



# Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 04:50 pm BST

PDB ID : 1OXW  
Title : The Crystal Structure of SeMet Patatin  
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Deposited on : 2003-04-03  
Resolution : 2.20 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

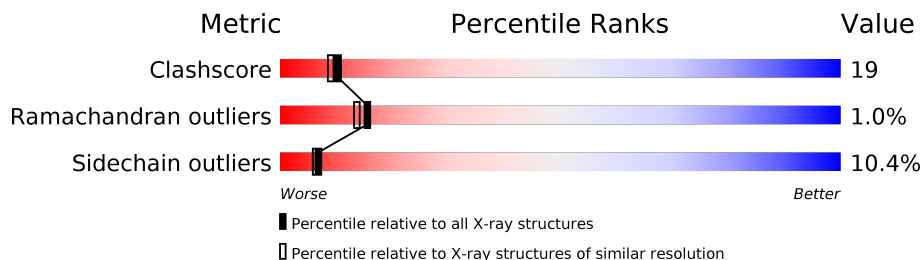
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	373	
1	B	373	
1	C	373	

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 8871 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 Patatin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	Se			
1	A	360	2787	1769	454	553	11	0	0	0
1	B	359	2782	1765	453	553	11	0	0	0
1	C	362	2804	1779	457	556	12	0	0	0

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	14	MSE	-	EXPRESSION TAG	UNP Q8LPW4
A	15	HIS	-	EXPRESSION TAG	UNP Q8LPW4
A	16	HIS	-	EXPRESSION TAG	UNP Q8LPW4
A	17	HIS	-	EXPRESSION TAG	UNP Q8LPW4
A	18	HIS	-	EXPRESSION TAG	UNP Q8LPW4
A	19	HIS	-	EXPRESSION TAG	UNP Q8LPW4
A	20	HIS	-	EXPRESSION TAG	UNP Q8LPW4
A	21	ALA	-	EXPRESSION TAG	UNP Q8LPW4
A	22	MSE	-	EXPRESSION TAG	UNP Q8LPW4
A	28	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
A	58	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
A	85	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
A	131	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
A	180	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
A	253	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
A	284	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
A	290	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
A	298	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
A	331	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
A	339	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
B	1014	MSE	-	EXPRESSION TAG	UNP Q8LPW4
B	1015	HIS	-	EXPRESSION TAG	UNP Q8LPW4
B	1016	HIS	-	EXPRESSION TAG	UNP Q8LPW4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1017	HIS	-	EXPRESSION TAG	UNP Q8LPW4
B	1018	HIS	-	EXPRESSION TAG	UNP Q8LPW4
B	1019	HIS	-	EXPRESSION TAG	UNP Q8LPW4
B	1020	HIS	-	EXPRESSION TAG	UNP Q8LPW4
B	1021	ALA	-	EXPRESSION TAG	UNP Q8LPW4
B	1022	MSE	-	EXPRESSION TAG	UNP Q8LPW4
B	1028	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
B	1058	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
B	1085	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
B	1131	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
B	1180	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
B	1253	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
B	1284	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
B	1290	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
B	1298	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
B	1331	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
B	1339	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
C	2014	MSE	-	EXPRESSION TAG	UNP Q8LPW4
C	2015	HIS	-	EXPRESSION TAG	UNP Q8LPW4
C	2016	HIS	-	EXPRESSION TAG	UNP Q8LPW4
C	2017	HIS	-	EXPRESSION TAG	UNP Q8LPW4
C	2018	HIS	-	EXPRESSION TAG	UNP Q8LPW4
C	2019	HIS	-	EXPRESSION TAG	UNP Q8LPW4
C	2020	HIS	-	EXPRESSION TAG	UNP Q8LPW4
C	2021	ALA	-	EXPRESSION TAG	UNP Q8LPW4
C	2022	MSE	-	EXPRESSION TAG	UNP Q8LPW4
C	2028	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
C	2058	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
C	2085	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
C	2131	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
C	2180	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
C	2253	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
C	2284	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
C	2290	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
C	2298	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
C	2331	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4
C	2339	MSE	MET	MODIFIED RESIDUE	UNP Q8LPW4

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	156	Total O 156 156	0	0

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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
2	B	169	Total	O	0	0
			169	169		
2	C	173	Total	O	0	0
			173	173		

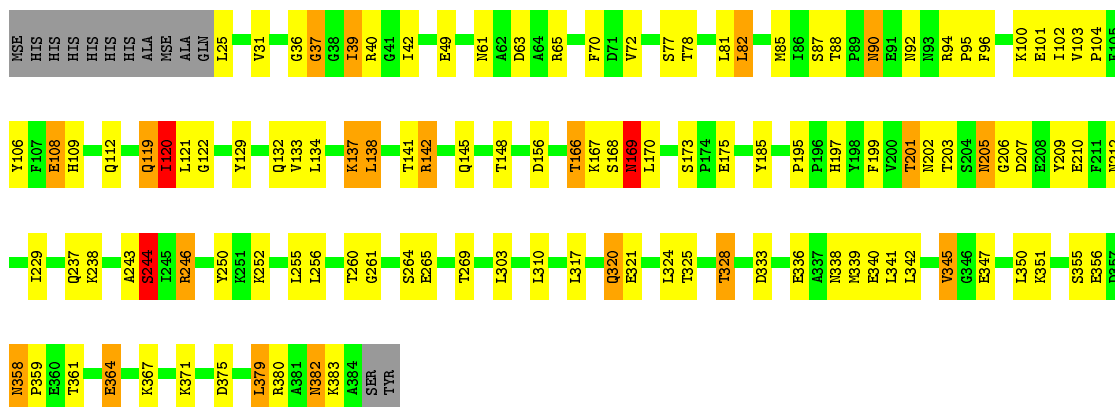
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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. 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. 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.

Note EDS was not executed.

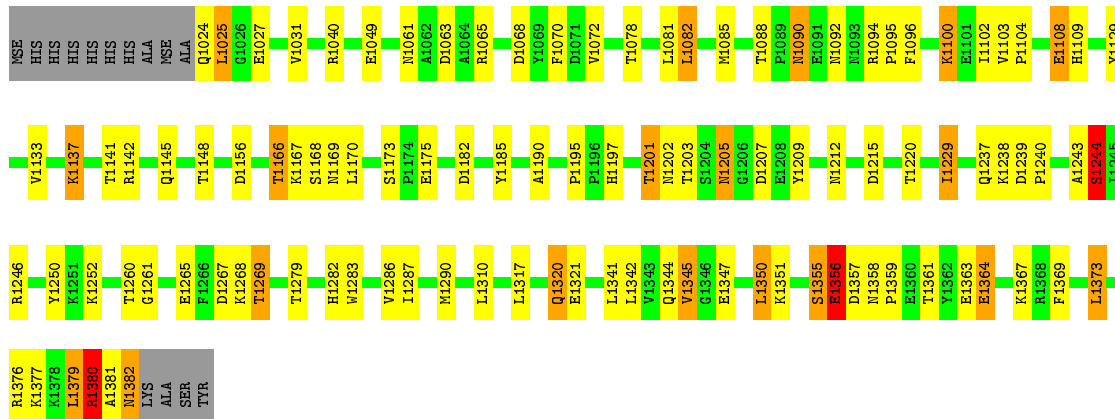
- Molecule 1: Patatin

Chain A: 



- Molecule 1: Patatin

Chain B: 



- Molecule 1: Patatin

Chain C: 

MSE	HIS	HIS	HIS	HIS	HIS	HIS	ALA	M2022	A2023	Q2024	L2025	M2028	G2036	G2037	G2038	T2039	R2040	G2041	L2042	L2048	E2049	Q2054	M2058	R2065	F2070	S2077	T2078	L2081	L2082	T2088	P2089	M2090	E2091	M2092	M2093	R2094	P2095	K2100	E2101	T2102	V2103	P2104	F2105	Y2106	F2107	E2108	Q2112
Y2129	V2133	L2134	Q2135	E2136	K2137	L2138	T2141	R2142	Q2145	T2148	D2156	T2157	K2158	T2166	K2167	S2168	M2169	S2173	P2174	E2175	D2182	Y2185	A2190	P2195	E2196	H2197	V2200	T2201	M2202	T2203	S2204	M2205	G2206	D2207	E2208	Y2209	M2212	V2213	D2215	T2220	Q2237	K2238					
A2243	S2244	L2245	R2246	Y2250	K2251	K2252	M2253	L2254	T2260	G2261	E2265	T2269	E2274	H2282	L2285	V2286	M2290	Q2308	P2309	A2310	Q2320	E2321	L2324	T2327	T2328	T2329	E2330	M2331	D2332	E2336	A2337	M2338	M2339	E2340	L2341	L2342	V2343	Q2344	Y2345	G2346	E2347	L2350	K2351	P2353			
D2357	M2358	T2361	E2364	R2380	K2383	ALA	SER	TTR																																							

## 4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	97.18Å 171.42Å 129.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20	Depositor
% Data completeness (in resolution range)	100.0 (20.00-2.20)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
Refinement program	X-PLOR 98.1	Depositor
R, $R_{free}$	0.220 , 0.272	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	8871	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP



## 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	0.45	0/2830	0.64	0/3825
1	B	0.44	0/2825	0.63	0/3819
1	C	0.44	0/2847	0.63	0/3847
All	All	0.45	0/8502	0.63	0/11491

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	2787	0	2756	106	0
1	B	2782	0	2746	105	0
1	C	2804	0	2773	104	0
2	A	156	0	0	2	0
2	B	169	0	0	3	0
2	C	173	0	0	5	0
All	All	8871	0	8275	312	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 19.

All (312) 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:B:1201:THR:HG22	1:B:1209:TYR:HB3	1.41	0.98
1:C:2201:THR:HG22	1:C:2209:TYR:HB3	1.46	0.97
1:C:2261:GLY:H	1:C:2320:GLN:HE22	1.11	0.96
1:A:201:THR:HG22	1:A:209:TYR:HB3	1.46	0.96
1:B:1261:GLY:H	1:B:1320:GLN:HE22	1.14	0.95
1:A:88:THR:HG23	1:A:141:THR:HG21	1.49	0.94
1:A:261:GLY:H	1:A:320:GLN:HE22	1.11	0.93
1:C:2022:MSE:N	1:C:2383:LYS:HZ2	1.67	0.91
1:B:1286:VAL:HG23	1:B:1290:MSE:HE2	1.52	0.89
1:B:1347:GLU:OE1	1:C:2024:GLN:HG2	1.72	0.89
1:B:1088:THR:HG23	1:B:1141:THR:HG21	1.57	0.85
1:A:106:TYR:O	1:A:339:MSE:HE1	1.78	0.83
1:C:2106:TYR:C	1:C:2339:MSE:HE1	2.01	0.81
1:C:2158:LYS:NZ	1:C:2212:ASN:HD22	1.80	0.80
1:C:2022:MSE:HB3	1:C:2383:LYS:HD2	1.66	0.78
1:B:1090:ASN:HD22	1:B:1090:ASN:C	1.86	0.78
1:C:2054:GLN:O	1:C:2058:MSE:HG3	1.84	0.77
1:A:324:LEU:HB3	1:A:328:THR:HG22	1.68	0.75
1:C:2049:GLU:HG3	1:C:2100:LYS:HA	1.69	0.75
1:C:2088:THR:HG23	1:C:2141:THR:HG21	1.68	0.75
1:C:2205:ASN:HD22	1:C:2207:ASP:H	1.33	0.74
1:B:1108:GLU:HG2	1:B:1109:HIS:CD2	2.23	0.73
1:B:1287:ILE:HA	1:B:1290:MSE:HE3	1.69	0.73
1:B:1175:GLU:O	1:B:1201:THR:HG21	1.89	0.73
1:C:2343:VAL:O	1:C:2347:GLU:HG3	1.87	0.73
1:C:2324:LEU:HD22	1:C:2328:THR:CG2	2.19	0.71
1:A:175:GLU:O	1:A:201:THR:HG21	1.90	0.71
1:C:2201:THR:HG23	1:C:2202:ASN:N	2.06	0.70
1:A:49:GLU:HG3	1:A:100:LYS:HA	1.72	0.70
1:A:90:ASN:HD22	1:A:90:ASN:C	1.93	0.70
1:A:261:GLY:H	1:A:320:GLN:NE2	1.90	0.69
1:B:1205:ASN:HD22	1:B:1207:ASP:H	1.40	0.69
1:B:1320:GLN:HE21	1:B:1321:GLU:H	1.40	0.69
1:C:2175:GLU:O	1:C:2201:THR:HG21	1.91	0.68
1:C:2090:ASN:C	1:C:2090:ASN:HD22	1.97	0.68
1:C:2250:TYR:HB2	1:C:2310:LEU:HD12	1.76	0.68
1:C:2320:GLN:HE21	1:C:2321:GLU:H	1.43	0.67
1:A:175:GLU:HG2	1:A:203:THR:HG22	1.76	0.67
1:B:1201:THR:HG23	1:B:1202:ASN:N	2.09	0.67
1:A:70:PHE:O	1:A:148:THR:HG21	1.95	0.67
1:A:201:THR:HG23	1:A:202:ASN:N	2.09	0.67
1:A:261:GLY:N	1:A:320:GLN:HE22	1.90	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:205:ASN:HD22	1:A:207:ASP:H	1.40	0.67
1:A:25:LEU:HD12	1:A:379:LEU:HD11	1.77	0.67
1:B:1369:PHE:CD2	1:B:1373:LEU:HD21	2.30	0.66
1:B:1250:TYR:HB2	1:B:1310:LEU:HD12	1.77	0.66
1:B:1379:LEU:HD23	1:B:1379:LEU:N	2.11	0.66
1:C:2205:ASN:ND2	1:C:2207:ASP:H	1.93	0.66
1:B:1049:GLU:HG3	1:B:1100:LYS:HA	1.78	0.65
1:C:2042:ILE:HD11	1:C:2339:MSE:HE3	1.77	0.65
1:C:2042:ILE:HD11	1:C:2339:MSE:CE	2.26	0.64
1:C:2142:ARG:H	1:C:2145:GLN:NE2	1.95	0.64
1:B:1175:GLU:HG2	1:B:1203:THR:HG22	1.80	0.64
1:C:2158:LYS:HZ3	1:C:2212:ASN:HD22	1.45	0.64
1:A:205:ASN:ND2	1:A:207:ASP:H	1.96	0.63
1:C:2175:GLU:HG2	1:C:2203:THR:HG22	1.79	0.63
1:B:1261:GLY:N	1:B:1320:GLN:HE22	1.93	0.63
1:A:320:GLN:HE21	1:A:321:GLU:H	1.45	0.63
1:B:1166:THR:HG23	1:B:1168:SER:H	1.64	0.63
1:A:229:ILE:HD11	1:A:255:LEU:HD22	1.80	0.63
1:C:2070:PHE:O	1:C:2148:THR:HG21	1.99	0.63
1:B:1287:ILE:HA	1:B:1290:MSE:CE	2.29	0.63
1:C:2134:LEU:O	1:C:2138:LEU:HB2	1.99	0.62
1:A:120:ILE:HD13	1:A:120:ILE:H	1.65	0.62
1:C:2175:GLU:HG3	1:C:2203:THR:HA	1.82	0.62
1:A:175:GLU:HG3	1:A:203:THR:HA	1.82	0.62
1:A:250:TYR:HB2	1:A:310:LEU:HD12	1.80	0.62
1:B:1369:PHE:O	1:B:1373:LEU:HD22	2.00	0.61
1:C:2168:SER:O	1:C:2169:ASN:HB2	1.99	0.61
1:B:1175:GLU:HG3	1:B:1203:THR:HA	1.81	0.61
1:A:324:LEU:HD22	1:A:328:THR:CG2	2.30	0.61
1:B:1070:PHE:O	1:B:1148:THR:HG21	2.00	0.61
1:C:2286:VAL:HG23	1:C:2290:MSE:HE3	1.82	0.61
1:C:2220:THR:O	1:C:2220:THR:HG22	2.00	0.61
1:A:256:LEU:HD13	1:A:317:LEU:HD23	1.81	0.61
1:B:1379:LEU:H	1:B:1379:LEU:HD23	1.66	0.61
1:C:2261:GLY:H	1:C:2320:GLN:NE2	1.90	0.61
1:C:2286:VAL:CG2	1:C:2290:MSE:HE3	2.31	0.61
1:B:1108:GLU:HG2	1:B:1109:HIS:NE2	2.16	0.60
1:B:1205:ASN:ND2	1:B:1207:ASP:H	1.97	0.60
1:A:168:SER:O	1:A:169:ASN:HB3	2.01	0.59
1:A:101:GLU:C	1:A:104:PRO:HD2	2.23	0.59
1:A:166:THR:HG23	1:A:168:SER:H	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2261:GLY:N	1:C:2320:GLN:HE22	1.90	0.59
1:B:1287:ILE:HD12	1:B:1290:MSE:HE3	1.83	0.58
1:A:82:LEU:HD22	1:A:102:ILE:HG21	1.84	0.58
1:A:90:ASN:ND2	1:A:94:ARG:H	2.01	0.58
1:B:1344:GLN:HG2	1:C:2024:GLN:OE1	2.02	0.58
1:A:324:LEU:HD22	1:A:328:THR:HG23	1.86	0.58
1:B:1361:THR:OG1	1:B:1364:GLU:HG2	2.04	0.58
1:C:2022:MSE:HE2	1:C:2383:LYS:HB3	1.85	0.57
1:A:39:ILE:HD13	1:A:333:ASP:O	2.05	0.57
1:B:1357:ASP:O	1:B:1359:PRO:HD3	2.05	0.57
1:B:1129:TYR:CE2	1:B:1133:VAL:HG21	2.40	0.57
1:C:2205:ASN:HD21	1:C:2207:ASP:HB2	1.70	0.57
1:B:1320:GLN:HA	1:B:1320:GLN:HE21	1.70	0.57
1:A:42:ILE:HD11	1:A:339:MSE:HE2	1.87	0.56
1:B:1090:ASN:ND2	1:B:1090:ASN:C	2.56	0.56
1:B:1129:TYR:O	1:B:1133:VAL:HG23	2.06	0.56
1:C:2142:ARG:H	1:C:2145:GLN:HE21	1.54	0.56
1:C:2361:THR:OG1	1:C:2364:GLU:HG2	2.06	0.56
1:A:36:GLY:HA3	1:A:77:SER:HB3	1.87	0.56
1:B:1367:LYS:HE2	2:B:3277:HOH:O	2.06	0.55
1:A:106:TYR:HB3	1:A:339:MSE:HE2	1.88	0.55
1:B:1261:GLY:H	1:B:1320:GLN:NE2	1.94	0.55
1:C:2082:LEU:HD22	1:C:2102:ILE:HG21	1.88	0.55
1:C:2090:ASN:ND2	1:C:2094:ARG:H	2.05	0.55
1:C:2106:TYR:O	1:C:2339:MSE:HE1	2.07	0.55
1:B:1082:LEU:O	1:B:1082:LEU:HD12	2.07	0.54
1:A:106:TYR:C	1:A:339:MSE:HE1	2.27	0.54
1:C:2158:LYS:HZ2	1:C:2212:ASN:HD22	1.51	0.54
1:A:137:LYS:HE3	2:A:3967:HOH:O	2.07	0.54
1:A:40:ARG:HB3	1:A:260:THR:HB	1.90	0.54
1:A:371:LYS:HE2	1:C:2351:LYS:HB3	1.89	0.53
1:C:2101:GLU:C	1:C:2104:PRO:HD2	2.28	0.53
1:B:1369:PHE:HD2	1:B:1373:LEU:HD21	1.69	0.53
1:C:2082:LEU:O	1:C:2082:LEU:HD12	2.09	0.53
1:C:2328:THR:HA	1:C:2338:ASN:HD21	1.74	0.53
1:A:142:ARG:H	1:A:145:GLN:NE2	2.06	0.53
1:A:382:ASN:ND2	1:A:383:LYS:N	2.57	0.53
1:B:1090:ASN:ND2	1:B:1094:ARG:H	2.07	0.53
1:B:1320:GLN:HE21	1:B:1321:GLU:N	2.05	0.53
1:B:1082:LEU:HD22	1:B:1102:ILE:HG21	1.90	0.52
1:C:2040:ARG:HD2	1:C:2260:THR:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:65:ARG:CB	1:A:95:PRO:HG2	2.39	0.52
1:B:1185:TYR:OH	1:B:1195:PRO:HD2	2.10	0.52
1:B:1065:ARG:CB	1:B:1095:PRO:HG2	2.39	0.52
1:A:324:LEU:HB3	1:A:328:THR:CG2	2.38	0.52
1:C:2201:THR:CG2	1:C:2202:ASN:N	2.71	0.52
1:A:39:ILE:HG22	1:A:339:MSE:HE3	1.91	0.52
1:B:1203:THR:OG1	1:B:1205:ASN:ND2	2.42	0.52
1:C:2320:GLN:HE21	1:C:2320:GLN:HA	1.74	0.51
1:A:361:THR:OG1	1:A:364:GLU:HG2	2.10	0.51
1:C:2282:HIS:HA	1:C:2285:LEU:HD12	1.92	0.51
1:C:2040:ARG:HB3	1:C:2260:THR:HB	1.92	0.51
1:C:2078:THR:HA	1:C:2081:LEU:HG	1.92	0.51
1:C:2106:TYR:HB3	1:C:2339:MSE:CE	2.41	0.51
1:C:2353:PRO:HA	1:C:2361:THR:HA	1.90	0.51
1:A:25:LEU:O	1:A:25:LEU:HD22	2.10	0.51
1:C:2129:TYR:CE2	1:C:2133:VAL:HG21	2.46	0.51
1:B:1142:ARG:H	1:B:1145:GLN:NE2	2.08	0.51
1:C:2090:ASN:C	1:C:2090:ASN:ND2	2.64	0.51
1:A:40:ARG:HD2	1:A:260:THR:O	2.11	0.51
1:A:39:ILE:CG2	1:A:339:MSE:HE3	2.41	0.51
1:B:1090:ASN:ND2	1:B:1092:ASN:H	2.09	0.50
1:B:1369:PHE:CD2	1:B:1373:LEU:CD2	2.94	0.50
1:B:1068:ASP:HB3	1:B:1377:LYS:HE3	1.93	0.50
1:A:166:THR:HG22	1:A:168:SER:O	2.12	0.50
1:A:129:TYR:O	1:A:133:VAL:HG23	2.12	0.50
1:C:2244:SER:HB3	2:C:3340:HOH:O	2.10	0.50
1:A:168:SER:O	1:A:169:ASN:CB	2.59	0.50
1:B:1103:VAL:HB	1:B:1104:PRO:HD3	1.92	0.50
1:B:1369:PHE:HD2	1:B:1373:LEU:CD2	2.24	0.50
1:A:382:ASN:ND2	1:A:383:LYS:H	2.10	0.50
1:A:129:TYR:CE2	1:A:133:VAL:HG21	2.47	0.49
1:B:1025:LEU:HD22	1:B:1376:ARG:HB2	1.93	0.49
1:B:1166:THR:HG23	1:B:1168:SER:N	2.27	0.49
1:A:261:GLY:HA2	1:A:321:GLU:O	2.13	0.49
1:C:2261:GLY:HA2	1:C:2321:GLU:O	2.12	0.49
1:B:1078:THR:HA	1:B:1081:LEU:HG	1.94	0.49
1:B:1201:THR:CG2	1:B:1202:ASN:N	2.76	0.49
1:B:1269:THR:HG22	2:B:3047:HOH:O	2.12	0.49
1:B:1380:ARG:HG2	1:B:1380:ARG:HH11	1.78	0.48
1:A:101:GLU:O	1:A:104:PRO:HD2	2.13	0.48
1:A:90:ASN:ND2	1:A:90:ASN:C	2.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1350:LEU:O	1:B:1363:GLU:HB2	2.13	0.48
1:B:1283:TRP:CZ3	1:B:1290:MSE:HE1	2.48	0.48
1:B:1320:GLN:CA	1:B:1320:GLN:HE21	2.26	0.48
1:A:185:TYR:OH	1:A:195:PRO:HD2	2.13	0.48
1:B:1355:SER:OG	1:B:1356:GLU:N	2.46	0.48
1:A:90:ASN:ND2	1:A:92:ASN:H	2.12	0.48
1:C:2185:TYR:OH	1:C:2195:PRO:HD2	2.14	0.48
1:A:175:GLU:HA	1:A:201:THR:CG2	2.43	0.48
1:C:2250:TYR:HB2	1:C:2310:LEU:CD1	2.43	0.48
1:C:2090:ASN:ND2	1:C:2092:ASN:H	2.12	0.48
1:A:379:LEU:HD23	1:A:379:LEU:N	2.29	0.47
1:A:132:GLN:NE2	2:A:4099:HOH:O	2.46	0.47
1:A:320:GLN:HE21	1:A:320:GLN:HA	1.79	0.47
1:B:1261:GLY:HA2	1:B:1321:GLU:O	2.14	0.47
1:C:2129:TYR:O	1:C:2133:VAL:HG23	2.14	0.47
1:A:166:THR:CG2	1:A:168:SER:O	2.63	0.47
1:A:197:HIS:HD1	1:A:199:PHE:HD2	1.62	0.47
1:B:1085:MSE:HE3	1:B:1102:ILE:HD12	1.94	0.47
1:C:2025:LEU:HA	1:C:2028:MSE:HE3	1.95	0.47
1:A:375:ASP:O	1:A:379:LEU:HG	2.15	0.47
1:C:2036:GLY:CA	1:C:2077:SER:HB3	2.45	0.47
1:C:2243:ALA:O	1:C:2244:SER:HB3	2.13	0.47
1:B:1061:ASN:OD1	1:B:1063:ASP:HB2	2.15	0.47
1:A:37:GLY:O	1:A:40:ARG:HB2	2.14	0.47
1:B:1379:LEU:CD2	1:B:1379:LEU:N	2.77	0.47
1:C:2173:SER:HA	1:C:2175:GLU:OE2	2.15	0.47
1:C:2320:GLN:HE21	1:C:2321:GLU:N	2.11	0.47
1:C:2237:GLN:HA	1:C:2246:ARG:HE	1.80	0.47
1:A:175:GLU:HA	1:A:201:THR:HG23	1.96	0.47
1:B:1361:THR:OG1	1:B:1364:GLU:CG	2.64	0.46
1:A:205:ASN:HD21	1:A:207:ASP:HB2	1.78	0.46
1:A:108:GLU:HG2	1:A:109:HIS:CD2	2.50	0.46
1:A:197:HIS:ND1	1:A:199:PHE:HD2	2.13	0.46
1:B:1205:ASN:HD21	1:B:1207:ASP:HB2	1.80	0.46
1:C:2065:ARG:CB	1:C:2095:PRO:HG2	2.44	0.46
1:A:167:LYS:O	1:A:167:LYS:HG2	2.14	0.46
1:A:203:THR:OG1	1:A:205:ASN:ND2	2.49	0.46
1:A:31:VAL:HG22	1:A:72:VAL:HB	1.97	0.46
1:A:175:GLU:CG	1:A:203:THR:HG22	2.44	0.46
1:A:229:ILE:HD12	1:A:303:LEU:CD2	2.46	0.46
1:C:2112:GLN:HB2	1:C:2129:TYR:CE2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:GLN:HE22	1:A:122:GLY:HA3	1.81	0.46
1:B:1082:LEU:C	1:B:1082:LEU:HD12	2.36	0.46
1:B:1382:ASN:ND2	1:B:1382:ASN:N	2.64	0.46
1:C:2175:GLU:HA	1:C:2201:THR:HG23	1.96	0.46
1:A:112:GLN:HB2	1:A:129:TYR:CE2	2.51	0.46
1:B:1148:THR:O	1:B:1167:LYS:HD3	2.16	0.46
1:C:2039:ILE:HD11	1:C:2330:GLU:O	2.16	0.46
1:A:202:ASN:ND2	1:A:206:GLY:O	2.48	0.45
1:B:1279:THR:H	1:B:1282:HIS:CD2	2.34	0.45
1:C:2175:GLU:HA	1:C:2201:THR:CG2	2.46	0.45
1:A:39:ILE:H	1:A:39:ILE:HG13	1.48	0.45
1:B:1175:GLU:HA	1:B:1201:THR:HG23	1.98	0.45
1:C:2101:GLU:O	1:C:2104:PRO:HD2	2.16	0.45
1:A:106:TYR:HB3	1:A:339:MSE:CE	2.46	0.45
1:A:250:TYR:HB2	1:A:310:LEU:CD1	2.47	0.45
1:A:320:GLN:HE21	1:A:321:GLU:N	2.12	0.45
1:B:1229:ILE:HA	1:B:1229:ILE:HD12	1.75	0.45
1:C:2182:ASP:OD1	1:C:2197:HIS:HE1	2.00	0.45
1:B:1283:TRP:HZ3	1:B:1290:MSE:HE1	1.81	0.45
1:A:237:GLN:HA	1:A:246:ARG:HE	1.82	0.45
1:A:61:ASN:OD1	1:A:63:ASP:HB2	2.16	0.45
1:A:82:LEU:O	1:A:82:LEU:HD12	2.16	0.45
1:B:1250:TYR:HB2	1:B:1310:LEU:CD1	2.44	0.45
1:A:156:ASP:HA	1:A:212:ASN:O	2.17	0.44
1:A:173:SER:HA	1:A:175:GLU:OE2	2.17	0.44
1:B:1175:GLU:CG	1:B:1203:THR:HG22	2.46	0.44
1:B:1341:LEU:O	1:B:1345:VAL:HG12	2.17	0.44
1:A:201:THR:CG2	1:A:202:ASN:N	2.74	0.44
1:A:243:ALA:O	1:A:244:SER:HB3	2.16	0.44
1:B:1237:GLN:HA	1:B:1246:ARG:HE	1.82	0.44
1:C:2042:ILE:HD11	1:C:2339:MSE:HE2	2.00	0.44
1:B:1320:GLN:NE2	1:B:1321:GLU:H	2.12	0.44
1:B:1040:ARG:HD2	1:B:1260:THR:O	2.18	0.44
1:C:2324:LEU:HB3	1:C:2328:THR:HG22	1.99	0.44
1:A:325:THR:O	1:A:328:THR:HB	2.17	0.44
1:B:1220:THR:O	1:B:1220:THR:HG22	2.18	0.44
1:A:36:GLY:CA	1:A:77:SER:HB3	2.47	0.44
1:B:1279:THR:H	1:B:1282:HIS:HD2	1.66	0.44
1:B:1369:PHE:CE2	1:B:1373:LEU:HD21	2.53	0.44
1:C:2203:THR:OG1	1:C:2207:ASP:HB2	2.17	0.44
1:C:2156:ASP:HA	1:C:2212:ASN:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:GLU:CA	1:A:201:THR:HG21	2.47	0.43
1:A:382:ASN:ND2	1:A:383:LYS:HG2	2.32	0.43
1:A:78:THR:HA	1:A:81:LEU:HG	1.99	0.43
1:A:205:ASN:HD22	1:A:205:ASN:C	2.21	0.43
1:B:1342:LEU:O	1:B:1345:VAL:HG13	2.17	0.43
1:B:1173:SER:HA	1:B:1175:GLU:OE2	2.17	0.43
1:A:134:LEU:O	1:A:138:LEU:HD22	2.18	0.43
1:B:1096:PHE:CZ	1:B:1137:LYS:HG2	2.54	0.43
1:B:1286:VAL:HG23	1:B:1290:MSE:CE	2.38	0.43
1:B:1203:THR:OG1	1:B:1207:ASP:HB2	2.18	0.43
1:B:1205:ASN:HD22	1:B:1205:ASN:C	2.21	0.43
1:C:2327:THR:OG1	1:C:2338:ASN:ND2	2.51	0.43
1:C:2023:ALA:HB1	2:C:3390:HOH:O	2.17	0.43
1:C:2203:THR:OG1	1:C:2205:ASN:ND2	2.52	0.43
1:B:1243:ALA:O	1:B:1244:SER:HB3	2.19	0.43
1:C:2265:GLU:HG2	2:C:3668:HOH:O	2.19	0.43
1:C:2197:HIS:HD2	2:C:4048:HOH:O	2.02	0.42
1:A:341:LEU:O	1:A:345:VAL:HG12	2.19	0.42
1:C:2037:GLY:O	1:C:2040:ARG:HB2	2.19	0.42
1:C:2082:LEU:HD12	1:C:2082:LEU:C	2.39	0.42
1:C:2308:GLN:HG2	2:C:3666:HOH:O	2.19	0.42
1:B:1031:VAL:HG22	1:B:1072:VAL:HB	2.02	0.42
1:B:1175:GLU:HA	1:B:1201:THR:CG2	2.49	0.42
1:A:170:LEU:HG	1:A:170:LEU:H	1.72	0.42
1:B:1320:GLN:HA	1:B:1320:GLN:NE2	2.33	0.42
1:A:336:GLU:O	1:A:340:GLU:HG3	2.20	0.42
1:A:82:LEU:C	1:A:82:LEU:HD12	2.40	0.42
1:C:2320:GLN:HE21	1:C:2320:GLN:CA	2.33	0.42
1:C:2049:GLU:HG3	1:C:2100:LYS:CA	2.46	0.42
1:A:342:LEU:HA	1:A:345:VAL:CG1	2.50	0.42
1:B:1355:SER:O	1:B:1356:GLU:C	2.58	0.42
1:C:2175:GLU:CD	1:C:2175:GLU:H	2.22	0.42
1:A:103:VAL:N	1:A:104:PRO:CD	2.82	0.42
1:A:361:THR:OG1	1:A:364:GLU:CG	2.67	0.42
1:B:1156:ASP:HA	1:B:1212:ASN:O	2.19	0.42
1:A:96:PHE:CZ	1:A:137:LYS:HG3	2.54	0.41
1:C:2324:LEU:HD22	1:C:2328:THR:HG22	2.01	0.41
1:A:119:GLN:NE2	1:A:121:LEU:C	2.73	0.41
1:A:229:ILE:HD12	1:A:303:LEU:HD21	2.02	0.41
1:C:2336:GLU:OE1	1:C:2340:GLU:OE2	2.38	0.41
1:A:203:THR:OG1	1:A:207:ASP:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1182:ASP:OD1	1:B:1197:HIS:HE1	2.02	0.41
1:C:2254:LEU:HA	1:C:2254:LEU:HD12	1.96	0.41
1:C:2342:LEU:HA	1:C:2345:VAL:CG1	2.51	0.41
1:B:1168:SER:O	1:B:1170:LEU:HG	2.21	0.41
1:B:1267:ASP:OD1	1:B:1268:LYS:NZ	2.50	0.41
1:B:1342:LEU:HA	1:B:1345:VAL:CG1	2.50	0.41
1:B:1381:ALA:HB1	1:B:1382:ASN:ND2	2.35	0.41
1:C:2205:ASN:C	1:C:2205:ASN:HD22	2.24	0.41
1:B:1170:LEU:HD21	2:B:3291:HOH:O	2.20	0.41
1:C:2039:ILE:H	1:C:2039:ILE:HG13	1.40	0.41
1:C:2320:GLN:NE2	1:C:2321:GLU:H	2.15	0.41
1:C:2358:ASN:HD22	1:C:2358:ASN:C	2.25	0.41
1:B:1357:ASP:O	1:B:1359:PRO:CD	2.67	0.40
1:C:2341:LEU:O	1:C:2345:VAL:HG12	2.21	0.40
1:B:1239:ASP:HA	1:B:1240:PRO:HD2	1.90	0.40
1:B:1380:ARG:HG2	1:B:1380:ARG:NH1	2.35	0.40
1:C:2048:LEU:HA	1:C:2048:LEU:HD23	1.91	0.40
1:C:2190:ALA:HA	1:C:2215:ASP:HB2	2.03	0.40
1:A:328:THR:HA	1:A:338:ASN:HD21	1.87	0.40
1:B:1190:ALA:HA	1:B:1215:ASP:HB2	2.03	0.40
1:B:1040:ARG:HB3	1:B:1260:THR:HB	2.02	0.40
1:C:2175:GLU:CA	1:C:2201:THR:HG21	2.51	0.40
1:C:2200:VAL:CG1	1:C:2201:THR:N	2.84	0.40
1:C:2158:LYS:HZ2	1:C:2212:ASN:ND2	2.16	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	358/373 (96%)	337 (94%)	15 (4%)	6 (2%)	<b>9</b> <b>6</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	357/373 (96%)	335 (94%)	19 (5%)	3 (1%)	19	19
1	C	360/373 (96%)	340 (94%)	18 (5%)	2 (1%)	25	26
All	All	1075/1119 (96%)	1012 (94%)	52 (5%)	11 (1%)	15	14

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	244	SER
1	A	358	ASN
1	B	1244	SER
1	B	1356	GLU
1	C	2244	SER
1	A	120	ILE
1	A	169	ASN
1	A	359	PRO
1	B	1380	ARG
1	C	2037	GLY
1	A	37	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	302/300 (101%)	265 (88%)	37 (12%)	4	4
1	B	302/300 (101%)	271 (90%)	31 (10%)	7	6
1	C	304/300 (101%)	278 (91%)	26 (9%)	10	10
All	All	908/900 (101%)	814 (90%)	94 (10%)	7	6

All (94) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	ILE
1	A	82	LEU
1	A	85	MSE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	87	SER
1	A	90	ASN
1	A	108	GLU
1	A	119	GLN
1	A	120	ILE
1	A	137	LYS
1	A	138	LEU
1	A	142	ARG
1	A	166	THR
1	A	169	ASN
1	A	201	THR
1	A	205	ASN
1	A	210	GLU
1	A	238	LYS
1	A	244	SER
1	A	246	ARG
1	A	252	LYS
1	A	264	SER
1	A	265	GLU
1	A	269	THR
1	A	320	GLN
1	A	328	THR
1	A	345	VAL
1	A	347	GLU
1	A	350	LEU
1	A	351	LYS
1	A	355	SER
1	A	356	GLU
1	A	358	ASN
1	A	364	GLU
1	A	367	LYS
1	A	379	LEU
1	A	380	ARG
1	A	382	ASN
1	B	1024	GLN
1	B	1025	LEU
1	B	1027	GLU
1	B	1082	LEU
1	B	1090	ASN
1	B	1100	LYS
1	B	1108	GLU
1	B	1137	LYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	B	1166	THR
1	B	1169	ASN
1	B	1201	THR
1	B	1205	ASN
1	B	1229	ILE
1	B	1238	LYS
1	B	1244	SER
1	B	1252	LYS
1	B	1265	GLU
1	B	1269	THR
1	B	1317	LEU
1	B	1320	GLN
1	B	1345	VAL
1	B	1350	LEU
1	B	1351	LYS
1	B	1355	SER
1	B	1356	GLU
1	B	1358	ASN
1	B	1364	GLU
1	B	1373	LEU
1	B	1379	LEU
1	B	1380	ARG
1	B	1382	ASN
1	C	2039	ILE
1	C	2082	LEU
1	C	2090	ASN
1	C	2100	LYS
1	C	2108	GLU
1	C	2136	GLU
1	C	2137	LYS
1	C	2138	LEU
1	C	2166	THR
1	C	2167	LYS
1	C	2201	THR
1	C	2205	ASN
1	C	2238	LYS
1	C	2244	SER
1	C	2252	LYS
1	C	2265	GLU
1	C	2269	THR
1	C	2274	GLU
1	C	2320	GLN

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Mol	Chain	Res	Type
1	C	2332	ASP
1	C	2345	VAL
1	C	2350	LEU
1	C	2357	ASP
1	C	2358	ASN
1	C	2364	GLU
1	C	2380	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	90	ASN
1	A	112	GLN
1	A	119	GLN
1	A	132	GLN
1	A	145	GLN
1	A	169	ASN
1	A	205	ASN
1	A	320	GLN
1	A	338	ASN
1	A	358	ASN
1	A	382	ASN
1	B	1024	GLN
1	B	1090	ASN
1	B	1112	GLN
1	B	1145	GLN
1	B	1169	ASN
1	B	1197	HIS
1	B	1202	ASN
1	B	1205	ASN
1	B	1282	HIS
1	B	1320	GLN
1	B	1338	ASN
1	B	1348	ASN
1	B	1358	ASN
1	B	1382	ASN
1	C	2090	ASN
1	C	2112	GLN
1	C	2119	GLN
1	C	2145	GLN
1	C	2197	HIS
1	C	2205	ASN

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Mol	Chain	Res	Type
1	C	2212	ASN
1	C	2320	GLN
1	C	2338	ASN
1	C	2358	ASN
1	C	2382	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 carbohydrates 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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.