



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 08:03 AM UTC

PDB ID : 1TAQ / pdb_00001taq
Title : STRUCTURE OF TAQ DNA POLYMERASE
Authors : Kim, Y.; Eom, S.H.; Wang, J.; Lee, D.-S.; Suh, S.W.; Steitz, T.A.
Deposited on : 1996-06-04
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)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

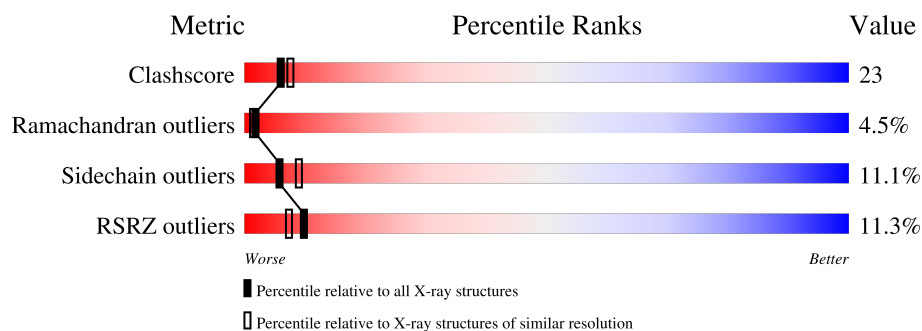
1 Overall quality at a glance

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)
RSRZ outliers	180081	4916 (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 $\leq 5\%$. 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	832	

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
3	ZN	A	900	-	-	-	X

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6747 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.

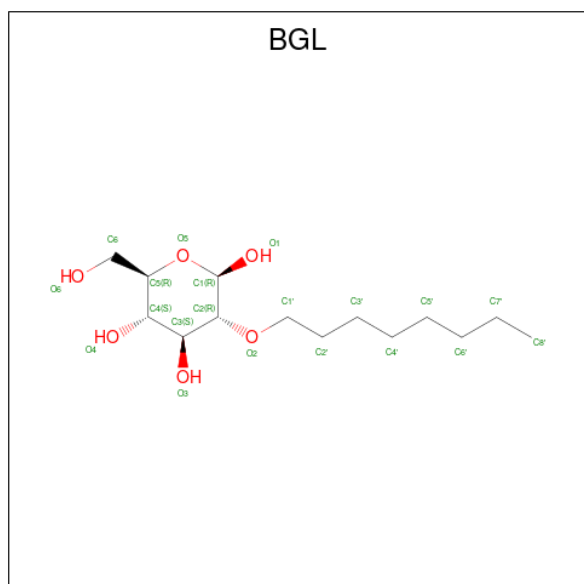
- Molecule 1 is a protein called TAQ DNA POLYMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	807	6432	4102	1145	1168	17	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	575	CYS	SER	conflict	UNP P19821
A	576	CYS	SER	conflict	UNP P19821
A	577	CYS	SER	conflict	UNP P19821
A	597	GLY	ALA	conflict	UNP P19821

- Molecule 2 is 2-O-octyl-beta-D-glucopyranose (CCD ID: BGL) (formula: $C_{14}H_{28}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	20	14	6	0	0

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	Zn 1	0	0

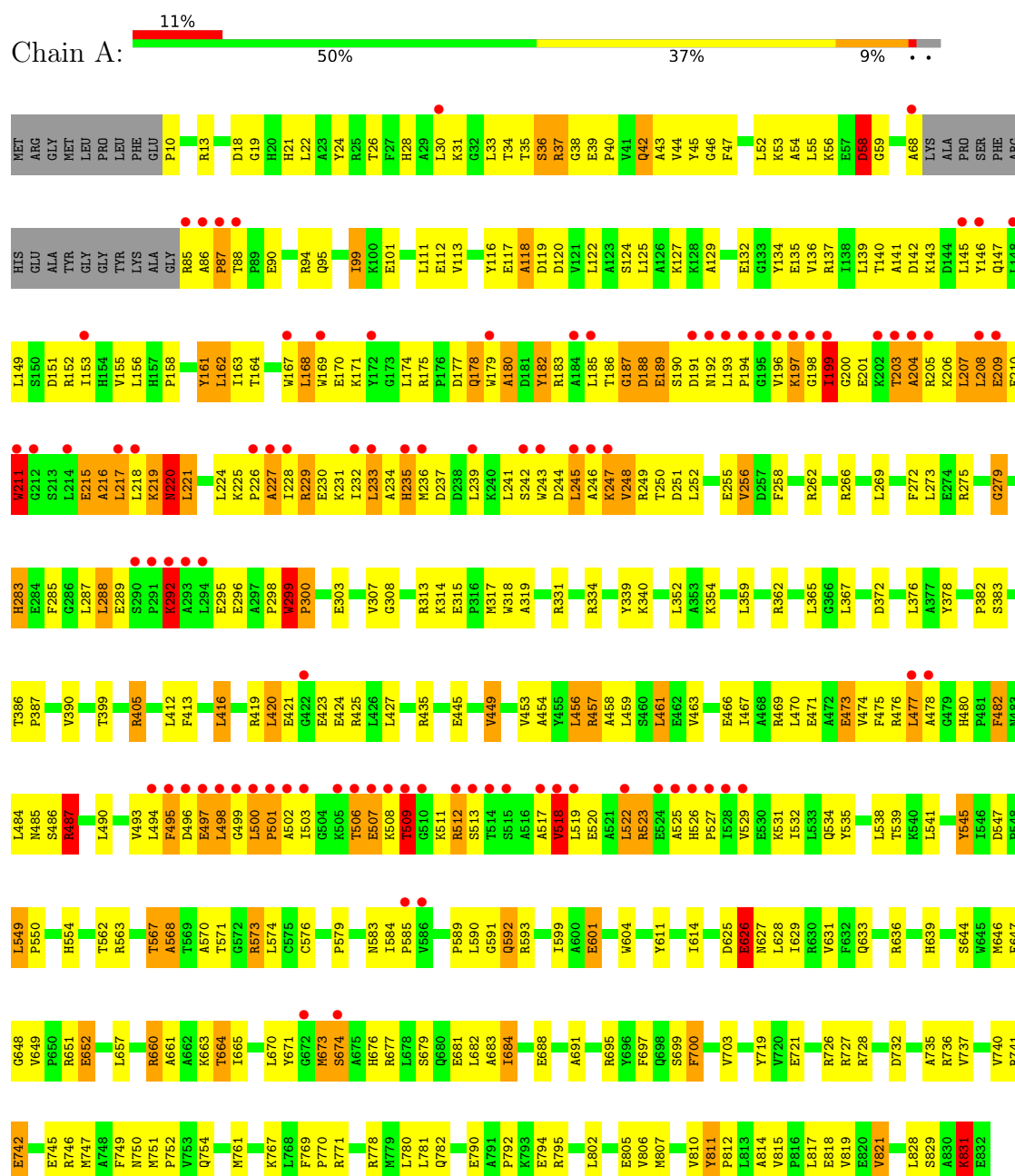
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	294	Total 294	O 294	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: TAQ DNA POLYMERASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	107.42Å 107.42Å 170.25Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.00 – 2.40 40.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-2.40) 72.7 (40.00-2.40)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.93 (at 2.39Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.202 , 0.323 0.209 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	37.3	Xtriage
Anisotropy	0.240	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 108.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.038 for -h,-k,l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6747	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.31% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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	0.60	1/6568 (0.0%)	1.13	55/8891 (0.6%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	518	VAL	CA-CB	5.27	1.59	1.54

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	215	GLU	N-CA-C	10.60	123.95	111.02
1	A	151	ASP	N-CA-C	-8.73	98.19	110.50
1	A	509	THR	N-CA-C	8.20	128.26	110.80
1	A	279	GLY	N-CA-C	-7.96	104.53	114.16
1	A	383	SER	N-CA-C	-7.84	103.73	113.38
1	A	33	LEU	N-CA-C	7.84	122.24	110.64
1	A	508	LYS	N-CA-C	7.21	121.20	109.59
1	A	135	GLU	N-CA-C	-7.04	97.25	108.73
1	A	584	ILE	N-CA-C	-7.04	102.06	108.95
1	A	211	TRP	N-CA-C	-6.93	104.71	113.72
1	A	258	PHE	N-CA-C	6.87	121.09	108.58
1	A	58	ASP	N-CA-C	6.86	125.41	110.80
1	A	269	LEU	N-CA-C	-6.85	103.89	111.36
1	A	498	LEU	N-CA-C	6.81	120.11	110.50
1	A	476	ARG	N-CA-C	-6.80	103.79	111.07
1	A	340	LYS	N-CA-C	-6.71	104.05	111.36
1	A	567	THR	N-CA-C	-6.50	103.45	108.78
1	A	525	ALA	N-CA-C	6.37	120.76	112.92
1	A	549	LEU	N-CA-C	6.27	121.40	113.25
1	A	495	PHE	N-CA-C	-6.26	105.95	113.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	628	LEU	N-CA-C	-6.23	103.80	111.40
1	A	308	GLY	N-CA-C	-6.22	101.25	111.38
1	A	299	TRP	N-CA-C	6.14	123.38	109.81
1	A	220	ASN	N-CA-C	6.12	123.84	110.80
1	A	101	GLU	N-CA-C	-6.09	104.55	111.07
1	A	554	HIS	CA-C-N	6.08	125.80	119.05
1	A	554	HIS	C-N-CA	6.08	125.80	119.05
1	A	416	LEU	N-CA-C	6.01	119.08	111.69
1	A	251	ASP	N-CA-C	5.89	119.23	112.57
1	A	568	ALA	N-CA-C	5.74	123.04	110.80
1	A	247	LYS	N-CA-C	-5.72	101.84	110.70
1	A	700	PHE	CA-C-N	5.57	125.23	119.05
1	A	700	PHE	C-N-CA	5.57	125.23	119.05
1	A	732	ASP	N-CA-C	5.54	119.78	113.19
1	A	449	VAL	CB-CA-C	-5.53	102.31	110.82
1	A	367	LEU	CA-C-N	5.50	123.62	119.66
1	A	367	LEU	C-N-CA	5.50	123.62	119.66
1	A	136	VAL	N-CA-C	5.42	115.76	108.17
1	A	339	TYR	N-CA-C	5.41	116.86	111.07
1	A	522	LEU	N-CA-C	5.34	119.65	113.18
1	A	477	LEU	N-CA-C	-5.29	101.64	110.17
1	A	545	TYR	N-CA-C	5.29	121.47	114.12
1	A	487	ARG	N-CA-C	5.26	122.00	110.80
1	A	289	GLU	N-CA-C	-5.21	107.45	112.97
1	A	811	TYR	CA-C-N	5.17	126.59	120.23
1	A	811	TYR	C-N-CA	5.17	126.59	120.23
1	A	599	ILE	N-CA-C	5.14	116.26	108.96
1	A	736	ARG	N-CA-C	-5.12	106.12	112.93
1	A	626	GLU	N-CA-C	5.05	117.52	111.71
1	A	153	ILE	CB-CA-C	-5.04	104.86	110.96
1	A	815	VAL	CA-C-N	-5.03	115.38	120.21
1	A	815	VAL	C-N-CA	-5.03	115.38	120.21
1	A	180	ALA	N-CA-C	-5.02	107.11	113.18
1	A	372	ASP	CA-C-N	5.01	124.79	119.28
1	A	372	ASP	C-N-CA	5.01	124.79	119.28

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	6432	0	6525	295	0
2	A	20	0	27	2	0
3	A	1	0	0	0	0
4	A	294	0	0	9	0
All	All	6747	0	6552	296	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 23.

All (296) 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:34:THR:HG22	1:A:40:PRO:HA	1.49	0.95
1:A:295:GLU:HG2	1:A:331:ARG:HG2	1.50	0.92
1:A:207:LEU:HD23	1:A:210:GLU:HB2	1.52	0.90
1:A:127:LYS:HG3	1:A:250:THR:HB	1.52	0.88
1:A:34:THR:HB	1:A:38:GLY:O	1.74	0.88
1:A:86:ALA:HB3	1:A:87:PRO:HD3	1.55	0.88
1:A:292:LYS:HE2	1:A:292:LYS:HA	1.64	0.78
1:A:68:ALA:HB2	1:A:112:GLU:HB2	1.62	0.78
1:A:44:VAL:HA	1:A:99:ILE:HD11	1.64	0.78
1:A:146:TYR:O	1:A:149:LEU:HB2	1.84	0.77
1:A:111:LEU:HD23	1:A:125:LEU:HD11	1.66	0.77
1:A:592:GLN:HG3	1:A:828:LEU:HD11	1.67	0.76
1:A:140:THR:HG21	1:A:145:LEU:HD12	1.67	0.75
1:A:183:ARG:HE	1:A:245:LEU:HD21	1.52	0.75
1:A:224:LEU:HB3	1:A:229:ARG:HB2	1.68	0.74
1:A:470:LEU:O	1:A:474:VAL:HG23	1.88	0.72
1:A:147:GLN:CD	1:A:248:VAL:HG21	2.14	0.72
1:A:18:ASP:O	1:A:22:LEU:HG	1.90	0.72
1:A:207:LEU:HB3	1:A:211:TRP:HE1	1.55	0.71
1:A:168:LEU:HD11	1:A:179:TRP:CD1	2.25	0.71
1:A:421:GLU:HA	1:A:427:LEU:HD21	1.72	0.71
1:A:660:ARG:O	1:A:664:THR:HG23	1.90	0.71
1:A:196:VAL:HB	1:A:204:ALA:HB2	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:466:GLU:HA	1:A:469:ARG:CZ	2.22	0.70
1:A:198:GLY:HA2	1:A:203:THR:HA	1.73	0.70
1:A:376:LEU:HD22	1:A:420:LEU:HD22	1.73	0.70
1:A:585:PRO:O	1:A:591:GLY:HA3	1.91	0.70
1:A:116:TYR:CZ	1:A:252:LEU:HD12	2.28	0.69
1:A:53:LYS:HA	1:A:56:LYS:HD3	1.75	0.68
1:A:186:THR:HG22	1:A:187:GLY:H	1.59	0.68
1:A:684:ILE:HG23	1:A:688:GLU:HB3	1.78	0.65
1:A:129:ALA:O	1:A:134:TYR:HB2	1.98	0.64
1:A:207:LEU:HB3	1:A:211:TRP:NE1	2.11	0.64
1:A:592:GLN:HG3	1:A:828:LEU:CD1	2.26	0.64
1:A:205:ARG:HA	1:A:208:LEU:HG	1.78	0.64
1:A:244:ASP:O	1:A:247:LYS:HB2	1.98	0.64
1:A:197:LYS:HD3	1:A:227:ALA:HB2	1.80	0.63
1:A:574:LEU:HD12	1:A:782:GLN:HE21	1.62	0.63
1:A:120:ASP:HB3	1:A:252:LEU:HD21	1.80	0.63
1:A:639:HIS:CD2	1:A:663:LYS:HA	2.34	0.62
1:A:458:ALA:HA	1:A:461:LEU:HD23	1.81	0.62
1:A:386:THR:O	1:A:390:VAL:HG23	1.99	0.62
1:A:771:ARG:HB3	1:A:802:LEU:HD21	1.81	0.62
1:A:231:LYS:HA	1:A:234:ALA:HB3	1.82	0.61
1:A:285:PHE:HA	1:A:288:LEU:HD21	1.82	0.61
1:A:146:TYR:HB2	1:A:179:TRP:CZ3	2.35	0.61
1:A:474:VAL:HG11	1:A:484:LEU:HD21	1.82	0.61
1:A:507:GLU:C	1:A:513:SER:HB2	2.25	0.61
1:A:216:ALA:HA	1:A:221:LEU:HB3	1.83	0.61
1:A:571:THR:HG21	1:A:754:GLN:OE1	2.01	0.60
1:A:68:ALA:HB2	1:A:112:GLU:CB	2.30	0.60
1:A:399:THR:O	1:A:405:ARG:HD3	2.02	0.60
1:A:526:HIS:HB2	1:A:529:VAL:HG22	1.84	0.60
1:A:200:GLY:O	1:A:201:GLU:HG2	2.02	0.59
1:A:124:SER:OG	1:A:252:LEU:HD23	2.02	0.59
1:A:18:ASP:OD2	1:A:21:HIS:HB2	2.01	0.59
1:A:819:VAL:HG12	1:A:821:VAL:HG12	1.83	0.59
1:A:527:PRO:O	1:A:531:LYS:HG2	2.03	0.58
1:A:482:PHE:HD1	1:A:482:PHE:H	1.51	0.58
1:A:182:TYR:CE2	1:A:208:LEU:HD13	2.38	0.58
1:A:425:ARG:HB2	4:A:1075:HOH:O	2.03	0.58
1:A:273:LEU:HB3	1:A:279:GLY:HA2	1.86	0.58
1:A:216:ALA:CA	1:A:221:LEU:HB3	2.33	0.58
1:A:471:GLU:HG2	1:A:475:PHE:CZ	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:697:PHE:HE1	1:A:703:VAL:HG12	1.68	0.58
1:A:721:GLU:O	1:A:752:PRO:HB3	2.04	0.57
2:A:833:BGL:O1	2:A:833:BGL:H1'2	2.04	0.57
1:A:227:ALA:H	1:A:230:GLU:HB3	1.68	0.57
1:A:771:ARG:HH11	1:A:771:ARG:HG2	1.69	0.57
1:A:769:PHE:HB3	1:A:770:PRO:HD3	1.85	0.57
1:A:661:ALA:O	1:A:665:ILE:HG13	2.05	0.57
1:A:182:TYR:CZ	1:A:208:LEU:HD13	2.40	0.56
1:A:229:ARG:C	1:A:229:ARG:HD2	2.31	0.56
1:A:30:LEU:HD13	1:A:45:TYR:HD2	1.69	0.56
1:A:86:ALA:CB	1:A:87:PRO:HD3	2.31	0.56
1:A:458:ALA:O	1:A:461:LEU:HG	2.05	0.56
1:A:13:ARG:NH1	1:A:13:ARG:HB2	2.21	0.56
1:A:534:GLN:O	1:A:538:LEU:HB2	2.05	0.56
1:A:199:ILE:HG13	1:A:226:PRO:O	2.04	0.56
1:A:127:LYS:HG3	1:A:250:THR:CB	2.33	0.56
1:A:244:ASP:HA	1:A:247:LYS:HG3	1.88	0.56
1:A:423:GLU:O	1:A:427:LEU:HG	2.06	0.56
1:A:671:TYR:CE1	1:A:673:MET:HA	2.40	0.56
1:A:218:LEU:O	1:A:219:LYS:HB2	2.06	0.56
1:A:249:ARG:HG3	1:A:252:LEU:HD21	1.88	0.55
1:A:454:ALA:O	1:A:457:ARG:HG3	2.06	0.55
1:A:43:ALA:HB3	1:A:95:GLN:OE1	2.06	0.55
1:A:473:GLU:HG2	1:A:531:LYS:HE2	1.87	0.55
1:A:673:MET:HG2	1:A:677:ARG:HB3	1.87	0.55
1:A:319:ALA:O	1:A:362:ARG:NH2	2.39	0.55
1:A:19:GLY:HA2	1:A:47:PHE:HE2	1.72	0.55
1:A:226:PRO:O	1:A:228:ILE:N	2.40	0.55
1:A:547:ASP:O	1:A:550:PRO:HD2	2.07	0.54
1:A:227:ALA:N	1:A:230:GLU:HB3	2.21	0.54
1:A:207:LEU:O	1:A:209:GLU:N	2.41	0.54
1:A:216:ALA:HB2	1:A:221:LEU:HD12	1.90	0.54
1:A:626:GLU:CD	1:A:626:GLU:H	2.14	0.54
1:A:466:GLU:HA	1:A:469:ARG:NH2	2.23	0.54
1:A:147:GLN:NE2	1:A:248:VAL:HG21	2.23	0.53
1:A:445:GLU:HG3	1:A:562:THR:O	2.07	0.53
1:A:767:LYS:O	1:A:770:PRO:HD2	2.09	0.53
1:A:215:GLU:OE1	1:A:218:LEU:HB2	2.09	0.53
1:A:627:ASN:O	1:A:631:VAL:HG23	2.09	0.53
1:A:742:GLU:O	1:A:746:ARG:HD3	2.08	0.53
1:A:299:TRP:CG	1:A:300:PRO:N	2.77	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:467:ILE:HD13	1:A:539:THR:HG22	1.91	0.53
1:A:216:ALA:HB2	1:A:221:LEU:HB3	1.90	0.53
1:A:85:ARG:N	1:A:88:THR:HG1	2.08	0.52
1:A:227:ALA:HA	1:A:231:LYS:HG2	1.90	0.52
1:A:780:LEU:HD11	1:A:790:GLU:HB2	1.91	0.52
1:A:10:PRO:HG3	1:A:152:ARG:HH12	1.74	0.52
1:A:520:GLU:O	1:A:523:ARG:HG2	2.09	0.52
1:A:590:LEU:HG	1:A:593:ARG:NH2	2.24	0.52
1:A:162:LEU:O	1:A:164:THR:HG23	2.10	0.52
1:A:141:ALA:HB2	1:A:158:PRO:HG2	1.92	0.52
1:A:116:TYR:CE2	1:A:252:LEU:HD12	2.46	0.51
1:A:585:PRO:HG2	1:A:591:GLY:CA	2.40	0.51
1:A:53:LYS:O	1:A:56:LYS:HB2	2.10	0.51
1:A:149:LEU:HD11	1:A:163:ILE:O	2.10	0.51
1:A:741:ARG:O	1:A:745:GLU:HG3	2.11	0.51
1:A:180:ALA:HA	1:A:245:LEU:HD12	1.93	0.50
1:A:459:LEU:O	1:A:463:VAL:HG23	2.11	0.50
1:A:246:ALA:C	1:A:248:VAL:H	2.19	0.50
1:A:295:GLU:CD	1:A:295:GLU:H	2.19	0.50
1:A:299:TRP:O	1:A:300:PRO:C	2.54	0.50
1:A:648:GLY:CA	2:A:833:BGL:H5'1	2.41	0.50
1:A:143:LYS:HB3	1:A:179:TRP:HH2	1.76	0.50
1:A:217:LEU:CD2	1:A:218:LEU:HG	2.42	0.50
1:A:216:ALA:CB	1:A:221:LEU:HB3	2.42	0.50
1:A:735:ALA:HB3	1:A:741:ARG:HB3	1.93	0.50
1:A:646:MET:O	1:A:695:ARG:HD3	2.12	0.50
1:A:728:ARG:HB2	1:A:751:MET:HE3	1.94	0.50
1:A:737:VAL:HB	1:A:740:VAL:HB	1.93	0.50
1:A:778:ARG:HG3	1:A:790:GLU:HB3	1.94	0.50
1:A:174:LEU:HD12	1:A:178:GLN:OE1	2.12	0.50
1:A:674:SER:OG	1:A:677:ARG:HB2	2.11	0.50
1:A:792:PRO:O	1:A:795:ARG:HB2	2.11	0.50
1:A:636:ARG:HG2	1:A:636:ARG:HH11	1.77	0.50
1:A:229:ARG:NH1	1:A:233:LEU:HD11	2.26	0.49
1:A:503:ILE:HG21	1:A:517:ALA:HB1	1.94	0.49
1:A:36:SER:O	1:A:37:ARG:HG3	2.12	0.49
1:A:217:LEU:HB2	1:A:232:ILE:HG23	1.94	0.49
1:A:262:ARG:N	1:A:262:ARG:HD2	2.28	0.49
1:A:299:TRP:C	1:A:299:TRP:CD2	2.88	0.49
1:A:673:MET:O	1:A:677:ARG:HD3	2.13	0.49
1:A:728:ARG:HD3	1:A:747:MET:HE3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:545:TYR:OH	1:A:583:ASN:HB2	2.12	0.49
1:A:541:LEU:HD23	1:A:590:LEU:HD13	1.94	0.49
1:A:54:ALA:CB	1:A:139:LEU:HD12	2.43	0.49
1:A:207:LEU:CD2	1:A:210:GLU:HB2	2.35	0.49
1:A:314:LYS:HE3	1:A:315:GLU:OE2	2.13	0.49
1:A:143:LYS:O	1:A:179:TRP:CZ3	2.66	0.49
1:A:198:GLY:HA2	1:A:203:THR:CA	2.41	0.49
1:A:629:ILE:HD13	1:A:814:ALA:HB1	1.95	0.49
1:A:295:GLU:O	1:A:331:ARG:HA	2.13	0.48
1:A:691:ALA:O	1:A:695:ARG:HG3	2.13	0.48
1:A:19:GLY:HA2	1:A:47:PHE:CE2	2.49	0.48
1:A:248:VAL:O	1:A:248:VAL:HG23	2.13	0.48
1:A:137:ARG:HB3	1:A:156:LEU:HD13	1.94	0.48
1:A:262:ARG:HD2	1:A:262:ARG:H	1.78	0.48
1:A:211:TRP:CZ3	1:A:228:ILE:HA	2.49	0.48
1:A:747:MET:HA	1:A:750:ASN:HB3	1.95	0.48
1:A:230:GLU:O	1:A:233:LEU:HD12	2.14	0.48
1:A:487:ARG:NH2	1:A:511:LYS:HE2	2.29	0.47
1:A:604:TRP:CE3	1:A:790:GLU:HG2	2.48	0.47
1:A:683:ALA:O	1:A:684:ILE:HD12	2.14	0.47
1:A:633:GLN:NE2	1:A:814:ALA:O	2.46	0.47
1:A:26:THR:HB	1:A:46:GLY:HA3	1.96	0.47
1:A:215:GLU:O	1:A:216:ALA:HB3	2.13	0.47
1:A:255:GLU:O	1:A:256:VAL:C	2.57	0.47
1:A:651:ARG:HG3	1:A:652:GLU:N	2.29	0.47
1:A:236:MET:O	1:A:237:ASP:HB2	2.14	0.47
1:A:719:TYR:CD1	1:A:727:ARG:HG3	2.49	0.47
1:A:42:GLN:NE2	1:A:42:GLN:H	2.12	0.47
1:A:34:THR:CG2	1:A:40:PRO:HA	2.34	0.47
1:A:496:ASP:C	1:A:497:GLU:HG3	2.39	0.47
1:A:208:LEU:N	1:A:211:TRP:HE1	2.13	0.47
1:A:246:ALA:C	1:A:248:VAL:N	2.72	0.47
1:A:625:ASP:OD2	1:A:700:PHE:HD1	1.98	0.47
1:A:272:PHE:HA	1:A:275:ARG:NH1	2.30	0.47
1:A:186:THR:OG1	1:A:208:LEU:HD21	2.15	0.46
1:A:283:HIS:ND1	1:A:283:HIS:C	2.73	0.46
1:A:119:ASP:HA	1:A:122:LEU:HD12	1.96	0.46
1:A:147:GLN:CD	1:A:180:ALA:HB2	2.41	0.46
1:A:155:VAL:HB	1:A:163:ILE:HB	1.97	0.46
1:A:164:THR:O	1:A:167:TRP:HB3	2.15	0.46
1:A:209:GLU:CD	1:A:209:GLU:H	2.24	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:629:ILE:O	1:A:633:GLN:HG2	2.16	0.46
1:A:545:TYR:O	1:A:549:LEU:HD22	2.15	0.46
1:A:563:ARG:O	1:A:576:CYS:HA	2.16	0.46
1:A:207:LEU:HD11	1:A:228:ILE:HG12	1.96	0.46
1:A:424:GLU:HG2	4:A:953:HOH:O	2.16	0.46
1:A:673:MET:O	1:A:674:SER:CB	2.65	0.45
1:A:68:ALA:HB3	1:A:113:VAL:O	2.16	0.45
1:A:376:LEU:HD11	1:A:413:PHE:CE1	2.52	0.45
1:A:498:LEU:HD12	1:A:499:GLY:H	1.80	0.45
1:A:313:ARG:HD3	1:A:318:TRP:O	2.16	0.45
1:A:671:TYR:HA	1:A:749:PHE:HE1	1.81	0.45
1:A:174:LEU:HD12	1:A:178:GLN:CD	2.41	0.45
1:A:477:LEU:O	1:A:478:ALA:HB3	2.16	0.45
1:A:507:GLU:OE1	1:A:517:ALA:HB2	2.17	0.45
1:A:44:VAL:HA	1:A:99:ILE:CD1	2.41	0.45
1:A:485:ASN:O	1:A:487:ARG:N	2.49	0.45
1:A:466:GLU:HG2	1:A:469:ARG:HH22	1.80	0.45
1:A:174:LEU:HD21	1:A:209:GLU:HB3	1.99	0.45
1:A:249:ARG:HG3	1:A:252:LEU:CD2	2.46	0.45
1:A:243:TRP:HD1	1:A:244:ASP:N	2.14	0.45
1:A:475:PHE:CZ	1:A:482:PHE:O	2.69	0.45
1:A:522:LEU:N	1:A:522:LEU:HD12	2.32	0.45
1:A:40:PRO:HD2	1:A:94:ARG:HH12	1.82	0.44
1:A:58:ASP:HB2	1:A:59:GLY:H	1.61	0.44
1:A:244:ASP:HA	1:A:247:LYS:CG	2.47	0.44
1:A:726:ARG:O	1:A:751:MET:HE1	2.17	0.44
1:A:529:VAL:C	1:A:532:ILE:HG22	2.43	0.44
1:A:111:LEU:HD22	1:A:256:VAL:HG11	1.99	0.44
1:A:140:THR:O	1:A:158:PRO:HD3	2.18	0.44
1:A:307:VAL:HG23	4:A:1126:HOH:O	2.17	0.44
1:A:40:PRO:HD2	1:A:94:ARG:NH1	2.32	0.44
1:A:482:PHE:CE2	1:A:493:VAL:HG21	2.52	0.44
1:A:601:GLU:HG3	4:A:1155:HOH:O	2.16	0.44
1:A:604:TRP:HE3	1:A:790:GLU:HG2	1.83	0.44
1:A:303:GLU:HA	4:A:1057:HOH:O	2.16	0.44
1:A:471:GLU:HG3	1:A:484:LEU:HD12	2.00	0.44
1:A:778:ARG:HD2	1:A:790:GLU:OE1	2.17	0.44
1:A:198:GLY:O	1:A:199:ILE:HB	2.18	0.44
1:A:761:MET:HB2	4:A:910:HOH:O	2.18	0.44
1:A:611:TYR:HB3	1:A:614:ILE:HB	2.00	0.44
1:A:296:GLU:OE2	1:A:334:ARG:NH1	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:506:THR:HG21	4:A:1145:HOH:O	2.16	0.43
1:A:697:PHE:CE1	1:A:703:VAL:HG12	2.52	0.43
1:A:233:LEU:C	1:A:235:HIS:H	2.24	0.43
1:A:674:SER:HG	1:A:677:ARG:HB2	1.83	0.43
1:A:189:GLU:C	1:A:191:ASP:H	2.26	0.43
1:A:317:MET:SD	1:A:362:ARG:HB2	2.58	0.43
1:A:456:LEU:HB3	4:A:984:HOH:O	2.18	0.43
1:A:187:GLY:O	1:A:188:ASP:C	2.62	0.43
1:A:207:LEU:HD22	1:A:211:TRP:CD1	2.54	0.43
1:A:807:MET:O	1:A:810:VAL:HG12	2.19	0.43
1:A:24:TYR:CZ	1:A:28:HIS:HE1	2.35	0.43
1:A:487:ARG:HH21	1:A:511:LYS:HE2	1.84	0.43
1:A:541:LEU:HD11	1:A:585:PRO:HD3	2.01	0.43
1:A:570:ALA:HB1	1:A:747:MET:HE1	1.99	0.43
1:A:771:ARG:HG2	1:A:771:ARG:NH1	2.32	0.43
1:A:378:TYR:CD1	1:A:567:THR:HB	2.53	0.43
1:A:190:SER:O	1:A:192:ASN:N	2.52	0.43
1:A:283:HIS:ND1	1:A:283:HIS:O	2.52	0.43
1:A:470:LEU:HD13	1:A:531:LYS:HE3	2.01	0.43
1:A:529:VAL:O	1:A:532:ILE:HG22	2.19	0.43
1:A:639:HIS:HD2	1:A:663:LYS:HA	1.79	0.43
1:A:490:LEU:O	1:A:494:LEU:HG	2.19	0.42
1:A:484:LEU:O	1:A:485:ASN:HB2	2.19	0.42
1:A:518:VAL:O	1:A:519:LEU:HB3	2.17	0.42
1:A:229:ARG:HH11	1:A:233:LEU:HD11	1.84	0.42
1:A:589:PRO:O	1:A:593:ARG:HG3	2.19	0.42
1:A:829:SER:C	1:A:831:LYS:N	2.76	0.42
1:A:58:ASP:O	1:A:137:ARG:NH2	2.53	0.42
1:A:146:TYR:HB2	1:A:179:TRP:CE3	2.54	0.42
1:A:117:GLU:O	1:A:118:ALA:C	2.62	0.42
1:A:412:LEU:O	1:A:416:LEU:HB2	2.20	0.42
1:A:35:THR:O	1:A:37:ARG:N	2.52	0.42
1:A:352:LEU:HD11	1:A:387:PRO:HG2	2.01	0.42
1:A:137:ARG:NH1	1:A:156:LEU:HD21	2.35	0.42
1:A:47:PHE:HB3	1:A:99:ILE:CD1	2.50	0.41
1:A:199:ILE:CG1	1:A:227:ALA:HB3	2.49	0.41
1:A:761:MET:HE1	1:A:807:MET:CE	2.49	0.41
1:A:34:THR:HG22	1:A:40:PRO:CA	2.34	0.41
1:A:99:ILE:HD13	1:A:99:ILE:HA	1.72	0.41
1:A:802:LEU:O	1:A:806:VAL:HG23	2.19	0.41
1:A:224:LEU:HG	1:A:225:LYS:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:647:PHE:O	1:A:649:VAL:HG13	2.20	0.41
1:A:567:THR:O	1:A:568:ALA:HB3	2.21	0.41
1:A:193:LEU:N	1:A:194:PRO:HD3	2.34	0.41
1:A:354:LYS:HE3	1:A:354:LYS:HB3	1.93	0.41
1:A:795:ARG:HG3	1:A:795:ARG:HH11	1.85	0.41
1:A:828:LEU:O	1:A:828:LEU:HG	2.21	0.41
1:A:230:GLU:O	1:A:234:ALA:HB2	2.20	0.41
1:A:239:LEU:C	1:A:241:LEU:H	2.28	0.41
1:A:419:ARG:NE	1:A:419:ARG:HA	2.36	0.41
1:A:466:GLU:HA	1:A:469:ARG:NH1	2.35	0.41
1:A:501:PRO:HB2	1:A:502:ALA:H	1.60	0.41
1:A:811:TYR:HA	1:A:812:PRO:HD2	1.86	0.41
1:A:175:ARG:HB2	1:A:177:ASP:OD1	2.21	0.41
1:A:220:ASN:O	1:A:221:LEU:HB2	2.21	0.41
1:A:256:VAL:O	1:A:256:VAL:HG13	2.21	0.41
1:A:500:LEU:HA	1:A:501:PRO:HD3	1.84	0.41
1:A:47:PHE:HB3	1:A:99:ILE:HD11	2.03	0.40
1:A:573:ARG:NH1	4:A:1034:HOH:O	2.54	0.40
1:A:676:HIS:O	1:A:679:SER:HB3	2.21	0.40
1:A:139:LEU:HD23	1:A:139:LEU:C	2.46	0.40
1:A:185:LEU:HD12	1:A:185:LEU:O	2.21	0.40
1:A:204:ALA:HA	1:A:211:TRP:HZ2	1.86	0.40
1:A:535:TYR:O	1:A:539:THR:HG23	2.21	0.40
1:A:193:LEU:HD13	1:A:242:SER:OG	2.22	0.40
1:A:794:GLU:O	1:A:795:ARG:HG2	2.21	0.40
1:A:199:ILE:HD11	1:A:226:PRO:HB2	2.03	0.40
1:A:512:ARG:HD2	1:A:512:ARG:O	2.22	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	803/832 (96%)	675 (84%)	92 (12%)	36 (4%)	2 1

All (36) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	37	ARG
1	A	87	PRO
1	A	161	TYR
1	A	208	LEU
1	A	220	ASN
1	A	221	LEU
1	A	256	VAL
1	A	292	LYS
1	A	299	TRP
1	A	487	ARG
1	A	501	PRO
1	A	674	SER
1	A	31	LYS
1	A	36	SER
1	A	188	ASP
1	A	203	THR
1	A	219	LYS
1	A	509	THR
1	A	58	ASP
1	A	197	LYS
1	A	204	ALA
1	A	227	ALA
1	A	486	SER
1	A	39	GLU
1	A	216	ALA
1	A	831	LYS
1	A	199	ILE
1	A	300	PRO
1	A	118	ALA
1	A	287	LEU
1	A	507	GLU
1	A	673	MET
1	A	187	GLY
1	A	382	PRO
1	A	248	VAL
1	A	298	PRO

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	665/683 (97%)	591 (89%)	74 (11%)	6 9

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	GLN
1	A	52	LEU
1	A	55	LEU
1	A	90	GLU
1	A	99	ILE
1	A	132	GLU
1	A	142	ASP
1	A	161	TYR
1	A	162	LEU
1	A	168	LEU
1	A	169	TRP
1	A	170	GLU
1	A	171	LYS
1	A	178	GLN
1	A	182	TYR
1	A	189	GLU
1	A	199	ILE
1	A	206	LYS
1	A	207	LEU
1	A	209	GLU
1	A	211	TRP
1	A	217	LEU
1	A	229	ARG
1	A	233	LEU
1	A	235	HIS
1	A	245	LEU
1	A	266	ARG
1	A	283	HIS
1	A	288	LEU
1	A	292	LYS

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Mol	Chain	Res	Type
1	A	359	LEU
1	A	365	LEU
1	A	405	ARG
1	A	420	LEU
1	A	435	ARG
1	A	449	VAL
1	A	453	VAL
1	A	456	LEU
1	A	457	ARG
1	A	461	LEU
1	A	473	GLU
1	A	480	HIS
1	A	482	PHE
1	A	487	ARG
1	A	495	PHE
1	A	497	GLU
1	A	500	LEU
1	A	506	THR
1	A	509	THR
1	A	512	ARG
1	A	518	VAL
1	A	523	ARG
1	A	573	ARG
1	A	579	PRO
1	A	592	GLN
1	A	601	GLU
1	A	626	GLU
1	A	644	SER
1	A	652	GLU
1	A	657	LEU
1	A	660	ARG
1	A	664	THR
1	A	670	LEU
1	A	681	GLU
1	A	682	LEU
1	A	684	ILE
1	A	699	SER
1	A	742	GLU
1	A	781	LEU
1	A	805	GLU
1	A	817	LEU
1	A	818	GLU

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Mol	Chain	Res	Type
1	A	821	VAL
1	A	831	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	HIS
1	A	154	HIS
1	A	443	HIS
1	A	485	ASN
1	A	566	GLN
1	A	613	GLN
1	A	639	HIS
1	A	782	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](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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	BGL	A	833	-	20,20,20	1.16	1 (5%)	24,25,25	2.26	9 (37%)

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	BGL	A	833	-	-	3/11/31/31	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	833	BGL	C4-C5	3.47	1.60	1.53

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	833	BGL	C6-C5-C4	5.71	127.05	113.02
2	A	833	BGL	O5-C5-C4	-4.07	102.36	109.70
2	A	833	BGL	C1-O5-C5	-3.63	106.62	113.65
2	A	833	BGL	O3-C3-C2	3.25	118.28	109.94
2	A	833	BGL	O4-C4-C3	3.10	117.68	110.38
2	A	833	BGL	O6-C6-C5	3.04	121.69	111.33
2	A	833	BGL	C3-C4-C5	-2.65	105.43	110.23
2	A	833	BGL	O2-C2-C3	2.05	113.94	109.83
2	A	833	BGL	O2-C1'-C2'	2.01	116.20	109.37

There are no chirality outliers.

All (3) torsion outliers are listed below:

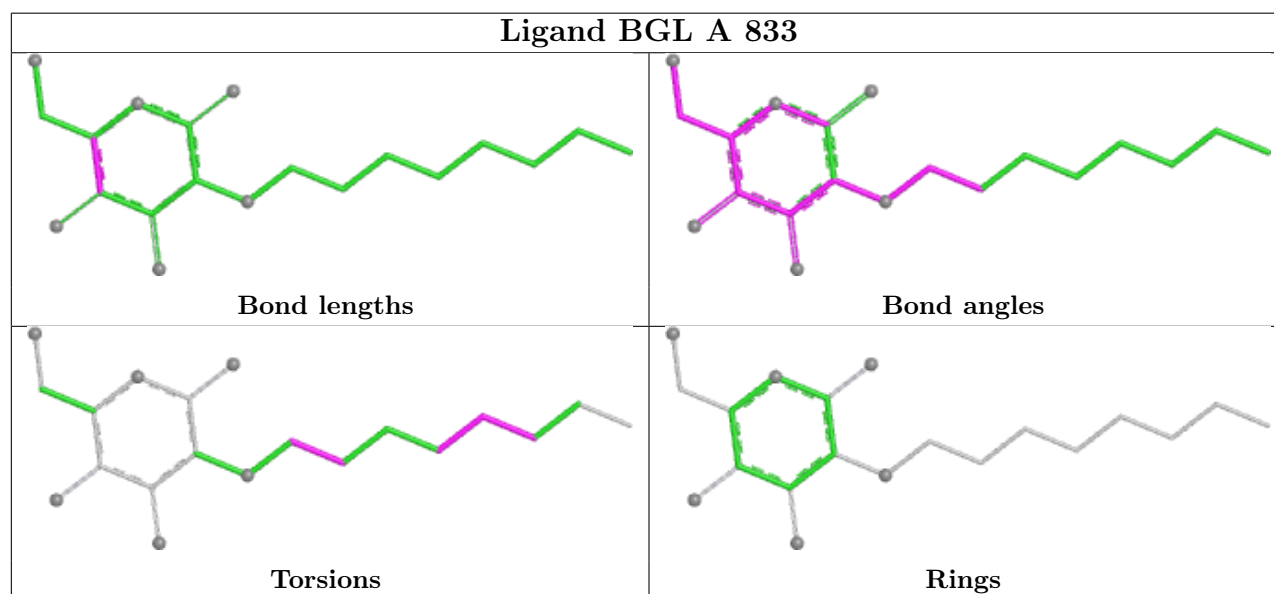
Mol	Chain	Res	Type	Atoms
2	A	833	BGL	C3'-C4'-C5'-C6'
2	A	833	BGL	O2-C1'-C2'-C3'
2	A	833	BGL	C4'-C5'-C6'-C7'

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	833	BGL	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	807/832 (96%)	0.42	91 (11%) 10 7	10, 43, 98, 100	0

All (91) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	217	LEU	5.8
1	A	525	ALA	5.6
1	A	228	ILE	5.5
1	A	232	ILE	5.5
1	A	204	ALA	5.0
1	A	196	VAL	4.9
1	A	194	PRO	4.7
1	A	211	TRP	4.5
1	A	169	TRP	4.4
1	A	198	GLY	4.2
1	A	86	ALA	4.2
1	A	208	LEU	4.1
1	A	509	THR	4.1
1	A	193	LEU	4.1
1	A	212	GLY	4.0
1	A	514	THR	4.0
1	A	510	GLY	4.0
1	A	203	THR	3.8
1	A	191	ASP	3.8
1	A	502	ALA	3.7
1	A	526	HIS	3.7
1	A	294	LEU	3.6
1	A	68	ALA	3.6
1	A	218	LEU	3.6
1	A	233	LEU	3.5
1	A	184	ALA	3.5
1	A	227	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	498	LEU	3.4
1	A	495	PHE	3.3
1	A	500	LEU	3.3
1	A	195	GLY	3.3
1	A	477	LEU	3.3
1	A	226	PRO	3.2
1	A	506	THR	3.2
1	A	293	ALA	3.1
1	A	239	LEU	3.1
1	A	503	ILE	3.0
1	A	236	MET	3.0
1	A	529	VAL	2.9
1	A	519	LEU	2.9
1	A	290	SER	2.8
1	A	205	ARG	2.7
1	A	167	TRP	2.7
1	A	214	LEU	2.7
1	A	209	GLU	2.7
1	A	246	ALA	2.7
1	A	247	LYS	2.6
1	A	185	LEU	2.6
1	A	508	LYS	2.6
1	A	501	PRO	2.6
1	A	478	ALA	2.6
1	A	494	LEU	2.6
1	A	85	ARG	2.5
1	A	87	PRO	2.5
1	A	527	PRO	2.5
1	A	507	GLU	2.5
1	A	243	TRP	2.5
1	A	245	LEU	2.5
1	A	517	ALA	2.5
1	A	672	GLY	2.5
1	A	497	GLU	2.5
1	A	172	TYR	2.4
1	A	197	LYS	2.4
1	A	528	ILE	2.4
1	A	496	ASP	2.4
1	A	522	LEU	2.4
1	A	674	SER	2.3
1	A	199	ILE	2.3
1	A	192	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	422	GLY	2.3
1	A	512	ARG	2.3
1	A	242	SER	2.2
1	A	148	LEU	2.2
1	A	515	SER	2.2
1	A	145	LEU	2.2
1	A	153	ILE	2.2
1	A	513	SER	2.2
1	A	30	LEU	2.2
1	A	146	TYR	2.2
1	A	499	GLY	2.2
1	A	524	GLU	2.2
1	A	518	VAL	2.1
1	A	235	HIS	2.1
1	A	88	THR	2.1
1	A	585	PRO	2.1
1	A	292	LYS	2.1
1	A	179	TRP	2.1
1	A	202	LYS	2.0
1	A	291	PRO	2.0
1	A	586	VAL	2.0
1	A	505	LYS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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, 95th 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.

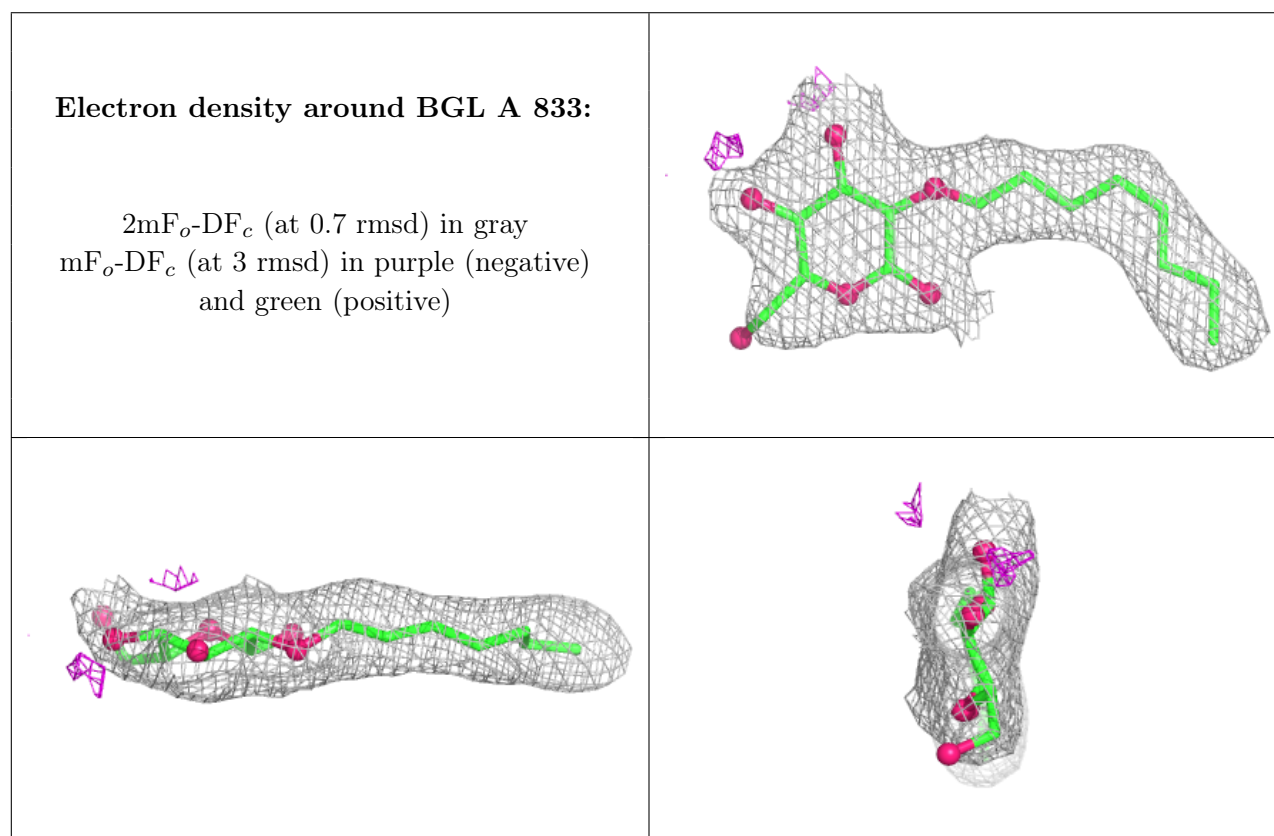
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	ZN	A	900	1/1	0.63	0.43	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	BGL	A	833	20/20	0.95	0.07	2,24,46,57	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.