



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 12:04 AM UTC

PDB ID : 1GHD / pdb_00001ghd
Title : Crystal structure of the glutaryl-7-aminocephalosporanic acid acylase by mad phasing
Authors : Ding, Y.; Jiang, W.; Mao, X.; He, H.; Zhang, S.; Tang, H.; Bartlam, M.; Ye, S.; Jiang, F.; Liu, Y.; Zhao, G.; Rao, Z.
Deposited on : 2000-12-07
Resolution : 2.40 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

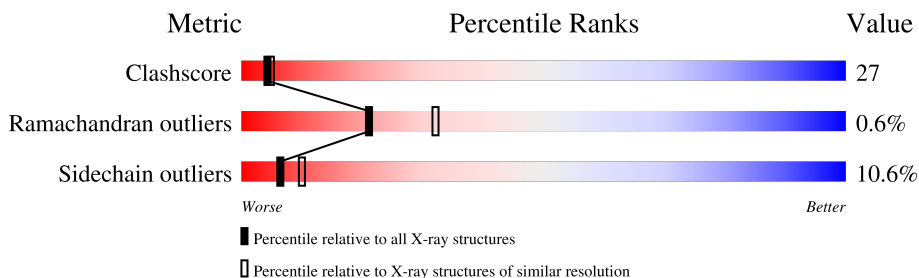
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	171	
2	B	522	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5504 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 GLUTARYL-7-AMINOCEPHALOSPORANIC ACID ACYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	153	Total	C	N	O	Se	0	0	0
			1201	764	212	224	1			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	147	MSE	MET	modified residue	UNP O86089

- Molecule 2 is a protein called GLUTARYL-7-AMINOCEPHALOSPORANIC ACID ACYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	520	Total	C	N	O	Se	0	0	0
			4105	2595	724	775	11			

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	64	MSE	MET	modified residue	UNP O86089
B	73	MSE	MET	modified residue	UNP O86089
B	149	MSE	MET	modified residue	UNP O86089
B	156	MSE	MET	modified residue	UNP O86089
B	172	MSE	MET	modified residue	UNP O86089
B	282	MSE	MET	modified residue	UNP O86089
B	294	MSE	MET	modified residue	UNP O86089
B	304	MSE	MET	modified residue	UNP O86089
B	416	MSE	MET	modified residue	UNP O86089
B	460	MSE	MET	modified residue	UNP O86089
B	473	MSE	MET	modified residue	UNP O86089

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	47	Total 47	O 47	0	0
3	B	151	Total 151	O 151	0	0

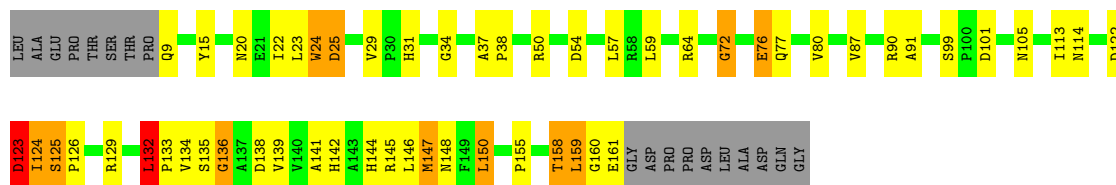
3 Residue-property plots

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. 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.

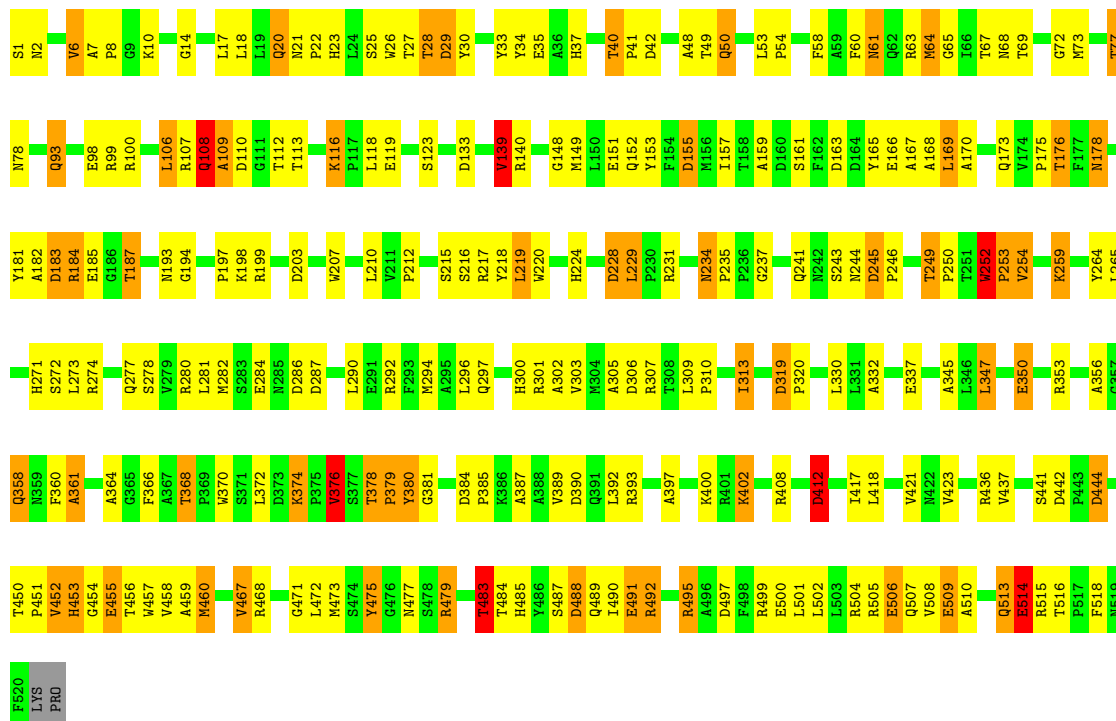
• Molecule 1: GLUTARYL-7-AMINOCEPHALOSPORANIC ACID ACYLASE

Chain A: 



• Molecule 2: GLUTARYL-7-AMINOCEPHALOSPORANIC ACID ACYLASE

Chain B: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	73.48Å 73.48Å 382.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.40	Depositor
% Data completeness (in resolution range)	97.8 (30.00-2.40)	Depositor
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.218 , 0.265	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5504	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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	1.07	6/1239 (0.5%)	1.44	23/1694 (1.4%)
2	B	1.04	15/4208 (0.4%)	1.51	79/5727 (1.4%)
All	All	1.05	21/5447 (0.4%)	1.49	102/7421 (1.4%)

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	123	ASP	CA-C	10.13	1.66	1.52
2	B	514	GLU	CG-CD	9.54	1.75	1.52
2	B	514	GLU	CB-CG	9.53	1.81	1.52
1	A	123	ASP	CB-CG	9.31	1.75	1.52
1	A	123	ASP	CA-CB	9.02	1.68	1.53
2	B	514	GLU	CA-CB	8.91	1.68	1.53
1	A	124	ILE	N-CA	7.87	1.56	1.46
2	B	514	GLU	CA-C	7.86	1.63	1.52
2	B	203	ASP	CA-CB	7.46	1.65	1.53
2	B	203	ASP	CG-OD2	6.80	1.38	1.25
2	B	509	GLU	CB-CG	6.56	1.72	1.52
2	B	509	GLU	CG-CD	6.28	1.67	1.52
2	B	509	GLU	CA-CB	6.12	1.63	1.53
2	B	234	ASN	C-O	-5.80	1.21	1.23
2	B	249	THR	CA-CB	5.78	1.60	1.53
2	B	246	PRO	CA-C	5.68	1.57	1.52
1	A	87	VAL	CA-CB	5.63	1.57	1.54
1	A	124	ILE	CA-C	5.52	1.59	1.52
2	B	515	ARG	N-CA	5.31	1.53	1.46
2	B	467	VAL	CA-CB	5.22	1.59	1.54
2	B	488	ASP	CB-CG	-5.22	1.39	1.52

All (102) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	378	THR	CA-C-N	-16.24	100.26	120.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	378	THR	C-N-CA	-16.24	100.26	120.23
2	B	252	TRP	CA-C-N	-15.60	100.33	119.84
2	B	252	TRP	C-N-CA	-15.60	100.33	119.84
1	A	132	LEU	CA-C-N	-12.98	103.62	119.84
1	A	132	LEU	C-N-CA	-12.98	103.62	119.84
2	B	361	ALA	N-CA-C	-12.02	93.76	110.35
1	A	125	SER	N-CA-C	11.39	125.88	109.48
2	B	514	GLU	OE1-CD-OE2	-10.52	97.66	122.90
1	A	123	ASP	OD1-CG-OD2	-9.95	99.02	122.90
2	B	487	SER	CA-C-N	9.62	133.56	120.38
2	B	487	SER	C-N-CA	9.62	133.56	120.38
2	B	364	ALA	N-CA-C	-9.50	97.43	110.35
2	B	175	PRO	N-CA-C	9.17	125.31	114.03
2	B	253	PRO	N-CA-C	-9.01	93.91	112.47
2	B	514	GLU	CB-CG-CD	8.52	127.08	112.60
2	B	29	ASP	N-CA-C	8.41	120.07	111.07
1	A	132	LEU	N-CA-C	8.41	128.39	109.81
2	B	178	ASN	N-CA-C	-8.34	95.95	109.96
2	B	488	ASP	N-CA-C	8.29	121.36	111.33
2	B	513	GLN	N-CA-C	-8.21	95.80	108.76
1	A	64	ARG	N-CA-C	-8.16	103.05	113.16
2	B	184	ARG	N-CA-C	-8.10	103.29	113.01
2	B	379	PRO	N-CA-C	-7.91	98.08	110.50
2	B	319	ASP	CA-C-N	7.73	127.27	118.85
2	B	319	ASP	C-N-CA	7.73	127.27	118.85
2	B	123	SER	N-CA-C	-7.58	98.72	110.17
2	B	139	VAL	CB-CA-C	-7.42	100.81	110.98
1	A	124	ILE	CB-CA-C	-7.33	99.26	111.29
2	B	313	ILE	CA-C-N	-7.31	111.24	119.28
2	B	313	ILE	C-N-CA	-7.31	111.24	119.28
2	B	477	ASN	N-CA-C	7.26	120.99	112.72
2	B	330	LEU	N-CA-C	-7.17	103.54	111.36
2	B	305	ALA	N-CA-C	-7.16	102.89	111.69
2	B	216	SER	N-CA-C	-7.13	104.70	113.19
2	B	500	GLU	N-CA-C	-6.95	100.71	110.50
2	B	378	THR	N-CA-C	6.92	125.09	109.81
1	A	113	ILE	N-CA-C	-6.88	103.81	110.42
1	A	72	GLY	CA-C-N	6.83	128.38	119.84
1	A	72	GLY	C-N-CA	6.83	128.38	119.84
2	B	484	THR	N-CA-C	-6.72	104.95	113.02
2	B	183	ASP	CB-CA-C	-6.64	96.25	109.33
2	B	108	GLN	N-CA-C	6.58	121.60	112.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	510	ALA	N-CA-C	6.57	121.03	112.89
2	B	98	GLU	N-CA-C	-6.56	99.33	109.76
2	B	374	LYS	CA-C-N	6.49	126.18	119.56
2	B	374	LYS	C-N-CA	6.49	126.18	119.56
2	B	390	ASP	N-CA-C	-6.46	104.33	111.82
1	A	54	ASP	N-CA-C	6.42	118.82	111.11
1	A	123	ASP	CB-CG-OD2	6.31	132.92	118.40
2	B	483	THR	CB-CA-C	-6.30	96.77	109.68
2	B	100	ARG	N-CA-C	-6.30	99.64	109.72
1	A	76	GLU	N-CA-C	6.29	118.14	111.28
2	B	514	GLU	CG-CD-OE1	6.24	132.75	118.40
1	A	123	ASP	CA-CB-CG	6.13	118.73	112.60
2	B	412	ASP	N-CA-C	-6.12	105.97	113.50
2	B	368	THR	CA-C-N	6.05	126.02	120.21
2	B	368	THR	C-N-CA	6.05	126.02	120.21
2	B	110	ASP	N-CA-C	-6.03	105.10	112.88
1	A	123	ASP	N-CA-C	-6.02	97.97	110.80
2	B	514	GLU	N-CA-C	-6.01	98.00	110.80
2	B	319	ASP	N-CA-C	-6.00	102.51	110.07
2	B	167	ALA	N-CA-C	-5.96	104.71	111.14
2	B	397	ALA	N-CA-C	-5.93	104.72	111.07
2	B	313	ILE	N-CA-C	5.90	120.04	112.67
2	B	436	ARG	N-CA-C	-5.87	99.62	108.96
2	B	265	LEU	N-CA-C	5.86	117.34	111.07
2	B	437	VAL	N-CA-C	5.86	117.03	108.53
2	B	203	ASP	N-CA-C	-5.81	102.86	110.53
2	B	228	ASP	N-CA-C	-5.67	106.40	113.38
2	B	170	ALA	N-CA-C	5.64	119.67	112.34
2	B	380	TYR	N-CA-C	5.58	117.76	108.99
1	A	136	GLY	N-CA-C	-5.58	106.02	112.83
2	B	444	ASP	N-CA-C	-5.46	101.40	109.86
1	A	72	GLY	N-CA-C	5.44	123.44	112.34
2	B	450	THR	CA-C-N	-5.44	112.47	120.46
2	B	450	THR	C-N-CA	-5.44	112.47	120.46
2	B	155	ASP	N-CA-C	-5.36	105.60	111.82
2	B	235	PRO	N-CA-C	5.36	117.23	110.70
2	B	229	LEU	N-CA-C	5.35	117.34	110.39
2	B	376	VAL	N-CA-CB	-5.33	105.02	111.94
2	B	402	LYS	N-CA-C	5.32	117.08	111.28
2	B	345	ALA	N-CA-C	5.32	117.49	111.11
1	A	105	ASN	N-CA-C	-5.30	105.58	111.36
2	B	246	PRO	N-CA-C	-5.29	104.24	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	182	ALA	CA-C-N	5.28	131.11	122.81
2	B	182	ALA	C-N-CA	5.28	131.11	122.81
1	A	147	MSE	N-CA-C	5.26	116.71	110.97
2	B	495	ARG	NE-CZ-NH1	-5.25	116.25	121.50
2	B	374	LYS	N-CA-C	-5.23	101.50	109.30
2	B	483	THR	N-CA-CB	5.22	117.83	110.36
2	B	148	GLY	N-CA-C	5.18	125.46	113.18
2	B	20	GLN	N-CA-C	-5.17	100.09	108.52
1	A	124	ILE	N-CA-C	5.15	120.06	109.34
2	B	203	ASP	CB-CA-C	5.08	120.09	109.68
1	A	24	TRP	CA-C-N	5.07	130.12	121.29
1	A	24	TRP	C-N-CA	5.07	130.12	121.29
2	B	442	ASP	N-CA-C	-5.07	102.90	110.20
1	A	150	LEU	N-CA-C	-5.06	100.02	110.80
2	B	501	LEU	N-CA-C	-5.05	101.01	109.24
2	B	516	THR	N-CA-C	5.04	119.62	108.73
2	B	273	LEU	N-CA-C	-5.01	106.01	111.82

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	1201	0	1118	52	0
2	B	4105	0	3936	241	0
3	A	47	0	0	2	0
3	B	151	0	0	8	0
All	All	5504	0	5054	280	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 (280) 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)
2:B:514:GLU:CD	2:B:514:GLU:CG	1.75	1.59
1:A:123:ASP:CB	1:A:123:ASP:CG	1.75	1.56
2:B:514:GLU:CG	2:B:514:GLU:CB	1.81	1.54
2:B:485:HIS:HE1	2:B:514:GLU:OE1	1.30	1.13
2:B:63:ARG:NH2	2:B:64:MSE:HE3	1.69	1.06
2:B:353:ARG:HD3	2:B:358:GLN:HE22	1.28	0.98
2:B:63:ARG:HH22	2:B:64:MSE:HE3	1.24	0.94
2:B:77:THR:HG21	2:B:220:TRP:HE1	1.34	0.93
2:B:485:HIS:CE1	2:B:514:GLU:OE1	2.22	0.92
2:B:244:ASN:HD22	2:B:274:ARG:HH22	0.93	0.92
2:B:20:GLN:HG2	2:B:67:THR:OG1	1.69	0.91
2:B:491:GLU:OE2	2:B:495:ARG:NH1	2.03	0.90
2:B:241:GLN:HG3	2:B:278:SER:OG	1.72	0.89
2:B:152:GLN:HE22	2:B:173:GLN:H	1.20	0.88
2:B:73:MSE:HB3	2:B:176:THR:HG22	1.56	0.87
2:B:152:GLN:NE2	2:B:173:GLN:H	1.73	0.85
2:B:77:THR:CG2	2:B:220:TRP:HE1	1.89	0.85
1:A:37:ALA:HB3	1:A:38:PRO:HD3	1.59	0.84
2:B:483:THR:HB	2:B:485:HIS:H	1.43	0.83
1:A:155:PRO:O	1:A:159:LEU:HB2	1.79	0.83
2:B:64:MSE:CE	2:B:159:ALA:HB3	2.09	0.83
2:B:64:MSE:HE1	2:B:159:ALA:HB3	1.61	0.83
1:A:158:THR:HB	2:B:78:ASN:OD1	1.79	0.82
2:B:244:ASN:ND2	2:B:274:ARG:HH22	1.77	0.80
2:B:307:ARG:NH1	2:B:379:PRO:HD2	1.96	0.80
1:A:144:HIS:HD2	1:A:148:ASN:HD22	1.27	0.78
2:B:307:ARG:HH12	2:B:379:PRO:HD2	1.45	0.78
2:B:50:GLN:HG2	2:B:53:LEU:HD12	1.65	0.78
2:B:479:ARG:HD3	3:B:537:HOH:O	1.82	0.77
2:B:50:GLN:HG2	2:B:53:LEU:CD1	2.14	0.77
2:B:58:PHE:HD2	2:B:67:THR:HG23	1.50	0.76
2:B:423:VAL:HG11	2:B:491:GLU:HB2	1.68	0.75
2:B:374:LYS:HB2	2:B:378:THR:HG23	1.69	0.75
2:B:21:ASN:ND2	2:B:297:GLN:HE21	1.85	0.74
1:A:114:ASN:HD21	1:A:134:VAL:H	1.34	0.74
2:B:229:LEU:O	2:B:231:ARG:HG3	1.88	0.74
2:B:183:ASP:HB3	2:B:185:GLU:H	1.52	0.73
2:B:106:LEU:HD12	2:B:116:LYS:HE3	1.71	0.73
1:A:147:MSE:SE	2:B:149:MSE:HE3	2.39	0.73
2:B:73:MSE:HE3	2:B:73:MSE:HA	1.70	0.73
2:B:374:LYS:HB2	2:B:378:THR:CG2	2.18	0.72
2:B:252:TRP:O	2:B:254:VAL:N	2.21	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:292:ARG:HG2	2:B:292:ARG:HH11	1.55	0.71
2:B:149:MSE:HE2	2:B:153:TYR:CE1	2.26	0.71
2:B:313:ILE:HD13	2:B:332:ALA:HB2	1.74	0.70
2:B:259:LYS:HE3	2:B:259:LYS:H	1.54	0.70
1:A:122:ASP:C	1:A:124:ILE:H	1.99	0.70
2:B:33:TYR:HB3	2:B:473:MSE:HE1	1.74	0.69
2:B:1:SER:HB2	2:B:23:HIS:CG	2.27	0.69
2:B:58:PHE:CD2	2:B:67:THR:HG23	2.27	0.69
2:B:64:MSE:HE2	2:B:181:TYR:HE1	1.58	0.69
1:A:144:HIS:HD2	1:A:148:ASN:ND2	1.91	0.69
2:B:33:TYR:CB	2:B:473:MSE:HE1	2.23	0.68
2:B:384:ASP:OD1	2:B:387:ALA:HB2	1.93	0.68
2:B:73:MSE:HB3	2:B:176:THR:CG2	2.23	0.67
2:B:64:MSE:HE2	2:B:181:TYR:CE1	2.29	0.67
2:B:108:GLN:O	2:B:109:ALA:CB	2.42	0.67
2:B:241:GLN:CG	2:B:278:SER:OG	2.42	0.67
2:B:244:ASN:HD22	2:B:274:ARG:NH2	1.79	0.67
2:B:224:HIS:HE1	2:B:264:TYR:OH	1.78	0.66
2:B:252:TRP:O	2:B:253:PRO:C	2.35	0.66
1:A:132:LEU:O	1:A:134:VAL:N	2.28	0.65
2:B:21:ASN:HD21	2:B:297:GLN:HE21	1.45	0.65
1:A:132:LEU:O	1:A:132:LEU:HD12	1.97	0.65
2:B:20:GLN:HA	2:B:67:THR:HG21	1.78	0.65
2:B:301:ARG:HG3	2:B:302:ALA:N	2.12	0.65
1:A:146:LEU:HD21	2:B:50:GLN:HG3	1.79	0.64
2:B:301:ARG:HD3	2:B:306:ASP:OD2	1.98	0.64
2:B:106:LEU:HD12	2:B:116:LYS:CE	2.27	0.64
1:A:91:ALA:CB	1:A:141:ALA:HB2	2.28	0.64
2:B:1:SER:CB	2:B:244:ASN:HD21	2.11	0.63
2:B:259:LYS:HE3	2:B:259:LYS:N	2.14	0.63
2:B:378:THR:O	2:B:379:PRO:C	2.36	0.63
1:A:142:HIS:HE1	3:B:567:HOH:O	1.81	0.63
2:B:1:SER:H3	2:B:22:PRO:HA	1.64	0.63
2:B:40:THR:HG22	2:B:42:ASP:H	1.63	0.63
1:A:77:GLN:NE2	1:A:77:GLN:HA	2.15	0.62
2:B:20:GLN:HG2	2:B:67:THR:HG1	1.63	0.62
1:A:20:ASN:HB3	2:B:518:PHE:CZ	2.35	0.62
2:B:455:GLU:HG3	2:B:458:VAL:HG21	1.81	0.61
2:B:61:ASN:ND2	2:B:64:MSE:H	1.98	0.61
2:B:108:GLN:HB2	2:B:112:THR:O	2.00	0.61
2:B:40:THR:HG23	2:B:41:PRO:HD2	1.80	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:485:HIS:HD2	2:B:488:ASP:OD2	1.83	0.61
2:B:1:SER:HB2	2:B:23:HIS:ND1	2.16	0.60
2:B:271:HIS:HD2	3:B:526:HOH:O	1.84	0.60
2:B:197:PRO:HB3	2:B:220:TRP:CD2	2.37	0.60
2:B:224:HIS:HD2	2:B:228:ASP:OD2	1.85	0.59
2:B:224:HIS:CE1	2:B:264:TYR:OH	2.55	0.59
2:B:67:THR:CG2	3:B:664:HOH:O	2.50	0.59
2:B:199:ARG:HD2	2:B:207:TRP:CE2	2.38	0.59
2:B:152:GLN:HE22	2:B:173:GLN:N	1.96	0.59
2:B:513:GLN:O	2:B:514:GLU:O	2.21	0.59
2:B:166:GLU:OE2	2:B:231:ARG:NH2	2.31	0.58
2:B:108:GLN:O	2:B:109:ALA:HB2	2.04	0.58
1:A:90:ARG:HH21	1:A:144:HIS:CE1	2.21	0.58
2:B:25:SER:CB	2:B:28:THR:HG23	2.33	0.58
2:B:67:THR:HG22	2:B:68:ASN:N	2.18	0.58
2:B:149:MSE:HE2	2:B:153:TYR:HE1	1.67	0.58
2:B:6:VAL:HG22	2:B:17:LEU:HB2	1.84	0.58
2:B:353:ARG:HD3	2:B:358:GLN:NE2	2.09	0.58
2:B:183:ASP:HB3	2:B:185:GLU:N	2.19	0.57
2:B:215:SER:C	2:B:217:ARG:H	2.11	0.57
2:B:26:TRP:CZ3	2:B:451:PRO:HG2	2.40	0.57
2:B:502:LEU:HD22	2:B:507:GLN:HB3	1.85	0.57
2:B:1:SER:HB2	2:B:23:HIS:HB2	1.88	0.56
2:B:378:THR:O	2:B:380:TYR:N	2.38	0.56
2:B:108:GLN:HA	2:B:108:GLN:NE2	2.19	0.56
2:B:133:ASP:C	2:B:133:ASP:OD1	2.49	0.56
1:A:31:HIS:HD2	2:B:37:HIS:ND1	2.04	0.56
2:B:370:TRP:HD1	2:B:379:PRO:HD3	1.70	0.56
1:A:122:ASP:C	1:A:124:ILE:N	2.63	0.56
2:B:78:ASN:OD1	2:B:139:VAL:HG13	2.05	0.56
2:B:108:GLN:CA	2:B:108:GLN:HE21	2.18	0.56
2:B:455:GLU:HG3	2:B:458:VAL:CG2	2.36	0.55
2:B:485:HIS:CE1	2:B:514:GLU:OE2	2.59	0.55
2:B:376:VAL:O	2:B:376:VAL:HG13	2.06	0.55
2:B:50:GLN:HG2	2:B:53:LEU:HD11	1.89	0.55
2:B:77:THR:CG2	2:B:220:TRP:NE1	2.66	0.55
1:A:90:ARG:HH21	1:A:144:HIS:HE1	1.54	0.54
2:B:505:ARG:HE	2:B:509:GLU:HG3	1.73	0.54
2:B:193:ASN:CG	2:B:194:GLY:N	2.66	0.54
2:B:77:THR:HB	3:B:665:HOH:O	2.08	0.54
2:B:27:THR:O	2:B:28:THR:C	2.49	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:67:THR:HG22	2:B:68:ASN:H	1.73	0.54
2:B:63:ARG:HH21	2:B:159:ALA:C	2.13	0.54
2:B:444:ASP:C	2:B:444:ASP:OD2	2.51	0.54
1:A:20:ASN:HB3	2:B:518:PHE:CE1	2.44	0.53
2:B:347:LEU:O	2:B:347:LEU:HD22	2.08	0.53
1:A:25:ASP:OD2	1:A:31:HIS:HE1	1.92	0.53
2:B:67:THR:HG21	3:B:664:HOH:O	2.08	0.53
2:B:181:TYR:OH	2:B:183:ASP:OD1	2.11	0.53
2:B:374:LYS:CB	2:B:378:THR:HG23	2.38	0.53
1:A:132:LEU:O	1:A:133:PRO:C	2.43	0.53
2:B:183:ASP:OD2	2:B:187:THR:HG23	2.09	0.53
1:A:9:GLN:HG3	1:A:9:GLN:O	2.08	0.52
1:A:24:TRP:O	2:B:513:GLN:O	2.27	0.52
2:B:2:ASN:ND2	2:B:274:ARG:HH11	2.08	0.52
2:B:77:THR:HG21	2:B:220:TRP:NE1	2.15	0.52
2:B:108:GLN:N	2:B:112:THR:O	2.42	0.52
2:B:8:PRO:HB3	2:B:14:GLY:O	2.09	0.51
2:B:108:GLN:NE2	2:B:108:GLN:CA	2.72	0.51
2:B:356:ALA:O	2:B:361:ALA:O	2.27	0.51
2:B:40:THR:HG23	2:B:41:PRO:CD	2.40	0.51
2:B:249:THR:N	2:B:250:PRO:CD	2.73	0.51
2:B:99:ARG:HH11	2:B:99:ARG:HG2	1.74	0.51
2:B:513:GLN:C	2:B:514:GLU:O	2.50	0.51
2:B:99:ARG:HG2	2:B:99:ARG:NH1	2.25	0.51
2:B:215:SER:C	2:B:217:ARG:N	2.68	0.51
2:B:350:GLU:OE1	2:B:402:LYS:NZ	2.41	0.51
2:B:441:SER:HB3	2:B:452:VAL:HG23	1.93	0.50
2:B:277:GLN:HG2	2:B:303:VAL:HG21	1.94	0.50
2:B:491:GLU:CD	2:B:495:ARG:NH1	2.68	0.50
2:B:212:PRO:HG2	2:B:218:TYR:CE2	2.46	0.50
2:B:6:VAL:HG21	2:B:17:LEU:HD12	1.94	0.50
2:B:152:GLN:HE21	2:B:173:GLN:HB2	1.77	0.50
1:A:129:ARG:O	1:A:132:LEU:HB2	2.12	0.50
2:B:61:ASN:C	2:B:61:ASN:HD22	2.20	0.49
2:B:198:LYS:HA	2:B:224:HIS:CE1	2.47	0.49
1:A:135:SER:O	1:A:136:GLY:C	2.55	0.49
2:B:1:SER:HB2	2:B:23:HIS:CB	2.42	0.49
1:A:91:ALA:HB1	1:A:141:ALA:HB2	1.94	0.49
2:B:7:ALA:O	2:B:8:PRO:C	2.55	0.49
2:B:408:ARG:NE	2:B:412:ASP:OD2	2.34	0.49
1:A:122:ASP:O	1:A:124:ILE:N	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1:SER:HB3	2:B:244:ASN:HD21	1.76	0.48
2:B:252:TRP:HA	2:B:252:TRP:CE3	2.48	0.48
2:B:485:HIS:HE1	2:B:514:GLU:OE2	1.93	0.48
2:B:376:VAL:O	2:B:376:VAL:CG1	2.61	0.48
2:B:25:SER:OG	2:B:28:THR:HG23	2.13	0.48
2:B:40:THR:CG2	2:B:42:ASP:H	2.26	0.48
2:B:294:MSE:HG2	2:B:460:MSE:HE3	1.95	0.48
2:B:380:TYR:CG	2:B:381:GLY:N	2.81	0.48
1:A:101:ASP:OD1	1:A:101:ASP:N	2.47	0.47
2:B:1:SER:N	2:B:22:PRO:HA	2.29	0.47
2:B:61:ASN:HB2	3:B:543:HOH:O	2.13	0.47
2:B:93:GLN:OE1	2:B:93:GLN:N	2.47	0.47
2:B:485:HIS:HE1	2:B:514:GLU:CD	2.10	0.47
1:A:160:GLY:O	1:A:161:GLU:C	2.58	0.47
2:B:10:LYS:NZ	2:B:282:MSE:O	2.46	0.47
2:B:149:MSE:HE2	2:B:153:TYR:CD1	2.49	0.47
1:A:76:GLU:O	1:A:80:VAL:HG23	2.14	0.47
2:B:64:MSE:CE	2:B:181:TYR:HE1	2.27	0.47
2:B:252:TRP:HA	2:B:252:TRP:HE3	1.80	0.47
2:B:64:MSE:HE1	2:B:165:TYR:HB2	1.97	0.47
2:B:35:GLU:CD	2:B:499:ARG:HH22	2.23	0.47
1:A:132:LEU:HD13	1:A:132:LEU:HA	1.65	0.46
2:B:29:ASP:OD2	2:B:30:TYR:N	2.48	0.46
2:B:99:ARG:NH1	2:B:119:GLU:OE1	2.48	0.46
2:B:106:LEU:O	2:B:113:THR:HA	2.15	0.46
2:B:73:MSE:CB	2:B:176:THR:HG22	2.36	0.46
2:B:151:GLU:OE2	2:B:155:ASP:OD2	2.33	0.46
2:B:237:GLY:HA3	2:B:253:PRO:HD2	1.96	0.46
2:B:504:ARG:NH1	2:B:506:GLU:OE2	2.48	0.46
1:A:139:VAL:HG13	2:B:54:PRO:HD3	1.97	0.46
2:B:20:GLN:NE2	2:B:457:TRP:HE1	2.14	0.46
2:B:513:GLN:O	2:B:514:GLU:HB2	2.16	0.46
2:B:456:THR:HG22	2:B:475:TYR:CE1	2.52	0.45
2:B:210:LEU:HD23	2:B:210:LEU:HA	1.81	0.45
2:B:1:SER:CB	2:B:23:HIS:HB2	2.47	0.45
2:B:40:THR:HG21	3:B:530:HOH:O	2.17	0.45
2:B:69:THR:OG1	2:B:178:ASN:HB2	2.16	0.45
2:B:281:LEU:HD22	2:B:296:LEU:HD22	1.98	0.45
1:A:34:GLY:O	2:B:41:PRO:HD3	2.17	0.45
2:B:385:PRO:O	2:B:389:VAL:HG23	2.16	0.45
1:A:99:SER:OG	1:A:101:ASP:OD1	2.24	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:140:ARG:CZ	2:B:219:LEU:HD22	2.47	0.44
2:B:417:ILE:HA	2:B:421:VAL:O	2.16	0.44
2:B:457:TRP:CZ2	2:B:459:ALA:HB2	2.52	0.44
2:B:63:ARG:HA	2:B:184:ARG:HD2	1.98	0.44
2:B:152:GLN:NE2	2:B:173:GLN:N	2.53	0.44
2:B:280:ARG:HD2	2:B:284:GLU:OE2	2.17	0.44
1:A:142:HIS:HD2	3:A:218:HOH:O	1.99	0.44
2:B:366:PHE:HA	2:B:381:GLY:O	2.18	0.44
2:B:489:GLN:OE1	2:B:499:ARG:NH1	2.49	0.44
1:A:132:LEU:HD12	1:A:132:LEU:C	2.42	0.44
2:B:107:ARG:HH11	2:B:107:ARG:HG2	1.82	0.44
1:A:15:TYR:CE1	2:B:505:ARG:HG2	2.53	0.44
2:B:1:SER:O	2:B:243:SER:HA	2.17	0.44
2:B:453:HIS:ND1	2:B:453:HIS:C	2.76	0.43
2:B:458:VAL:O	2:B:471:GLY:HA2	2.17	0.43
2:B:252:TRP:HB3	2:B:253:PRO:HD3	2.01	0.43
1:A:72:GLY:CA	2:B:107:ARG:HB3	2.48	0.43
2:B:294:MSE:SE	2:B:460:MSE:HE3	2.69	0.43
2:B:292:ARG:HG2	2:B:292:ARG:NH1	2.26	0.43
1:A:135:SER:N	1:A:138:ASP:OD2	2.44	0.43
1:A:144:HIS:CD2	1:A:148:ASN:ND2	2.79	0.43
2:B:61:ASN:HD21	2:B:64:MSE:H	1.64	0.43
2:B:72:GLY:O	2:B:73:MSE:C	2.62	0.43
2:B:140:ARG:HG2	2:B:220:TRP:CH2	2.54	0.43
2:B:313:ILE:HD13	2:B:332:ALA:CB	2.45	0.43
2:B:34:TYR:O	2:B:48:ALA:HA	2.19	0.43
2:B:152:GLN:NE2	2:B:173:GLN:HB2	2.33	0.43
2:B:454:GLY:O	2:B:455:GLU:C	2.62	0.42
1:A:114:ASN:HD21	1:A:134:VAL:HG22	1.84	0.42
1:A:114:ASN:ND2	1:A:134:VAL:HG22	2.34	0.42
2:B:508:VAL:O	2:B:509:GLU:C	2.62	0.42
2:B:301:ARG:HG2	2:B:303:VAL:HG23	2.00	0.42
2:B:492:ARG:HD3	2:B:497:ASP:HB3	2.02	0.42
2:B:181:TYR:CD2	2:B:181:TYR:C	2.97	0.42
2:B:374:LYS:HB2	2:B:378:THR:HG21	2.01	0.42
2:B:2:ASN:HD21	2:B:274:ARG:HH11	1.67	0.42
2:B:280:ARG:HD3	2:B:376:VAL:HG13	2.02	0.42
2:B:347:LEU:HD22	2:B:347:LEU:C	2.45	0.42
2:B:108:GLN:HA	2:B:108:GLN:HE21	1.82	0.42
2:B:417:ILE:O	2:B:418:LEU:HD23	2.19	0.42
1:A:72:GLY:HA2	2:B:107:ARG:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:145:ARG:HD3	3:A:218:HOH:O	2.19	0.42
2:B:187:THR:HA	2:B:234:ASN:OD1	2.19	0.42
2:B:241:GLN:CD	2:B:241:GLN:C	2.88	0.42
2:B:380:TYR:CD2	2:B:381:GLY:N	2.88	0.42
2:B:393:ARG:HG3	2:B:393:ARG:HH11	1.85	0.42
1:A:125:SER:HA	1:A:126:PRO:HD3	1.90	0.42
2:B:64:MSE:HE3	2:B:159:ALA:HB3	1.94	0.42
2:B:252:TRP:O	2:B:252:TRP:CE3	2.73	0.42
2:B:309:LEU:N	2:B:310:PRO:CD	2.82	0.42
1:A:90:ARG:NH2	1:A:144:HIS:HE1	2.17	0.41
2:B:60:PHE:HA	2:B:65:GLY:HA2	2.01	0.41
2:B:492:ARG:CD	2:B:497:ASP:O	2.68	0.41
2:B:107:ARG:HG2	2:B:107:ARG:NH1	2.36	0.41
2:B:485:HIS:CD2	2:B:488:ASP:OD2	2.70	0.41
2:B:168:ALA:O	2:B:169:LEU:C	2.63	0.41
2:B:33:TYR:C	2:B:473:MSE:HE1	2.45	0.41
2:B:300:HIS:HD2	2:B:337:GLU:OE1	2.04	0.41
2:B:472:LEU:HD23	2:B:499:ARG:HG3	2.02	0.41
2:B:489:GLN:O	2:B:492:ARG:HB2	2.21	0.41
1:A:22:ILE:C	1:A:23:LEU:HD12	2.46	0.41
2:B:245:ASP:OD2	2:B:245:ASP:N	2.52	0.41
2:B:380:TYR:CD2	2:B:380:TYR:C	2.98	0.41
1:A:132:LEU:O	1:A:132:LEU:CD1	2.69	0.41
2:B:2:ASN:HB2	2:B:21:ASN:HB3	2.02	0.41
2:B:319:ASP:HA	2:B:320:PRO:HD3	1.80	0.41
2:B:360:PHE:C	2:B:361:ALA:O	2.57	0.41
1:A:25:ASP:HB2	1:A:29:VAL:HB	2.03	0.40
1:A:31:HIS:CD2	2:B:37:HIS:ND1	2.87	0.40
2:B:370:TRP:HD1	2:B:379:PRO:CD	2.34	0.40
2:B:490:ILE:HD12	2:B:490:ILE:HA	1.77	0.40
2:B:63:ARG:NH2	2:B:161:SER:N	2.70	0.40
2:B:199:ARG:HD2	2:B:207:TRP:CD2	2.56	0.40
2:B:504:ARG:O	2:B:505:ARG:C	2.64	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	151/171 (88%)	139 (92%)	10 (7%)	2 (1%)	9	14
2	B	518/522 (99%)	477 (92%)	39 (8%)	2 (0%)	30	43
All	All	669/693 (96%)	616 (92%)	49 (7%)	4 (1%)	21	32

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	132	LEU
2	B	109	ALA
2	B	514	GLU
1	A	123	ASP

5.3.2 Protein sidechains

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	117/130 (90%)	109 (93%)	8 (7%)	14	25
2	B	429/420 (102%)	379 (88%)	50 (12%)	5	7
All	All	546/550 (99%)	488 (89%)	58 (11%)	6	10

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	ASP
1	A	50	ARG

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Mol	Chain	Res	Type
1	A	57	LEU
1	A	59	LEU
1	A	132	LEU
1	A	150	LEU
1	A	158	THR
1	A	159	LEU
2	B	6	VAL
2	B	18	LEU
2	B	28	THR
2	B	40	THR
2	B	49	THR
2	B	50	GLN
2	B	61	ASN
2	B	64	MSE
2	B	77	THR
2	B	93	GLN
2	B	106	LEU
2	B	108	GLN
2	B	116	LYS
2	B	118	LEU
2	B	139	VAL
2	B	157	ILE
2	B	163	ASP
2	B	169	LEU
2	B	176	THR
2	B	187	THR
2	B	219	LEU
2	B	245	ASP
2	B	252	TRP
2	B	254	VAL
2	B	259	LYS
2	B	272	SER
2	B	286	ASP
2	B	287	ASP
2	B	290	LEU
2	B	347	LEU
2	B	350	GLU
2	B	358	GLN
2	B	368	THR
2	B	372	LEU
2	B	376	VAL
2	B	392	LEU

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Mol	Chain	Res	Type
2	B	400	LYS
2	B	412	ASP
2	B	452	VAL
2	B	453	HIS
2	B	455	GLU
2	B	460	MSE
2	B	467	VAL
2	B	468	ARG
2	B	475	TYR
2	B	479	ARG
2	B	483	THR
2	B	491	GLU
2	B	492	ARG
2	B	506	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	HIS
1	A	52	HIS
1	A	55	ASN
1	A	77	GLN
1	A	114	ASN
1	A	130	GLN
1	A	142	HIS
1	A	144	HIS
1	A	148	ASN
2	B	2	ASN
2	B	20	GLN
2	B	21	ASN
2	B	61	ASN
2	B	84	GLN
2	B	108	GLN
2	B	152	GLN
2	B	224	HIS
2	B	244	ASN
2	B	271	HIS
2	B	300	HIS
2	B	358	GLN
2	B	485	HIS
2	B	507	GLN

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 oligosaccharides 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.