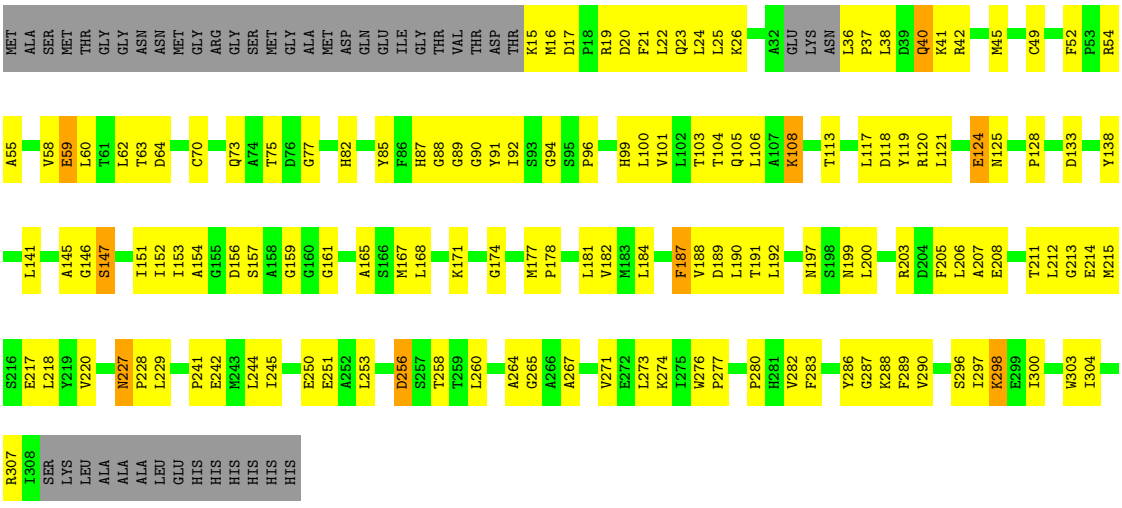
Chain C:



• Molecule 1: Esterase/lipase

Chain D:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	117.32Å 126.83Å 233.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.80 19.99 – 2.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.80) 98.3 (19.99-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.15 (at 2.79Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.233 , 0.282 0.232 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	33.6	Xtriage
Anisotropy	0.658	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 59.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	9129	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 37.76 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.0858e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, BME

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	0.38	0/2280	0.66	0/3096
1	B	0.38	0/2274	0.63	0/3088
1	C	0.36	0/2231	0.65	0/3028
1	D	0.35	0/2232	0.61	0/3030
All	All	0.37	0/9017	0.64	0/12242

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

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	2235	0	2224	122	0
1	B	2229	0	2219	104	0
1	C	2187	0	2178	125	0
1	D	2188	0	2182	125	0
2	A	4	0	6	1	0
2	B	4	0	6	1	0
2	C	4	0	5	3	0
2	D	4	0	6	4	0
3	A	10	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	35	0	0	0	0
3	C	10	0	0	0	0
3	D	15	0	0	1	0
4	A	63	0	0	5	0
4	B	56	0	0	4	0
4	C	49	0	0	6	0
4	D	36	0	0	10	0
All	All	9129	0	8826	474	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 27.

All (474) 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:A:157:SER:OG	2:A:325:BME:S2	2.06	1.13
1:D:58:VAL:HG11	1:D:104:THR:HB	1.37	1.04
1:A:33:GLU:HG3	1:A:36:LEU:HB2	1.46	0.98
1:C:152:ILE:HD12	1:C:304:ILE:HG23	1.50	0.93
1:A:37:PRO:HB2	1:A:40:GLN:HG3	1.49	0.93
1:A:225:ARG:CB	1:A:225:ARG:HH21	1.83	0.92
1:C:81:ALA:HB1	1:C:308:ILE:HD13	1.48	0.91
1:C:106:LEU:HD23	1:C:297:ILE:HG23	1.51	0.91
1:D:152:ILE:HD12	1:D:304:ILE:HG23	1.51	0.91
1:A:152:ILE:HD12	1:A:304:ILE:HG23	1.52	0.90
1:C:183:MET:HB3	1:C:186:PRO:HG3	1.55	0.89
1:B:206:LEU:O	2:B:330:BME:H12	1.78	0.84
1:A:36:LEU:HD11	1:A:40:GLN:HB2	1.58	0.83
1:A:33:GLU:CG	1:A:36:LEU:HB2	2.11	0.80
1:B:80:ALA:HB3	1:B:150:ARG:NH1	1.97	0.80
1:C:216:SER:O	1:C:220:VAL:HG12	1.81	0.79
1:D:227:ASN:ND2	1:D:229:LEU:H	1.81	0.79
1:C:81:ALA:CB	1:C:308:ILE:HD13	2.12	0.78
1:A:19:ARG:HA	1:A:22:LEU:HD12	1.64	0.78
1:D:197:ASN:HD22	1:D:197:ASN:H	1.32	0.78
1:C:82:HIS:HD2	1:C:115:TRP:HE1	1.29	0.77
1:D:87:HIS:HB2	1:D:99:HIS:CD2	2.20	0.77
1:C:225:ARG:NH2	1:C:225:ARG:HB2	2.01	0.76
1:C:225:ARG:HB2	1:C:225:ARG:HH21	1.51	0.75
1:A:227:ASN:C	1:A:227:ASN:HD22	1.88	0.75
1:A:287:GLY:HA2	1:A:293:ALA:HB3	1.67	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:36:LEU:HD11	1:D:40:GLN:HG2	1.69	0.75
1:A:194:ARG:HG3	4:A:333:HOH:O	1.86	0.74
1:A:225:ARG:HH21	1:A:225:ARG:HB3	1.53	0.74
1:C:87:HIS:HB2	1:C:99:HIS:CD2	2.21	0.74
1:C:40:GLN:HA	1:C:40:GLN:OE1	1.87	0.73
1:C:167:MET:HE1	1:C:178:PRO:HD3	1.70	0.73
1:D:25:LEU:HD22	1:D:206:LEU:HD21	1.70	0.73
1:C:37:PRO:HB3	1:C:41:LYS:HE2	1.69	0.73
1:B:227:ASN:C	1:B:227:ASN:HD22	1.92	0.73
1:B:242:GLU:HG3	4:B:370:HOH:O	1.88	0.72
1:D:227:ASN:HD22	1:D:229:LEU:H	1.35	0.72
1:B:167:MET:HE1	1:B:178:PRO:HD3	1.70	0.72
1:A:159:GLY:O	1:A:163:THR:HG22	1.90	0.72
1:A:36:LEU:CD1	1:A:40:GLN:HB2	2.20	0.71
1:A:293:ALA:O	1:A:297:ILE:HG12	1.90	0.71
1:B:31:LYS:HD2	1:B:31:LYS:N	2.06	0.71
1:C:106:LEU:CD2	1:C:297:ILE:HG23	2.20	0.71
1:C:41:LYS:C	1:C:43:ALA:H	1.94	0.71
1:A:194:ARG:H	1:A:197:ASN:HD22	1.38	0.70
1:B:247:VAL:HG23	1:B:251:GLU:OE2	1.92	0.70
1:B:227:ASN:HD22	1:B:228:PRO:N	1.90	0.70
1:C:190:LEU:HD22	1:C:230:ILE:CG2	2.21	0.70
1:B:167:MET:HB3	1:B:177:MET:HE1	1.73	0.69
1:C:227:ASN:ND2	1:C:229:LEU:H	1.90	0.69
1:D:214:GLU:O	1:D:218:LEU:HG	1.92	0.69
1:D:96:PRO:HG2	1:D:118:ASP:HB2	1.75	0.69
1:B:167:MET:CE	1:B:178:PRO:HD3	2.23	0.69
1:A:227:ASN:HD22	1:A:228:PRO:N	1.90	0.68
1:D:120:ARG:HD3	1:D:133:ASP:OD2	1.92	0.68
1:D:203:ARG:HD2	1:D:250:GLU:OE1	1.93	0.68
1:B:196:SER:O	1:B:200:LEU:HB2	1.93	0.68
1:D:215:MET:CE	2:D:326:BME:H21	2.24	0.68
1:C:251:GLU:HB3	4:C:332:HOH:O	1.93	0.68
1:A:183:MET:HB3	1:A:186:PRO:HG3	1.76	0.68
1:D:205:PHE:O	1:D:206:LEU:HD23	1.93	0.68
1:C:114:LEU:HD23	1:C:115:TRP:N	2.09	0.67
1:D:288:LYS:HD3	4:D:352:HOH:O	1.94	0.67
1:C:227:ASN:HD22	1:C:229:LEU:H	1.41	0.67
1:C:72:ARG:HG2	1:C:72:ARG:HH11	1.59	0.66
1:A:121:LEU:O	1:A:124:GLU:HG2	1.95	0.66
1:B:159:GLY:O	1:B:163:THR:HG23	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:274:LYS:HG3	1:B:272:GLU:HG2	1.78	0.66
1:B:80:ALA:HB3	1:B:150:ARG:HH11	1.57	0.66
1:C:47:ALA:O	1:C:50:GLU:HG2	1.95	0.66
1:C:52:PHE:HB3	1:C:101:VAL:CG1	2.26	0.66
2:C:325:BME:C1	4:C:359:HOH:O	2.43	0.66
1:A:99:HIS:HE1	1:A:156:ASP:OD2	1.79	0.66
1:C:242:GLU:HB3	1:C:270:SER:HB3	1.77	0.65
1:C:211:THR:O	1:C:215:MET:HG3	1.97	0.65
1:A:160:GLY:O	1:A:163:THR:HG23	1.95	0.65
1:A:194:ARG:H	1:A:197:ASN:ND2	1.94	0.65
1:D:106:LEU:HD23	1:D:297:ILE:HG23	1.78	0.65
1:A:33:GLU:HG3	1:A:36:LEU:CB	2.24	0.64
1:A:225:ARG:HH21	1:A:225:ARG:HB2	1.59	0.64
1:A:34:LYS:HG3	1:A:35:ASN:H	1.62	0.63
1:C:55:ALA:HB3	1:C:104:THR:HB	1.80	0.63
1:D:87:HIS:HD2	1:D:88:GLY:O	1.80	0.63
1:C:53:PRO:HD3	1:C:288:LYS:NZ	2.13	0.63
1:D:192:LEU:HA	1:D:197:ASN:OD1	1.99	0.63
1:A:81:ALA:HB2	1:A:308:ILE:HG21	1.79	0.63
1:D:22:LEU:HA	1:D:25:LEU:HD12	1.81	0.62
1:A:225:ARG:CB	1:A:225:ARG:NH2	2.61	0.62
1:C:167:MET:CE	1:C:178:PRO:HD3	2.29	0.62
1:A:81:ALA:HB1	1:A:308:ILE:HD13	1.81	0.62
1:C:87:HIS:HD2	1:C:88:GLY:O	1.82	0.62
1:D:21:PHE:HZ	1:D:286:TYR:CD2	2.18	0.62
1:B:49:CYS:HA	1:B:52:PHE:HD2	1.65	0.61
1:C:52:PHE:HB3	1:C:101:VAL:HG13	1.82	0.61
1:B:214:GLU:HG2	1:B:217:GLU:CB	2.30	0.61
2:C:325:BME:H11	4:C:359:HOH:O	1.97	0.61
1:D:82:HIS:HB2	1:D:151:ILE:HD13	1.82	0.61
1:A:287:GLY:HA2	1:A:293:ALA:CB	2.30	0.61
1:D:90:GLY:HA3	1:D:215:MET:SD	2.39	0.61
1:C:25:LEU:HD22	1:C:206:LEU:HD21	1.82	0.61
1:C:262:GLU:HG2	1:C:263:ARG:HD3	1.80	0.61
1:D:215:MET:HE1	2:D:326:BME:H21	1.82	0.61
1:B:246:HIS:HD2	1:B:296:SER:OG	1.83	0.60
1:C:181:LEU:HD12	1:C:243:MET:HE2	1.81	0.60
1:D:211:THR:O	1:D:215:MET:HG3	2.01	0.60
1:A:20:ASP:O	1:A:23:GLN:HB3	2.01	0.60
1:C:296:SER:O	1:C:300:ILE:HG13	2.02	0.60
1:A:177:MET:CE	1:A:240:LEU:HD23	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:227:ASN:ND2	1:A:229:LEU:H	1.99	0.59
1:B:203:ARG:HB3	4:B:338:HOH:O	2.01	0.59
1:C:49:CYS:SG	1:C:98:THR:HG22	2.43	0.59
1:A:185:SER:OG	1:A:251:GLU:OE2	2.21	0.59
1:B:86:PHE:O	1:B:159:GLY:HA3	2.03	0.59
1:C:55:ALA:O	1:C:58:VAL:HG22	2.03	0.59
1:B:79:GLY:C	1:B:81:ALA:H	2.06	0.59
1:D:17:ASP:HB3	1:D:20:ASP:OD2	2.02	0.59
1:B:189:ASP:OD2	1:B:191:THR:HG23	2.03	0.59
1:D:227:ASN:HD22	1:D:229:LEU:N	1.99	0.59
1:B:217:GLU:HB2	1:B:225:ARG:NH1	2.17	0.58
1:D:36:LEU:HG	1:D:40:GLN:HB3	1.85	0.58
1:D:267:ALA:HB2	4:D:336:HOH:O	2.03	0.58
1:C:37:PRO:O	1:C:38:LEU:HB2	2.03	0.58
1:A:23:GLN:O	1:A:27:ILE:HG13	2.03	0.58
1:C:26:LYS:HG2	1:C:30:GLU:OE1	2.02	0.58
1:C:82:HIS:CD2	1:C:115:TRP:HE1	2.18	0.58
1:D:87:HIS:HB2	1:D:99:HIS:HD2	1.67	0.58
1:D:245:ILE:HB	1:D:273:LEU:HD23	1.86	0.58
1:D:296:SER:O	1:D:300:ILE:HG13	2.04	0.58
1:A:152:ILE:CD1	1:A:304:ILE:HG23	2.30	0.57
1:C:21:PHE:HZ	1:C:286:TYR:CD2	2.23	0.57
1:B:167:MET:HB3	1:B:177:MET:CE	2.34	0.57
1:B:245:ILE:HB	1:B:273:LEU:HD23	1.87	0.57
1:D:36:LEU:CD1	1:D:40:GLN:HG2	2.33	0.57
1:A:216:SER:O	1:A:220:VAL:HG23	2.05	0.57
1:C:72:ARG:HD3	1:C:115:TRP:CZ2	2.40	0.57
1:A:36:LEU:HD12	1:A:41:LYS:N	2.20	0.57
1:D:15:LYS:HE2	1:D:287:GLY:O	2.05	0.57
1:B:211:THR:HG23	4:B:360:HOH:O	2.04	0.56
1:A:135:VAL:HG21	1:A:169:LYS:HD2	1.87	0.56
1:C:220:VAL:O	1:C:223:GLU:HB2	2.04	0.56
1:D:58:VAL:HG13	4:D:339:HOH:O	2.05	0.56
1:A:153:ILE:HG22	1:A:163:THR:HB	1.87	0.56
1:B:153:ILE:HG12	1:B:178:PRO:HG3	1.88	0.56
1:B:214:GLU:HG2	1:B:217:GLU:HB2	1.87	0.56
1:B:274:LYS:HD3	1:B:276:TRP:CZ2	2.39	0.56
1:D:63:THR:HG23	1:D:64:ASP:N	2.19	0.56
1:A:33:GLU:CD	1:A:33:GLU:H	2.07	0.56
1:A:23:GLN:HE21	1:A:23:GLN:HA	1.71	0.56
1:A:90:GLY:HA3	1:A:215:MET:CG	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:194:ARG:N	1:A:197:ASN:HD22	2.03	0.56
1:A:233:VAL:CG2	1:A:259:THR:HG22	2.36	0.56
1:C:47:ALA:HA	1:C:50:GLU:OE1	2.05	0.56
1:A:100:LEU:O	1:A:104:THR:HG23	2.05	0.56
1:C:172:GLU:O	1:C:172:GLU:HG2	2.06	0.56
1:D:212:LEU:HA	1:D:215:MET:HE2	1.88	0.56
1:C:106:LEU:O	1:C:110:SER:HB3	2.05	0.56
1:C:227:ASN:HD22	1:C:227:ASN:C	2.08	0.56
1:D:55:ALA:O	1:D:58:VAL:HG12	2.06	0.56
1:D:199:ASN:O	1:D:200:LEU:HD23	2.06	0.55
1:A:91:TYR:HE2	1:A:162:LEU:HD21	1.71	0.55
1:B:152:ILE:CG1	1:B:308:ILE:HD11	2.35	0.55
1:A:177:MET:HE2	1:A:240:LEU:HD23	1.89	0.55
1:A:109:GLN:NE2	1:A:298:LYS:HD2	2.22	0.55
1:C:58:VAL:HG21	1:C:104:THR:HB	1.89	0.55
1:A:225:ARG:HB2	1:A:225:ARG:NH2	2.19	0.55
1:A:81:ALA:CB	1:A:308:ILE:HG21	2.35	0.55
1:C:41:LYS:C	1:C:43:ALA:N	2.60	0.55
1:C:242:GLU:CB	1:C:270:SER:HB3	2.37	0.55
1:C:300:ILE:O	1:C:304:ILE:HG13	2.06	0.55
1:D:208:GLU:HB2	1:D:211:THR:HG22	1.89	0.55
1:D:207:ALA:HB1	1:D:212:LEU:HD11	1.87	0.54
1:C:139:ARG:O	1:C:142:LEU:HB2	2.07	0.54
1:D:87:HIS:HE1	4:D:329:HOH:O	1.90	0.54
1:A:87:HIS:HD2	1:A:88:GLY:O	1.91	0.54
1:C:71:ILE:HD12	1:C:96:PRO:HB2	1.89	0.54
1:C:106:LEU:HD23	1:C:297:ILE:CG2	2.31	0.54
1:A:63:THR:HG23	1:A:70:CYS:SG	2.48	0.54
1:A:138:TYR:CZ	1:A:178:PRO:HG3	2.43	0.54
1:B:214:GLU:O	1:B:217:GLU:HB3	2.07	0.54
1:D:197:ASN:H	1:D:197:ASN:ND2	2.00	0.54
1:D:282:VAL:O	1:D:282:VAL:HG12	2.08	0.53
1:A:61:THR:HG21	1:A:72:ARG:NH2	2.24	0.53
1:C:24:LEU:O	1:C:27:ILE:HG12	2.08	0.53
1:A:68:VAL:HB	1:A:117:LEU:HD11	1.89	0.53
1:C:262:GLU:HB2	1:D:258:THR:HG21	1.89	0.53
1:B:58:VAL:HA	1:B:75:THR:HG22	1.89	0.53
1:C:181:LEU:HG	1:C:241:PRO:HG2	1.90	0.53
1:C:227:ASN:HD22	1:C:229:LEU:N	2.05	0.53
1:D:105:GLN:HA	1:D:105:GLN:NE2	2.23	0.53
1:D:165:ALA:HA	1:D:168:LEU:HD12	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:251:GLU:CD	1:A:281:HIS:HA	2.29	0.53
1:B:296:SER:O	1:B:300:ILE:HG13	2.08	0.53
1:D:146:GLY:O	1:D:147:SER:HB2	2.08	0.53
1:B:298:LYS:HD2	1:B:299:GLU:N	2.24	0.52
1:C:102:LEU:HB2	1:C:285:MET:HG2	1.91	0.52
1:D:124:GLU:N	1:D:124:GLU:OE1	2.42	0.52
1:B:87:HIS:HB2	1:B:99:HIS:CD2	2.45	0.52
1:D:82:HIS:CD2	1:D:145:ALA:HB2	2.45	0.52
1:B:181:LEU:HG	1:B:241:PRO:HG2	1.92	0.52
1:B:227:ASN:HB3	1:B:230:ILE:HD12	1.92	0.52
1:A:274:LYS:HD3	1:A:276:TRP:CE2	2.45	0.52
1:D:244:LEU:HD22	1:D:303:TRP:CG	2.45	0.51
1:B:127:PHE:CD1	1:B:128:PRO:HA	2.44	0.51
1:B:242:GLU:OE2	1:B:307:ARG:HD3	2.09	0.51
1:D:99:HIS:O	1:D:103:THR:HG23	2.11	0.51
1:D:156:ASP:O	1:D:159:GLY:N	2.39	0.51
1:D:298:LYS:HB2	1:D:298:LYS:NZ	2.26	0.51
1:B:98:THR:OG1	1:B:99:HIS:HD2	1.93	0.51
1:C:139:ARG:HA	1:C:142:LEU:HD12	1.91	0.51
1:C:249:SER:OG	1:C:278:ASP:N	2.43	0.51
1:D:119:TYR:HB3	4:D:344:HOH:O	2.10	0.51
1:D:227:ASN:HD22	1:D:227:ASN:C	2.14	0.51
1:A:90:GLY:HA3	1:A:215:MET:HG2	1.92	0.51
1:D:153:ILE:HD13	1:D:178:PRO:HG2	1.93	0.51
1:C:152:ILE:CD1	1:C:304:ILE:HG23	2.30	0.51
1:D:121:LEU:O	1:D:125:ASN:HB2	2.10	0.51
1:B:85:TYR:HA	1:B:154:ALA:O	2.10	0.51
1:C:273:LEU:HD13	1:C:274:LYS:N	2.25	0.51
1:B:37:PRO:HB2	1:B:40:GLN:HG3	1.93	0.51
1:C:109:GLN:HB2	1:C:301:CYS:SG	2.50	0.51
1:B:196:SER:HB2	1:B:200:LEU:HD12	1.92	0.50
1:B:217:GLU:OE1	1:B:220:VAL:HB	2.11	0.50
1:D:264:ALA:HB3	1:D:271:VAL:HG21	1.94	0.50
1:A:169:LYS:O	1:A:169:LYS:HD3	2.11	0.50
1:A:90:GLY:HA3	1:A:215:MET:SD	2.51	0.50
1:A:26:LYS:HD2	1:A:205:PHE:CZ	2.46	0.50
1:A:90:GLY:O	1:A:91:TYR:HB2	2.11	0.50
1:B:62:LEU:HD23	1:B:62:LEU:H	1.75	0.50
1:C:185:SER:N	1:C:186:PRO:HD3	2.25	0.50
1:A:34:LYS:NZ	1:A:35:ASN:HB2	2.27	0.50
1:A:65:LEU:O	1:A:68:VAL:HG23	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:150:ARG:HA	1:B:308:ILE:HG23	1.94	0.50
1:C:15:LYS:HE3	1:C:287:GLY:O	2.12	0.50
1:C:156:ASP:O	1:C:159:GLY:N	2.44	0.50
1:A:194:ARG:O	1:A:197:ASN:HB2	2.12	0.50
1:C:90:GLY:HA2	1:C:158:ALA:HB2	1.92	0.50
1:D:153:ILE:N	1:D:153:ILE:HD12	2.27	0.50
1:A:154:ALA:HA	1:A:182:VAL:O	2.12	0.50
1:D:251:GLU:HB3	4:D:330:HOH:O	2.11	0.50
1:C:190:LEU:HD22	1:C:230:ILE:HG22	1.94	0.49
1:B:286:TYR:O	1:B:290:VAL:HG22	2.13	0.49
1:D:105:GLN:HE21	1:D:105:GLN:CA	2.24	0.49
1:A:227:ASN:HD22	1:A:228:PRO:CD	2.25	0.49
1:A:296:SER:O	1:A:300:ILE:HG13	2.11	0.49
1:C:37:PRO:CB	1:C:41:LYS:HE2	2.41	0.49
1:B:227:ASN:C	1:B:227:ASN:ND2	2.64	0.49
1:C:223:GLU:OE2	1:C:223:GLU:HA	2.13	0.49
1:A:274:LYS:HD3	1:A:276:TRP:CZ2	2.47	0.49
1:A:208:GLU:HB2	1:A:211:THR:OG1	2.13	0.49
1:C:233:VAL:HG22	1:C:259:THR:HG22	1.95	0.49
1:A:14:THR:O	1:A:15:LYS:HD3	2.13	0.49
1:B:54:ARG:HH11	1:B:54:ARG:HG3	1.78	0.48
1:A:225:ARG:NH1	4:A:386:HOH:O	2.46	0.48
1:C:17:ASP:HB3	1:C:20:ASP:OD2	2.13	0.48
1:D:153:ILE:HD13	1:D:178:PRO:CG	2.44	0.48
1:D:184:LEU:N	1:D:184:LEU:HD12	2.28	0.48
1:B:226:LYS:O	1:B:227:ASN:C	2.51	0.48
1:C:61:THR:HG21	1:C:72:ARG:NH2	2.28	0.48
1:B:79:GLY:C	1:B:81:ALA:N	2.67	0.48
1:A:151:ILE:HG22	1:A:152:ILE:N	2.29	0.48
1:B:308:ILE:HG22	1:B:308:ILE:O	2.13	0.48
1:A:68:VAL:HG11	1:A:133:ASP:HB3	1.94	0.48
1:D:161:GLY:HA2	1:D:188:VAL:HG12	1.96	0.48
1:D:213:GLY:O	1:D:217:GLU:HG3	2.14	0.48
1:A:55:ALA:HA	3:A:323:SO4:O3	2.14	0.48
1:A:227:ASN:C	1:A:227:ASN:ND2	2.60	0.48
1:C:85:TYR:HA	1:C:154:ALA:O	2.14	0.48
1:D:37:PRO:O	1:D:41:LYS:HG3	2.14	0.48
1:B:139:ARG:NH1	1:B:175:LEU:HD11	2.28	0.48
1:B:185:SER:HB3	1:B:281:HIS:CE1	2.49	0.47
1:D:54:ARG:O	1:D:55:ALA:C	2.52	0.47
1:D:37:PRO:HB2	1:D:40:GLN:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:138:TYR:CE2	1:D:178:PRO:HG3	2.50	0.47
1:D:227:ASN:HD22	1:D:228:PRO:N	2.12	0.47
1:B:62:LEU:HD23	1:B:62:LEU:N	2.30	0.47
1:C:53:PRO:HD3	1:C:288:LYS:CE	2.44	0.47
1:B:50:GLU:HA	4:B:366:HOH:O	2.14	0.47
1:B:171:LYS:HB2	1:B:177:MET:SD	2.54	0.47
1:B:291:ASN:HD22	1:B:292:ALA:N	2.12	0.47
1:D:303:TRP:O	1:D:307:ARG:HG2	2.15	0.47
1:C:177:MET:HB3	1:C:241:PRO:HD3	1.96	0.47
1:D:52:PHE:HB3	1:D:101:VAL:HG22	1.95	0.47
1:D:73:GLN:NE2	1:D:104:THR:HG22	2.28	0.47
1:A:36:LEU:CD1	1:A:41:LYS:N	2.77	0.47
1:A:105:GLN:HA	1:A:105:GLN:NE2	2.30	0.47
1:C:20:ASP:O	1:C:23:GLN:HB2	2.15	0.47
1:D:90:GLY:O	1:D:91:TYR:HB2	2.14	0.47
1:A:87:HIS:HE1	4:A:329:HOH:O	1.98	0.47
1:B:90:GLY:O	1:B:91:TYR:HB2	2.15	0.47
1:D:55:ALA:HA	3:D:323:SO4:O3	2.15	0.47
1:A:183:MET:CB	1:A:186:PRO:HG3	2.43	0.47
1:B:209:PRO:O	1:B:213:GLY:N	2.48	0.47
1:C:182:VAL:HG11	1:C:300:ILE:CG2	2.45	0.47
1:D:70:CYS:HB3	1:D:117:LEU:HD12	1.97	0.47
1:D:189:ASP:N	1:D:256:ASP:OD1	2.48	0.47
1:D:276:TRP:HA	1:D:277:PRO:HD3	1.75	0.47
1:B:169:LYS:O	1:B:172:GLU:HB3	2.15	0.46
1:B:291:ASN:HD22	1:B:291:ASN:C	2.17	0.46
1:D:289:PHE:N	1:D:289:PHE:CD1	2.83	0.46
1:C:81:ALA:HB1	1:C:308:ILE:CD1	2.33	0.46
1:C:102:LEU:O	1:C:105:GLN:HB2	2.15	0.46
1:A:69:PRO:HB2	1:A:118:ASP:HB3	1.97	0.46
1:B:264:ALA:O	1:B:265:GLY:C	2.53	0.46
1:C:197:ASN:O	1:C:201:ALA:HB2	2.16	0.46
1:B:114:LEU:HD23	1:B:114:LEU:C	2.35	0.46
1:D:82:HIS:ND1	1:D:113:THR:OG1	2.48	0.46
1:D:256:ASP:O	1:D:260:LEU:HB2	2.15	0.46
1:B:97:SER:O	1:B:99:HIS:N	2.48	0.46
1:C:160:GLY:HA2	1:C:163:THR:HG23	1.98	0.46
1:C:192:LEU:HA	4:C:334:HOH:O	2.15	0.46
1:D:276:TRP:CD1	1:D:276:TRP:N	2.83	0.46
1:A:44:GLY:O	1:A:48:LEU:HB2	2.16	0.46
1:C:204:ASP:OD2	1:C:207:ALA:HB3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:253:LEU:HB2	4:D:330:HOH:O	2.16	0.46
1:A:167:MET:HB3	1:A:177:MET:HE3	1.98	0.46
1:B:54:ARG:HG3	1:B:54:ARG:NH1	2.31	0.46
1:D:120:ARG:HB3	1:D:125:ASN:CB	2.46	0.46
1:B:48:LEU:C	1:B:50:GLU:H	2.19	0.46
1:B:85:TYR:CB	1:B:114:LEU:HD21	2.46	0.46
1:B:185:SER:HB2	1:B:282:VAL:HG22	1.98	0.46
1:C:40:GLN:C	1:C:42:ARG:N	2.70	0.46
1:C:135:VAL:HG21	1:C:169:LYS:HD3	1.96	0.46
1:A:288:LYS:HD3	1:A:289:PHE:CZ	2.51	0.45
1:B:168:LEU:HD23	1:B:240:LEU:HD21	1.99	0.45
1:C:38:LEU:C	1:C:40:GLN:N	2.66	0.45
1:C:52:PHE:HB3	1:C:101:VAL:HG11	1.97	0.45
1:A:34:LYS:HZ3	1:A:35:ASN:HB2	1.81	0.45
1:D:157:SER:OG	2:D:326:BME:S2	2.69	0.45
1:A:308:ILE:HG22	1:A:308:ILE:O	2.16	0.45
1:B:63:THR:OG1	1:B:64:ASP:N	2.47	0.45
1:D:75:THR:CG2	1:D:108:LYS:HA	2.46	0.45
1:C:243:MET:HG2	1:C:271:VAL:HG22	1.98	0.45
1:B:188:VAL:O	1:B:231:SER:HA	2.17	0.45
1:C:287:GLY:HA2	1:C:293:ALA:HB3	1.99	0.45
1:C:80:ALA:O	1:C:150:ARG:HG2	2.17	0.45
1:C:183:MET:C	1:C:184:LEU:HD12	2.37	0.45
1:C:251:GLU:CD	1:C:281:HIS:HA	2.37	0.45
1:D:165:ALA:O	1:D:168:LEU:HB2	2.16	0.45
1:A:244:LEU:HD22	1:A:303:TRP:CG	2.51	0.45
1:C:167:MET:HA	1:C:170:ALA:HB3	1.98	0.45
1:C:289:PHE:N	1:C:289:PHE:CD1	2.85	0.45
1:B:283:PHE:O	1:B:285:MET:N	2.50	0.45
1:C:72:ARG:HG2	1:C:72:ARG:NH1	2.30	0.45
1:B:269:VAL:O	1:B:271:VAL:HG23	2.16	0.44
1:D:138:TYR:CZ	1:D:178:PRO:HG3	2.52	0.44
1:A:203:ARG:HD2	1:A:250:GLU:OE1	2.16	0.44
1:B:191:THR:HG21	1:B:226:LYS:HE2	1.99	0.44
1:C:159:GLY:O	1:C:163:THR:HG23	2.17	0.44
1:D:16:MET:HE1	1:D:289:PHE:HD2	1.81	0.44
1:A:14:THR:HA	4:A:340:HOH:O	2.17	0.44
1:A:99:HIS:CE1	1:A:156:ASP:OD2	2.66	0.44
1:C:307:ARG:HD3	4:C:357:HOH:O	2.17	0.44
1:D:36:LEU:CG	1:D:40:GLN:HG2	2.47	0.44
1:D:59:GLU:HA	4:D:358:HOH:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:212:LEU:O	1:B:213:GLY:O	2.36	0.44
1:D:105:GLN:HA	1:D:105:GLN:HE21	1.80	0.44
1:D:303:TRP:CZ3	1:D:307:ARG:HG3	2.53	0.44
1:B:34:LYS:HB3	1:B:34:LYS:HE2	1.83	0.44
1:B:291:ASN:O	1:B:295:ILE:HG13	2.17	0.44
1:D:22:LEU:O	1:D:25:LEU:HB2	2.17	0.44
1:D:52:PHE:CB	1:D:101:VAL:HG22	2.48	0.44
1:A:123:PRO:HB3	1:A:218:LEU:HD22	2.00	0.44
1:A:274:LYS:HA	1:B:271:VAL:O	2.18	0.44
1:A:151:ILE:CG2	1:A:152:ILE:N	2.81	0.44
1:B:287:GLY:HA2	1:B:293:ALA:HB3	1.98	0.44
1:B:303:TRP:CD1	1:B:307:ARG:NH2	2.86	0.44
1:C:244:LEU:HD22	1:C:303:TRP:CG	2.53	0.43
1:D:181:LEU:HG	1:D:241:PRO:HG2	2.00	0.43
1:A:269:VAL:HG12	1:A:270:SER:N	2.32	0.43
1:A:93:SER:HA	1:A:121:LEU:HD13	1.99	0.43
1:D:141:LEU:HG	1:D:151:ILE:CD1	2.48	0.43
1:B:281:HIS:CD2	1:B:282:VAL:HG23	2.52	0.43
1:C:184:LEU:HD12	1:C:184:LEU:N	2.34	0.43
1:B:195:TRP:CD1	1:B:199:ASN:ND2	2.86	0.43
1:B:255:SER:HA	1:B:258:THR:OG1	2.18	0.43
1:C:17:ASP:O	1:C:20:ASP:N	2.48	0.43
1:C:100:LEU:O	1:C:104:THR:HG23	2.18	0.43
1:B:34:LYS:H	1:B:34:LYS:HG2	1.47	0.43
1:B:283:PHE:C	1:B:285:MET:H	2.21	0.43
1:D:100:LEU:O	1:D:104:THR:HG23	2.19	0.43
1:A:19:ARG:O	1:A:22:LEU:HB2	2.18	0.43
1:A:36:LEU:HD12	1:A:41:LYS:CA	2.49	0.43
1:A:220:VAL:O	1:A:223:GLU:HB2	2.19	0.43
2:C:325:BME:H12	4:C:359:HOH:O	2.14	0.43
1:D:153:ILE:N	1:D:153:ILE:CD1	2.82	0.43
1:B:251:GLU:OE1	1:B:281:HIS:ND1	2.32	0.43
1:B:64:ASP:HA	1:B:70:CYS:SG	2.59	0.42
1:D:177:MET:HA	1:D:178:PRO:HD3	1.90	0.42
1:B:68:VAL:HA	1:B:69:PRO:HD3	1.90	0.42
1:C:184:LEU:N	1:C:184:LEU:CD1	2.82	0.42
1:D:117:LEU:HG	4:D:344:HOH:O	2.19	0.42
1:B:200:LEU:O	1:B:201:ALA:C	2.57	0.42
1:C:68:VAL:CG1	1:C:117:LEU:HD11	2.49	0.42
1:C:138:TYR:CE1	1:C:167:MET:HE1	2.54	0.42
1:C:272:GLU:HG2	1:D:274:LYS:HG3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:GLY:HA2	1:A:163:THR:CG2	2.49	0.42
1:A:242:GLU:OE2	1:A:307:ARG:HD2	2.19	0.42
1:C:15:LYS:HG3	1:C:289:PHE:O	2.20	0.42
1:C:49:CYS:CB	1:C:98:THR:HG22	2.49	0.42
1:C:207:ALA:HB1	1:C:212:LEU:HD11	2.01	0.42
1:C:286:TYR:CD1	1:C:286:TYR:N	2.86	0.42
1:D:280:PRO:O	1:D:283:PHE:HB3	2.18	0.42
1:A:33:GLU:HG3	1:A:36:LEU:CG	2.50	0.42
1:A:63:THR:HG23	1:A:64:ASP:N	2.34	0.42
1:B:212:LEU:O	1:B:213:GLY:C	2.58	0.42
1:A:46:GLU:O	1:A:50:GLU:HB2	2.19	0.42
1:A:105:GLN:O	1:A:109:GLN:HG3	2.20	0.42
1:A:109:GLN:HE21	1:A:298:LYS:HD2	1.84	0.42
1:A:258:THR:HG21	1:B:262:GLU:HB2	2.02	0.42
1:A:45:MET:O	1:A:49:CYS:HB2	2.19	0.42
1:B:227:ASN:HD22	1:B:228:PRO:CD	2.33	0.42
1:C:188:VAL:O	1:C:231:SER:HA	2.18	0.42
1:C:281:HIS:O	1:C:282:VAL:C	2.56	0.42
1:D:215:MET:HE3	2:D:326:BME:H21	2.01	0.42
1:A:114:LEU:C	1:A:114:LEU:HD23	2.40	0.42
1:A:168:LEU:HD21	1:A:240:LEU:HD11	2.02	0.42
1:D:105:GLN:NE2	1:D:105:GLN:CA	2.83	0.42
1:D:182:VAL:HG11	1:D:300:ILE:CG2	2.49	0.42
1:C:40:GLN:C	1:C:42:ARG:H	2.23	0.41
1:C:220:VAL:HG13	1:C:221:GLY:N	2.35	0.41
1:D:117:LEU:HD12	1:D:117:LEU:HA	1.87	0.41
1:D:191:THR:O	1:D:192:LEU:C	2.57	0.41
1:A:145:ALA:O	1:A:150:ARG:NH2	2.53	0.41
1:B:208:GLU:HB3	1:B:209:PRO:HD2	2.02	0.41
1:D:42:ARG:O	1:D:45:MET:HB3	2.20	0.41
1:D:290:VAL:HG23	1:D:290:VAL:O	2.21	0.41
1:C:227:ASN:ND2	1:C:228:PRO:HD2	2.35	0.41
1:A:122:ALA:HB1	1:A:123:PRO:HA	2.02	0.41
1:B:126:PRO:O	1:B:129:ALA:HB2	2.21	0.41
1:C:59:GLU:O	1:C:73:GLN:HA	2.21	0.41
1:C:164:THR:HG21	1:C:232:PRO:HB3	2.01	0.41
1:C:171:LYS:NZ	1:C:239:GLY:HA3	2.35	0.41
1:D:23:GLN:O	1:D:26:LYS:HB3	2.19	0.41
1:B:38:LEU:O	1:B:42:ARG:HG3	2.19	0.41
1:B:227:ASN:ND2	1:B:229:LEU:H	2.19	0.41
1:D:187:PHE:CE2	1:D:190:LEU:HD12	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:LEU:HD12	1:A:41:LYS:HB2	2.03	0.41
1:A:167:MET:HB3	1:A:177:MET:CE	2.49	0.41
1:C:183:MET:CB	1:C:186:PRO:HG3	2.38	0.41
1:D:300:ILE:O	1:D:304:ILE:HG13	2.21	0.41
1:A:263:ARG:O	1:A:267:ALA:N	2.51	0.41
1:D:141:LEU:CD2	1:D:151:ILE:HD12	2.50	0.41
1:A:28:ASN:HD22	1:A:28:ASN:HA	1.68	0.41
1:A:48:LEU:C	1:A:50:GLU:H	2.23	0.41
1:A:90:GLY:CA	1:A:215:MET:HG2	2.51	0.41
1:A:229:LEU:HA	1:A:229:LEU:HD12	1.86	0.41
1:B:41:LYS:HE2	1:B:41:LYS:HB2	1.95	0.41
1:B:126:PRO:O	1:B:129:ALA:CB	2.69	0.41
1:B:152:ILE:HD13	1:B:180:GLY:N	2.36	0.41
1:C:81:ALA:HB2	1:C:308:ILE:HG21	2.01	0.41
1:C:276:TRP:HA	1:C:277:PRO:HD3	1.84	0.41
1:C:283:PHE:C	1:C:285:MET:H	2.22	0.41
1:D:16:MET:CE	1:D:289:PHE:HD2	2.33	0.41
1:D:26:LYS:HB2	1:D:205:PHE:CE2	2.56	0.41
1:D:197:ASN:ND2	1:D:197:ASN:N	2.69	0.41
1:D:265:GLY:C	1:D:267:ALA:H	2.25	0.41
1:D:60:LEU:N	4:D:358:HOH:O	2.37	0.41
1:D:171:LYS:O	1:D:174:GLY:N	2.52	0.41
1:B:109:GLN:HB2	1:B:301:CYS:SG	2.61	0.40
1:B:262:GLU:HG2	1:B:263:ARG:HD3	2.02	0.40
1:C:48:LEU:O	1:C:51:ARG:HB3	2.21	0.40
1:D:38:LEU:HD21	1:D:92:ILE:HB	2.02	0.40
1:D:85:TYR:HA	1:D:154:ALA:O	2.21	0.40
1:A:181:LEU:HG	1:A:241:PRO:HG2	2.03	0.40
1:B:261:ALA:HA	1:B:271:VAL:HG11	2.02	0.40
1:D:190:LEU:HD23	1:D:220:VAL:HG23	2.03	0.40
1:C:29:ALA:HB1	1:C:208:GLU:OE1	2.20	0.40
1:B:26:LYS:O	1:B:27:ILE:C	2.59	0.40
1:D:16:MET:HE1	1:D:289:PHE:CD2	2.56	0.40
1:D:214:GLU:OE2	1:D:218:LEU:HD11	2.20	0.40
1:A:36:LEU:HA	1:A:37:PRO:HD3	2.00	0.40
1:A:298:LYS:HE2	4:A:353:HOH:O	2.21	0.40
1:B:224:ASP:C	1:B:226:LYS:N	2.74	0.40
1:C:21:PHE:CZ	1:C:286:TYR:CD2	3.08	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	295/336 (88%)	258 (88%)	33 (11%)	4 (1%)	11 34
1	B	294/336 (88%)	247 (84%)	40 (14%)	7 (2%)	6 20
1	C	287/336 (85%)	244 (85%)	40 (14%)	3 (1%)	15 44
1	D	287/336 (85%)	247 (86%)	35 (12%)	5 (2%)	9 29
All	All	1163/1344 (86%)	996 (86%)	148 (13%)	19 (2%)	9 31

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	98	THR
1	B	213	GLY
1	B	284	GLN
1	A	49	CYS
1	A	97	SER
1	A	98	THR
1	B	77	GLY
1	B	49	CYS
1	D	77	GLY
1	D	147	SER
1	A	278	ASP
1	C	209	PRO
1	C	307	ARG
1	B	209	PRO
1	D	89	GLY
1	D	108	LYS
1	B	79	GLY
1	C	282	VAL
1	D	94	GLY

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	237/265 (89%)	221 (93%)	16 (7%)	16	42
1	B	236/265 (89%)	222 (94%)	14 (6%)	19	49
1	C	231/265 (87%)	214 (93%)	17 (7%)	13	37
1	D	231/265 (87%)	217 (94%)	14 (6%)	18	48
All	All	935/1060 (88%)	874 (94%)	61 (6%)	17	44

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	GLN
1	A	28	ASN
1	A	33	GLU
1	A	64	ASP
1	A	68	VAL
1	A	128	PRO
1	A	139	ARG
1	A	163	THR
1	A	184	LEU
1	A	215	MET
1	A	225	ARG
1	A	227	ASN
1	A	229	LEU
1	A	242	GLU
1	A	260	LEU
1	A	273	LEU
1	B	28	ASN
1	B	35	ASN
1	B	51	ARG
1	B	56	GLU
1	B	62	LEU
1	B	150	ARG
1	B	172	GLU
1	B	214	GLU

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Mol	Chain	Res	Type
1	B	227	ASN
1	B	246	HIS
1	B	260	LEU
1	B	291	ASN
1	B	298	LYS
1	B	307	ARG
1	C	30	GLU
1	C	73	GLN
1	C	97	SER
1	C	98	THR
1	C	101	VAL
1	C	111	SER
1	C	128	PRO
1	C	172	GLU
1	C	192	LEU
1	C	210	ASP
1	C	225	ARG
1	C	227	ASN
1	C	229	LEU
1	C	233	VAL
1	C	256	ASP
1	C	291	ASN
1	C	307	ARG
1	D	19	ARG
1	D	24	LEU
1	D	40	GLN
1	D	49	CYS
1	D	59	GLU
1	D	62	LEU
1	D	124	GLU
1	D	128	PRO
1	D	167	MET
1	D	187	PHE
1	D	227	ASN
1	D	242	GLU
1	D	256	ASP
1	D	298	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	GLN

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Mol	Chain	Res	Type
1	A	28	ASN
1	A	73	GLN
1	A	87	HIS
1	A	99	HIS
1	A	105	GLN
1	A	109	GLN
1	A	197	ASN
1	A	227	ASN
1	B	23	GLN
1	B	28	ASN
1	B	73	GLN
1	B	87	HIS
1	B	99	HIS
1	B	105	GLN
1	B	109	GLN
1	B	197	ASN
1	B	199	ASN
1	B	227	ASN
1	B	246	HIS
1	B	291	ASN
1	C	82	HIS
1	C	87	HIS
1	C	197	ASN
1	C	227	ASN
1	C	291	ASN
1	D	73	GLN
1	D	87	HIS
1	D	99	HIS
1	D	105	GLN
1	D	197	ASN
1	D	227	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)

18 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	BME	D	326	-	3,3,3	0.54	0	1,2,2	0.37	0
3	SO4	B	324	-	4,4,4	0.30	0	6,6,6	0.08	0
2	BME	B	330	-	3,3,3	0.32	0	1,2,2	1.33	0
2	BME	C	325	-	3,3,3	0.52	0	1,2,2	0.43	0
3	SO4	B	329	-	4,4,4	0.28	0	6,6,6	0.06	0
3	SO4	C	324	-	4,4,4	0.28	0	6,6,6	0.09	0
3	SO4	C	323	-	4,4,4	0.26	0	6,6,6	0.05	0
3	SO4	B	328	-	4,4,4	0.28	0	6,6,6	0.09	0
3	SO4	A	323	-	4,4,4	0.31	0	6,6,6	0.10	0
3	SO4	B	326	-	4,4,4	0.28	0	6,6,6	0.08	0
2	BME	A	325	-	3,3,3	0.34	0	1,2,2	0.52	0
3	SO4	B	325	-	4,4,4	0.29	0	6,6,6	0.12	0
3	SO4	A	324	-	4,4,4	0.32	0	6,6,6	0.10	0
3	SO4	D	325	-	4,4,4	0.30	0	6,6,6	0.11	0
3	SO4	B	323	-	4,4,4	0.28	0	6,6,6	0.14	0
3	SO4	D	324	-	4,4,4	0.32	0	6,6,6	0.09	0
3	SO4	B	327	-	4,4,4	0.29	0	6,6,6	0.06	0
3	SO4	D	323	-	4,4,4	0.26	0	6,6,6	0.06	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BME	D	326	-	-	0/1/1/1	-
2	BME	B	330	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BME	C	325	-	-	0/1/1/1	-
2	BME	A	325	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	330	BME	O1-C1-C2-S2

There are no ring outliers.

6 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	326	BME	4	0
2	B	330	BME	1	0
2	C	325	BME	3	0
3	A	323	SO4	1	0
2	A	325	BME	1	0
3	D	323	SO4	1	0

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, 95^{th} 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	297/336 (88%)	-0.53	1 (0%)	94	93	9, 28, 54, 72	1 (0%)
1	B	296/336 (88%)	-0.52	2 (0%)	87	84	9, 28, 50, 73	1 (0%)
1	C	291/336 (86%)	-0.47	5 (1%)	70	63	14, 31, 58, 72	1 (0%)
1	D	291/336 (86%)	-0.40	0	100	100	8, 33, 62, 74	1 (0%)
All	All	1175/1344 (87%)	-0.48	8 (0%)	87	84	8, 30, 58, 74	4 (0%)

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	77	GLY	3.8
1	B	77	GLY	2.9
1	A	33	GLU	2.8
1	C	37	PRO	2.8
1	C	30	GLU	2.6
1	C	76	ASP	2.4
1	C	38	LEU	2.2
1	B	33	GLU	2.1

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	SO4	B	329	5/5	0.14	0.60	151,151,151,151	0
3	SO4	B	328	5/5	0.75	0.35	113,113,114,114	0
2	BME	D	326	4/4	0.77	0.80	1,1,1,2	4
2	BME	C	325	4/4	0.79	0.75	1,1,1,5	4
3	SO4	B	325	5/5	0.83	0.30	76,76,77,78	0
3	SO4	B	326	5/5	0.86	0.32	114,114,115,115	0
3	SO4	B	327	5/5	0.86	0.30	101,102,103,103	0
2	BME	A	325	4/4	0.87	0.76	1,1,1,4	4
3	SO4	A	324	5/5	0.88	0.30	87,88,89,89	0
2	BME	B	330	4/4	0.88	0.53	4,5,5,7	4
3	SO4	D	325	5/5	0.90	0.23	80,81,82,82	0
3	SO4	C	324	5/5	0.93	0.24	83,83,84,84	0
3	SO4	D	324	5/5	0.93	0.21	61,61,63,63	0
3	SO4	C	323	5/5	0.93	0.27	82,82,82,83	0
3	SO4	B	324	5/5	0.95	0.16	109,109,110,110	0
3	SO4	D	323	5/5	0.95	0.26	74,75,75,76	0
3	SO4	A	323	5/5	0.96	0.18	61,61,63,63	0
3	SO4	B	323	5/5	0.98	0.14	52,53,53,54	0

6.5 Other polymers (i)

There are no such residues in this entry.