



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:34 PM GMT

PDB ID : 1KXR
Title : Crystal Structure of Calcium-Bound Protease Core of Calpain I
Authors : Moldoveanu, T.; Hosfield, C.M.; Lim, D.; Elce, J.S.; Jia, Z.; Davies, P.L.
Deposited on : 2002-02-01
Resolution : 2.07 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

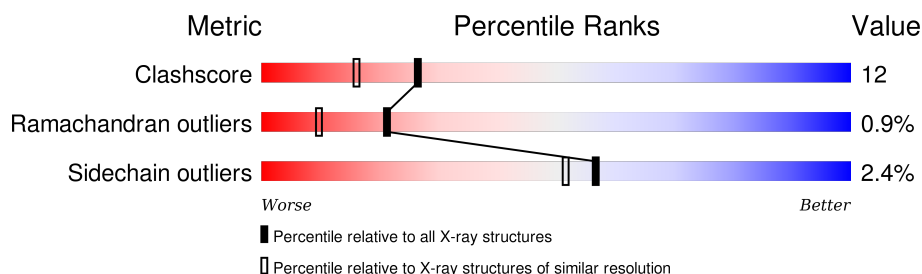
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.07 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	102246	1910 (2.08-2.04)
Ramachandran outliers	100387	1893 (2.08-2.04)
Sidechain outliers	100360	1893 (2.08-2.04)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	339	
1	B	339	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5517 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 thiol protease DOMAINS I AND II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	320	Total	C	N	O	S	0	0	0
			2573	1648	434	483	8			
1	B	321	Total	C	N	O	S	0	0	0
			2581	1654	435	484	8			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	26	MET	-	INITIATING MET	UNP P97571
A	115	SER	CYS	ENGINEERED	UNP P97571
A	357	LEU	-	EXPRESSION TAG	UNP P97571
A	358	GLU	-	EXPRESSION TAG	UNP P97571
A	359	HIS	-	EXPRESSION TAG	UNP P97571
A	360	HIS	-	EXPRESSION TAG	UNP P97571
A	361	HIS	-	EXPRESSION TAG	UNP P97571
A	362	HIS	-	EXPRESSION TAG	UNP P97571
A	363	HIS	-	EXPRESSION TAG	UNP P97571
A	364	HIS	-	EXPRESSION TAG	UNP P97571
B	26	MET	-	INITIATING MET	UNP P97571
B	115	SER	CYS	ENGINEERED	UNP P97571
B	357	LEU	-	EXPRESSION TAG	UNP P97571
B	358	GLU	-	EXPRESSION TAG	UNP P97571
B	359	HIS	-	EXPRESSION TAG	UNP P97571
B	360	HIS	-	EXPRESSION TAG	UNP P97571
B	361	HIS	-	EXPRESSION TAG	UNP P97571
B	362	HIS	-	EXPRESSION TAG	UNP P97571
B	363	HIS	-	EXPRESSION TAG	UNP P97571
B	364	HIS	-	EXPRESSION TAG	UNP P97571

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total 2	Ca 2	0	0
2	A	2	Total 2	Ca 2	0	0

- Molecule 3 is water.

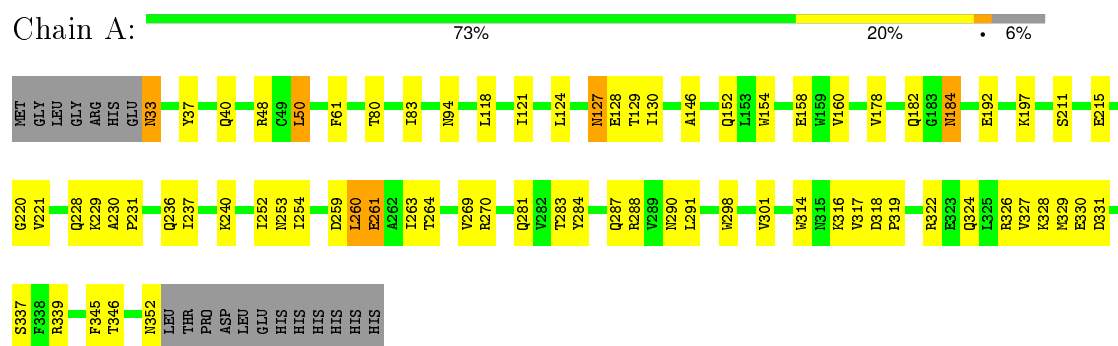
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	169	Total 169	O 169	0	0
3	B	190	Total 190	O 190	0	0

3 Residue-property plots

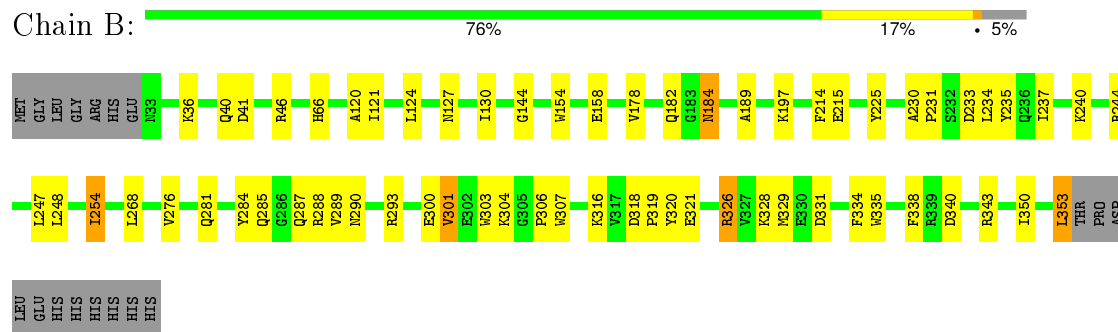
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

- Molecule 1: thiol protease DOMAINS I AND II



- Molecule 1: thiol protease DOMAINS I AND II



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	149.44Å 40.49Å 132.33Å 90.00° 105.96° 90.00°	Depositor
Resolution (Å)	30.00 – 2.07	Depositor
% Data completeness (in resolution range)	92.0 (30.00-2.07)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.213 , 0.256	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5517	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.33	0/2640	0.57	2/3581 (0.1%)
1	B	0.33	0/2648	0.57	0/3592
All	All	0.33	0/5288	0.57	2/7173 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	33	ASN	CB-CA-C	5.33	121.06	110.40
1	A	339	ARG	CB-CA-C	5.33	121.06	110.40

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	2573	0	2473	67	0
1	B	2581	0	2484	58	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	169	0	0	5	0
3	B	190	0	0	8	0
All	All	5517	0	4957	123	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 12.

All (123) 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:254:ILE:HG12	1:A:270:ARG:NH1	1.67	1.08
1:A:254:ILE:HG12	1:A:270:ARG:HH11	0.89	1.03
1:A:254:ILE:HB	1:A:270:ARG:HD2	1.35	1.03
1:A:263:ILE:HG12	1:A:269:VAL:HG22	1.42	0.99
1:A:184:ASN:H	1:A:184:ASN:HD22	1.18	0.91
1:A:263:ILE:HG22	1:A:264:THR:N	1.87	0.87
1:A:263:ILE:HG22	1:A:264:THR:H	1.35	0.85
1:B:184:ASN:H	1:B:184:ASN:HD22	1.28	0.82
1:A:50:LEU:HD13	1:A:146:ALA:HB2	1.61	0.82
1:A:254:ILE:CB	1:A:270:ARG:HD2	2.10	0.81
1:B:234:LEU:HD12	1:B:338:PHE:HZ	1.47	0.77
1:A:237:ILE:HA	1:A:240:LYS:HE2	1.70	0.74
1:A:281:GLN:HG2	1:A:290:ASN:HD22	1.53	0.73
1:A:263:ILE:CG2	1:A:264:THR:H	2.00	0.73
1:B:234:LEU:HD12	1:B:338:PHE:CZ	2.25	0.71
1:B:254:ILE:HD12	1:B:254:ILE:H	1.54	0.70
1:A:281:GLN:HG2	1:A:290:ASN:ND2	2.07	0.69
1:B:40:GLN:HE22	1:B:197:LYS:NZ	1.91	0.69
1:A:184:ASN:N	1:A:184:ASN:HD22	1.89	0.68
1:A:283:THR:HG21	1:B:316:LYS:HA	1.76	0.68
1:A:263:ILE:CG2	1:A:264:THR:N	2.56	0.67
1:B:154:TRP:CZ3	1:B:158:GLU:HA	2.31	0.65
1:A:127:ASN:C	1:A:127:ASN:HD22	2.01	0.64
1:A:317:VAL:HG23	1:A:322:ARG:HB3	1.80	0.63
1:B:46:ARG:HH21	1:B:144:GLY:HA3	1.64	0.62
1:A:211:SER:O	1:A:215:GLU:HG3	1.99	0.62
1:A:288:ARG:NH2	1:B:285:GLN:HE21	1.96	0.62
1:A:253:ASN:ND2	3:A:446:HOH:O	2.32	0.61
1:A:40:GLN:HE22	1:A:197:LYS:NZ	1.98	0.60
1:A:324:GLN:HG3	1:A:324:GLN:O	2.00	0.60
1:B:66:HIS:CD2	3:B:448:HOH:O	2.52	0.60
1:A:182:GLN:HG3	3:A:451:HOH:O	2.02	0.59
1:A:220:GLY:HA3	1:A:352:ASN:HD22	1.67	0.59
1:B:182:GLN:HG3	3:B:443:HOH:O	2.02	0.58
1:A:237:ILE:HA	1:A:240:LYS:CE	2.32	0.58
1:B:254:ILE:CD1	1:B:254:ILE:H	2.12	0.58
1:A:326:ARG:NH1	1:A:328:LYS:HE3	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:281:GLN:HG2	1:B:290:ASN:ND2	2.18	0.57
1:A:184:ASN:ND2	1:A:184:ASN:H	1.96	0.57
1:B:254:ILE:HD12	1:B:254:ILE:N	2.21	0.56
1:B:225:TYR:HE2	1:B:350:ILE:HD12	1.72	0.55
1:A:326:ARG:HG2	1:A:327:VAL:N	2.22	0.54
1:A:352:ASN:O	1:A:352:ASN:OD1	2.26	0.54
1:A:221:VAL:O	1:A:352:ASN:N	2.35	0.53
1:B:40:GLN:HE22	1:B:197:LYS:HZ3	1.55	0.53
1:B:240:LYS:HD3	1:B:244:ARG:NH2	2.24	0.53
1:A:94:ASN:HB2	3:A:439:HOH:O	2.08	0.53
1:A:48:ARG:HB2	1:A:48:ARG:NH1	2.23	0.53
1:B:284:TYR:CD2	1:B:316:LYS:HB2	2.43	0.52
1:B:215:GLU:HG3	3:B:453:HOH:O	2.08	0.52
1:A:317:VAL:CG2	1:A:322:ARG:HB3	2.40	0.52
1:B:340:ASP:HA	1:B:343:ARG:NH1	2.24	0.52
1:B:244:ARG:HD2	3:B:471:HOH:O	2.10	0.51
1:B:304:LYS:HE2	3:B:548:HOH:O	2.10	0.51
1:A:314:TRP:O	1:A:317:VAL:HG22	2.10	0.51
1:A:124:LEU:HD11	1:A:130:ILE:HG22	1.94	0.50
1:A:291:LEU:HD23	1:A:337:SER:HA	1.93	0.50
1:A:228:GLN:HE22	1:A:346:THR:HB	1.77	0.50
1:A:314:TRP:HB3	1:A:326:ARG:HH21	1.77	0.50
1:B:120:ALA:HA	1:B:214:PHE:HE1	1.76	0.49
1:B:281:GLN:HG2	1:B:290:ASN:HD22	1.76	0.49
1:A:80:THR:HA	1:A:83:ILE:HD12	1.95	0.49
1:B:235:TYR:CE2	1:B:290:ASN:HB3	2.48	0.49
1:B:319:PRO:HG3	3:B:436:HOH:O	2.13	0.48
1:A:236:GLN:O	1:A:240:LYS:HG2	2.14	0.48
1:A:127:ASN:HD21	1:A:129:THR:HB	1.78	0.48
1:B:326:ARG:HG3	3:B:397:HOH:O	2.14	0.48
1:B:326:ARG:NH2	1:B:328:LYS:HE3	2.29	0.48
1:A:314:TRP:CB	1:A:326:ARG:HH21	2.27	0.47
1:B:36:LYS:HE3	1:B:41:ASP:HB2	1.95	0.47
1:B:340:ASP:HA	1:B:343:ARG:HH12	1.78	0.47
1:A:121:ILE:O	1:A:124:LEU:HB3	2.14	0.47
1:B:254:ILE:HD11	3:B:538:HOH:O	2.15	0.47
1:B:329:MET:HE2	1:B:331:ASP:OD2	2.15	0.47
1:B:121:ILE:O	1:B:124:LEU:HB3	2.15	0.46
1:A:252:ILE:HG12	1:A:345:PHE:HA	1.96	0.46
1:B:184:ASN:HD22	1:B:184:ASN:N	1.98	0.46
1:A:283:THR:HA	1:A:287:GLN:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:254:ILE:HG21	1:A:270:ARG:CZ	2.46	0.46
1:A:154:TRP:CZ3	1:A:158:GLU:HA	2.51	0.46
1:A:263:ILE:HD11	1:A:298:TRP:HZ3	1.79	0.46
1:B:288:ARG:HG2	1:B:288:ARG:HH11	1.80	0.46
1:B:40:GLN:NE2	1:B:197:LYS:HZ3	2.13	0.45
1:A:260:LEU:N	1:A:260:LEU:HD12	2.31	0.45
1:B:184:ASN:H	1:B:184:ASN:ND2	2.07	0.45
1:B:40:GLN:HE22	1:B:197:LYS:HZ1	1.64	0.44
1:A:284:TYR:CE2	1:A:316:LYS:HB2	2.52	0.44
1:A:319:PRO:HA	1:A:322:ARG:HG2	2.00	0.44
1:A:229:LYS:HG2	3:A:477:HOH:O	2.17	0.44
1:B:318:ASP:OD1	1:B:320:TYR:HB3	2.18	0.44
1:B:353:LEU:N	1:B:353:LEU:HD13	2.33	0.43
1:B:284:TYR:CE2	1:B:316:LYS:HB2	2.53	0.43
1:B:268:LEU:HD21	1:B:303:TRP:HB2	2.00	0.43
1:A:40:GLN:HE22	1:A:197:LYS:HZ3	1.64	0.43
1:A:152:GLN:HA	1:A:160:VAL:O	2.18	0.43
1:B:230:ALA:HA	1:B:231:PRO:HD3	1.88	0.43
1:B:284:TYR:HB3	1:B:289:VAL:HG21	2.00	0.42
1:A:61:PHE:HB2	1:A:197:LYS:HG3	2.00	0.42
1:B:293:ARG:HB2	1:B:335:TRP:CE3	2.55	0.42
1:B:248:LEU:HB2	1:B:276:VAL:HB	2.01	0.42
1:A:37:TYR:HB2	1:A:160:VAL:HG12	2.00	0.42
1:A:263:ILE:HD11	1:A:298:TRP:CZ3	2.55	0.42
1:B:318:ASP:OD2	1:B:321:GLU:HG3	2.20	0.42
1:A:184:ASN:ND2	1:A:184:ASN:N	2.60	0.41
1:B:281:GLN:HB3	1:B:288:ARG:HD3	2.02	0.41
1:A:40:GLN:NE2	1:A:197:LYS:HZ3	2.18	0.41
1:A:263:ILE:HA	1:A:269:VAL:HA	2.01	0.41
1:A:182:GLN:CG	3:A:451:HOH:O	2.66	0.41
1:B:233:ASP:O	1:B:237:ILE:HG13	2.19	0.41
1:A:330:GLU:HA	1:A:330:GLU:OE1	2.21	0.41
1:B:288:ARG:NH1	1:B:288:ARG:HG2	2.36	0.41
1:B:304:LYS:HA	1:B:304:LYS:HD3	1.85	0.41
1:B:247:LEU:C	1:B:248:LEU:HD12	2.41	0.41
1:A:230:ALA:HA	1:A:231:PRO:HD3	1.91	0.41
1:A:178:VAL:HG12	1:A:192:GLU:OE2	2.21	0.41
1:B:124:LEU:HD11	1:B:130:ILE:HG22	2.02	0.41
1:B:303:TRP:HB3	1:B:334:PHE:CD1	2.56	0.41
1:B:300:GLU:HG3	1:B:301:VAL:HG23	2.03	0.41
1:B:234:LEU:HD13	1:B:234:LEU:C	2.42	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:306:PRO:O	1:B:307:TRP:HB2	2.21	0.40
1:B:178:VAL:CG1	1:B:189:ALA:HA	2.52	0.40
1:A:37:TYR:HB2	1:A:160:VAL:CG1	2.51	0.40
1:A:329:MET:HE2	1:A:331:ASP:OD2	2.21	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	318/339 (94%)	298 (94%)	16 (5%)	4 (1%)	15	5
1	B	319/339 (94%)	302 (95%)	15 (5%)	2 (1%)	30	17
All	All	637/678 (94%)	600 (94%)	31 (5%)	6 (1%)	21	10

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	259	ASP
1	A	261	GLU
1	B	287	GLN
1	A	260	LEU
1	A	301	VAL
1	B	301	VAL

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	272/291 (94%)	264 (97%)	8 (3%)	50	43
1	B	273/291 (94%)	268 (98%)	5 (2%)	66	63
All	All	545/582 (94%)	532 (98%)	13 (2%)	57	51

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	ASN
1	A	50	LEU
1	A	118	LEU
1	A	127	ASN
1	A	128	GLU
1	A	184	ASN
1	A	261	GLU
1	A	318	ASP
1	B	127	ASN
1	B	184	ASN
1	B	254	ILE
1	B	326	ARG
1	B	353	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (35) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	ASN
1	A	40	GLN
1	A	44	ASN
1	A	51	GLN
1	A	52	ASN
1	A	57	GLN
1	A	66	HIS
1	A	76	ASN
1	A	94	ASN
1	A	96	GLN
1	A	127	ASN
1	A	152	GLN
1	A	155	GLN
1	A	182	GLN
1	A	184	ASN

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Mol	Chain	Res	Type
1	A	253	ASN
1	A	281	GLN
1	A	285	GLN
1	A	290	ASN
1	A	352	ASN
1	B	40	GLN
1	B	52	ASN
1	B	66	HIS
1	B	76	ASN
1	B	94	ASN
1	B	96	GLN
1	B	127	ASN
1	B	132	HIS
1	B	152	GLN
1	B	184	ASN
1	B	236	GLN
1	B	253	ASN
1	B	281	GLN
1	B	285	GLN
1	B	290	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.