



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 07:48 AM UTC

PDB ID : 2G7K / pdb_00002g7k
Title : Structure of the Light Chain of Botulinum Neurotoxin, Serotype A Bound to small Molecule Inhibitors
Authors : Fu, Z.; Baldwin, M.R.; Boldt, G.E.; Crawford, A.; Janda, K.D.; Barbieri, J.T.; Kim, J.-J.P.
Deposited on : 2006-02-28
Resolution : 2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ 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
Xtriage (Phenix)	:	2.0
EDS	:	3.0
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

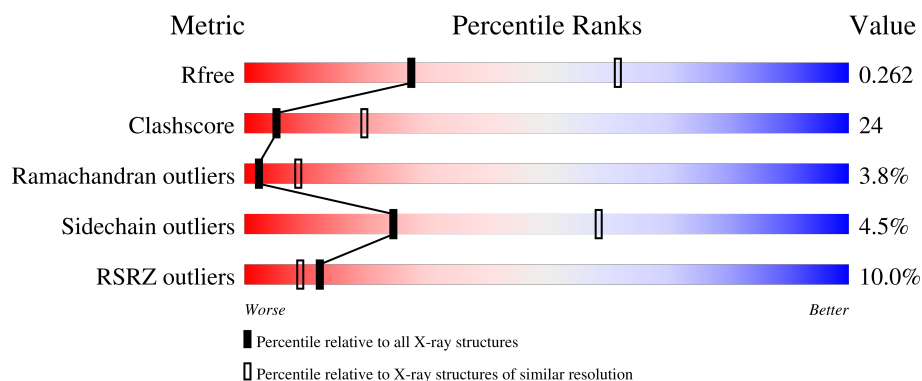
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	425	
1	B	425	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6481 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 Botulinum neurotoxin type A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	401	Total	C	N	O	S	0	0	0
			3247	2084	536	620	7			
1	B	399	Total	C	N	O	S	0	0	0
			3234	2076	534	617	7			

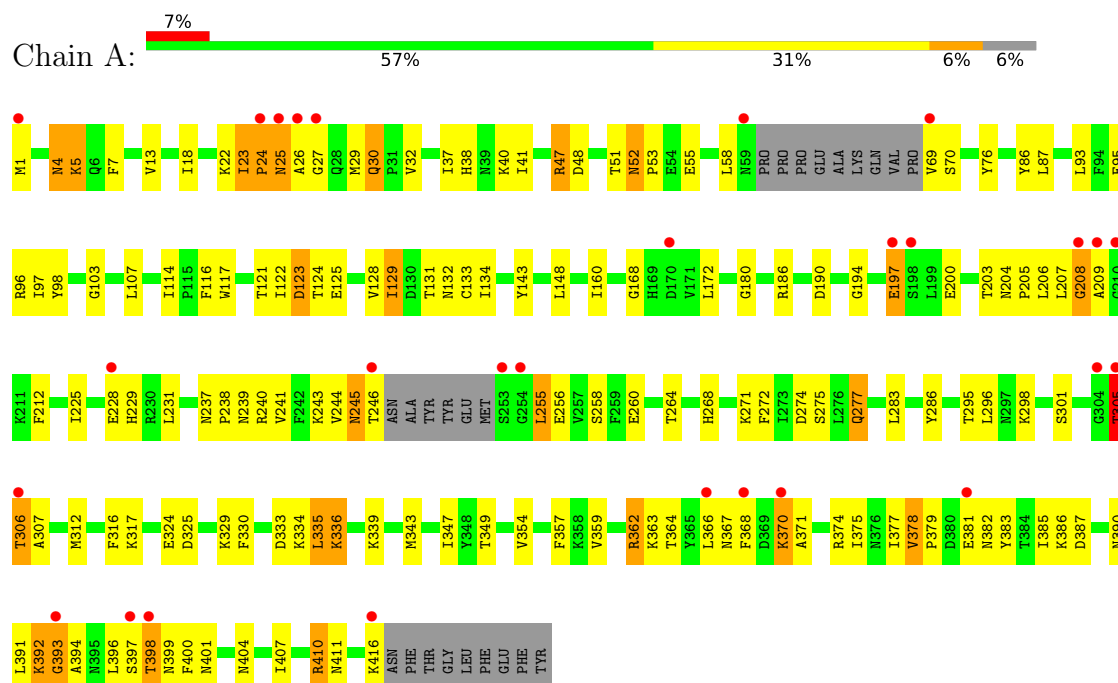
There are 2 discrepancies between the modelled and reference sequences:

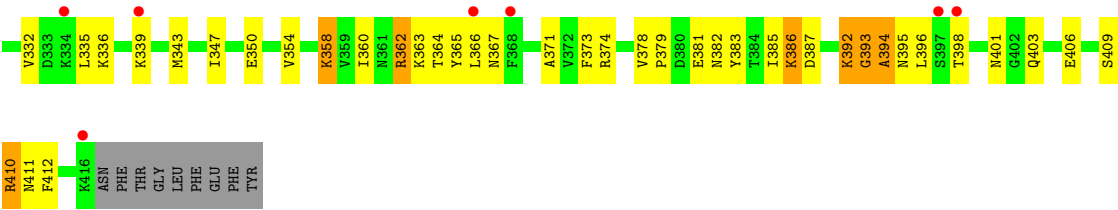
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q45894
B	1	MET	-	initiating methionine	UNP Q45894

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 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: Botulinum neurotoxin type A





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	69.10Å 110.09Å 167.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.98 – 2.80 29.98 – 2.80	Depositor EDS
% Data completeness (in resolution range)	94.9 (29.98-2.80) 94.8 (29.98-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.03 (at 2.80Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.223 , 0.265 0.223 , 0.262	Depositor DCC
R_{free} test set	3059 reflections (10.03%)	wwPDB-VP
Wilson B-factor (Å ²)	36.8	Xtriage
Anisotropy	0.160	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 56.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	6481	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.20% 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

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	0.51	1/3317 (0.0%)	0.99	20/4482 (0.4%)
1	B	0.47	0/3304	0.94	7/4464 (0.2%)
All	All	0.49	1/6621 (0.0%)	0.96	27/8946 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	378	VAL	CA-CB	5.11	1.57	1.54

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	399	ASN	N-CA-C	-8.01	103.46	113.23
1	A	26	ALA	N-CA-C	-6.88	103.98	112.38
1	A	131	THR	N-CA-C	-6.63	105.18	113.20
1	A	317	LYS	N-CA-C	-6.44	104.34	111.36
1	A	129	ILE	N-CA-C	-6.43	97.72	106.85
1	A	286	TYR	N-CA-C	-6.42	104.20	111.07
1	B	39	ASN	N-CA-C	6.17	118.51	111.11
1	A	334	LYS	N-CA-C	6.16	118.78	111.33
1	A	305	THR	N-CA-C	6.13	123.85	110.80
1	B	41	ILE	N-CA-C	6.12	116.73	108.17
1	A	23	ILE	CA-C-N	-6.09	113.69	119.90
1	A	23	ILE	C-N-CA	-6.09	113.69	119.90
1	B	26	ALA	N-CA-C	-5.90	104.93	111.36
1	B	363	LYS	N-CA-C	-5.87	106.28	113.50
1	A	52	ASN	CA-C-N	5.76	124.97	118.97
1	A	52	ASN	C-N-CA	5.76	124.97	118.97
1	B	160	ILE	N-CA-C	5.72	117.00	111.91
1	A	121	THR	N-CA-C	-5.67	106.35	113.72
1	A	47	ARG	N-CA-C	-5.56	100.91	109.76
1	A	30	GLN	N-CA-C	-5.38	102.86	110.29
1	A	4	ASN	N-CA-C	5.32	117.87	108.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	272	PHE	N-CA-C	-5.29	106.78	113.18
1	A	336	LYS	N-CA-C	-5.13	105.39	111.69
1	A	41	ILE	N-CA-C	5.12	115.35	107.77
1	B	395	ASN	N-CA-C	-5.10	106.90	113.02
1	A	186	ARG	N-CA-C	-5.07	102.14	109.59
1	B	382	ASN	N-CA-C	-5.03	107.10	113.43

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	3247	0	3192	135	0
1	B	3234	0	3178	182	0
All	All	6481	0	6370	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 24.

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:A:410:ARG:HH11	1:A:410:ARG:HB2	1.05	1.08
1:A:387:ASP:OD2	1:A:392:LYS:HG3	1.55	1.04
1:A:410:ARG:HB2	1:A:410:ARG:NH1	1.74	1.02
1:B:5:LYS:HD3	1:B:7:PHE:HE2	1.29	0.98
1:B:410:ARG:HH11	1:B:410:ARG:HB2	1.27	0.96
1:A:343:MET:HA	1:A:347:ILE:HD12	1.44	0.95
1:A:410:ARG:HH11	1:A:410:ARG:CB	1.80	0.95
1:A:225:ILE:O	1:A:228:GLU:HG2	1.66	0.94
1:A:209:ALA:H	1:A:404:ASN:HD21	1.18	0.89
1:B:265:PHE:HE2	1:B:362:ARG:HH12	1.20	0.88
1:B:122:ILE:HG22	1:B:124:THR:HG22	1.56	0.87
1:B:5:LYS:HD3	1:B:7:PHE:CE2	2.10	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:117:TRP:CE2	1:B:128:VAL:HB	2.11	0.85
1:B:362:ARG:HH11	1:B:362:ARG:HB2	1.42	0.84
1:B:374:ARG:HH11	1:B:374:ARG:HG3	1.44	0.82
1:B:5:LYS:CD	1:B:7:PHE:HE2	1.92	0.82
1:B:387:ASP:OD2	1:B:392:LYS:HG3	1.79	0.81
1:B:410:ARG:HB2	1:B:410:ARG:NH1	1.97	0.79
1:B:204:ASN:ND2	1:B:206:LEU:H	1.81	0.79
1:B:325:ASP:OD2	1:B:329:LYS:HB3	1.83	0.79
1:A:228:GLU:HG3	1:A:229:HIS:N	1.98	0.77
1:B:362:ARG:HH11	1:B:362:ARG:CB	1.96	0.77
1:B:228:GLU:HG3	1:B:229:HIS:H	1.51	0.76
1:A:391:LEU:O	1:A:397:SER:HB3	1.85	0.76
1:A:275:SER:HB2	1:B:243:LYS:HG2	1.66	0.76
1:B:362:ARG:HB2	1:B:362:ARG:NH1	2.01	0.75
1:A:305:THR:C	1:A:307:ALA:H	1.95	0.75
1:B:5:LYS:CB	1:B:7:PHE:CE2	2.71	0.73
1:B:300:LYS:O	1:B:309:LEU:HD22	1.88	0.73
1:B:181:SER:O	1:B:231:LEU:HD23	1.89	0.73
1:A:268:HIS:CE1	1:B:268:HIS:HB3	2.24	0.73
1:B:255:LEU:HD12	1:B:255:LEU:O	1.89	0.72
1:B:204:ASN:C	1:B:204:ASN:HD22	1.97	0.71
1:B:5:LYS:HB2	1:B:7:PHE:CE2	2.24	0.71
1:A:70:SER:HA	1:A:160:ILE:HD11	1.72	0.71
1:B:5:LYS:HB2	1:B:7:PHE:CZ	2.26	0.70
1:B:122:ILE:CG2	1:B:124:THR:HG22	2.21	0.70
1:A:397:SER:O	1:A:398:THR:HG23	1.92	0.70
1:A:209:ALA:N	1:A:404:ASN:HD21	1.90	0.70
1:B:172:LEU:H	1:B:172:LEU:HD23	1.56	0.70
1:A:239:ASN:HD21	1:A:240:ARG:HH12	1.39	0.69
1:B:78:SER:O	1:B:83:LYS:HE3	1.94	0.68
1:A:324:GLU:HB2	1:A:330:PHE:CE1	2.29	0.68
1:B:116:PHE:HA	1:B:316:PHE:CE1	2.29	0.68
1:B:134:ILE:HG23	1:B:148:LEU:HD21	1.76	0.67
1:B:266:GLY:HA2	1:B:270:ALA:HB2	1.75	0.67
1:A:245:ASN:HD22	1:A:246:THR:N	1.93	0.67
1:A:305:THR:C	1:A:307:ALA:N	2.51	0.66
1:B:169:HIS:CD2	1:B:171:VAL:H	2.13	0.66
1:B:96:ARG:HA	1:B:385:ILE:HG23	1.78	0.66
1:A:382:ASN:HB3	1:A:411:ASN:OD1	1.95	0.66
1:A:225:ILE:O	1:A:228:GLU:CG	2.44	0.65
1:A:4:ASN:O	1:A:5:LYS:HB3	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:335:LEU:HD12	1:A:339:LYS:HE3	1.79	0.64
1:A:305:THR:O	1:A:307:ALA:N	2.31	0.64
1:A:354:VAL:HG12	1:B:201:VAL:HG21	1.80	0.64
1:B:312:MET:O	1:B:315:VAL:HG22	1.98	0.64
1:B:204:ASN:HD22	1:B:205:PRO:N	1.97	0.63
1:B:124:THR:HA	1:B:299:ALA:HA	1.78	0.63
1:A:335:LEU:O	1:A:339:LYS:HG3	1.99	0.62
1:B:228:GLU:HG3	1:B:229:HIS:N	2.13	0.62
1:A:239:ASN:HD21	1:A:240:ARG:NH1	1.98	0.62
1:B:130:ASP:OD2	1:B:130:ASP:N	2.30	0.62
1:B:396:LEU:HA	1:B:401:ASN:HB2	1.81	0.62
1:A:204:ASN:HD22	1:A:205:PRO:N	1.98	0.61
1:A:245:ASN:HD22	1:A:245:ASN:C	2.08	0.60
1:A:29:MET:HE2	1:A:30:GLN:O	2.01	0.60
1:B:125:GLU:HA	1:B:301:SER:O	2.02	0.60
1:A:225:ILE:CG2	1:A:264:THR:HG23	2.32	0.60
1:B:315:VAL:HG23	1:B:316:PHE:N	2.16	0.60
1:B:315:VAL:CG2	1:B:316:PHE:N	2.64	0.60
1:A:392:LYS:O	1:A:394:ALA:N	2.34	0.60
1:A:204:ASN:HD22	1:A:204:ASN:C	2.10	0.59
1:A:197:GLU:OE2	1:A:207:LEU:HB2	2.02	0.59
1:B:225:ILE:O	1:B:228:GLU:HG3	2.03	0.59
1:A:325:ASP:OD2	1:A:329:LYS:HB3	2.03	0.59
1:B:34:ALA:HB2	1:B:44:ILE:HG12	1.84	0.59
1:A:22:LYS:O	1:A:24:PRO:HD3	2.02	0.59
1:A:122:ILE:HG22	1:A:124:THR:HG22	1.83	0.59
1:A:204:ASN:ND2	1:A:206:LEU:H	2.01	0.59
1:A:47:ARG:CZ	1:A:58:LEU:HD13	2.33	0.58
1:B:50:PHE:O	1:B:52:ASN:N	2.37	0.58
1:B:224:LEU:O	1:B:227:ALA:HB3	2.03	0.58
1:A:228:GLU:HG3	1:A:229:HIS:H	1.69	0.58
1:B:127:LYS:HG2	1:B:128:VAL:N	2.18	0.58
1:B:106:LEU:O	1:B:110:ILE:HG13	2.04	0.57
1:A:204:ASN:HD22	1:A:205:PRO:CD	2.17	0.57
1:B:392:LYS:O	1:B:394:ALA:N	2.37	0.57
1:A:241:VAL:HG12	1:A:258:SER:HA	1.86	0.57
1:B:161:GLN:HG3	1:B:161:GLN:O	2.04	0.57
1:A:400:PHE:CZ	1:B:201:VAL:HG12	2.40	0.56
1:B:50:PHE:C	1:B:52:ASN:H	2.13	0.56
1:B:22:LYS:HB2	1:B:135:ASN:HB2	1.87	0.56
1:B:204:ASN:HB3	1:B:207:LEU:HD13	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:302:ILE:HB	1:B:309:LEU:HD12	1.87	0.56
1:B:358:LYS:HB2	1:B:358:LYS:NZ	2.20	0.56
1:A:13:VAL:HA	1:A:18:ILE:HG22	1.86	0.56
1:B:101:ASP:HA	1:B:104:ARG:NH1	2.21	0.56
1:B:225:ILE:O	1:B:228:GLU:CG	2.54	0.56
1:B:23:ILE:HG22	1:B:26:ALA:HB2	1.87	0.56
1:B:5:LYS:CD	1:B:7:PHE:CE2	2.78	0.56
1:B:5:LYS:HB3	1:B:7:PHE:CE2	2.40	0.56
1:A:324:GLU:HB2	1:A:330:PHE:CD1	2.41	0.56
1:A:134:ILE:HD13	1:A:148:LEU:HD13	1.88	0.55
1:A:40:LYS:HE3	1:A:114:ILE:HD11	1.89	0.55
1:B:169:HIS:CG	1:B:170:ASP:N	2.74	0.55
1:B:392:LYS:O	1:B:393:GLY:C	2.49	0.55
1:A:69:VAL:HG23	1:A:416:LYS:HD3	1.87	0.55
1:B:374:ARG:HH11	1:B:374:ARG:CG	2.18	0.55
1:B:204:ASN:ND2	1:B:204:ASN:C	2.65	0.55
1:B:134:ILE:HD13	1:B:148:LEU:HD13	1.89	0.55
1:A:245:ASN:C	1:A:245:ASN:ND2	2.65	0.54
1:B:266:GLY:CA	1:B:270:ALA:HB2	2.36	0.54
1:B:360:ILE:HG22	1:B:403:GLN:CD	2.32	0.54
1:A:69:VAL:CG2	1:A:416:LYS:HD3	2.38	0.54
1:A:204:ASN:HD22	1:A:205:PRO:HD2	1.72	0.54
1:A:194:GLY:HA2	1:A:212:PHE:O	2.07	0.54
1:A:200:GLU:HB2	1:A:203:THR:HG23	1.90	0.54
1:A:93:LEU:HD21	1:A:377:ILE:HD13	1.89	0.53
1:B:343:MET:HA	1:B:347:ILE:HD12	1.89	0.53
1:B:7:PHE:HE1	1:B:37:ILE:HA	1.74	0.53
1:A:396:LEU:HA	1:A:401:ASN:HB2	1.91	0.53
1:A:255:LEU:HD23	1:A:256:GLU:N	2.24	0.53
1:B:373:PHE:CD2	1:B:412:PHE:HB3	2.44	0.53
1:B:406:GLU:HA	1:B:406:GLU:OE1	2.09	0.53
1:A:392:LYS:O	1:A:393:GLY:C	2.51	0.53
1:B:117:TRP:CD2	1:B:312:MET:HE2	2.44	0.53
1:B:120:SER:OG	1:B:125:GLU:HB2	2.08	0.53
1:B:371:ALA:HB1	1:B:373:PHE:CE1	2.44	0.53
1:B:386:LYS:HB2	1:B:386:LYS:NZ	2.24	0.53
1:B:225:ILE:HA	1:B:228:GLU:HG2	1.90	0.53
1:B:169:HIS:CD2	1:B:172:LEU:HG	2.44	0.52
1:B:190:ASP:O	1:B:374:ARG:HD2	2.08	0.52
1:A:381:GLU:N	1:A:381:GLU:CD	2.67	0.52
1:B:374:ARG:HG3	1:B:374:ARG:NH1	2.19	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:229:HIS:ND1	1:A:260:GLU:OE2	2.41	0.52
1:A:359:VAL:O	1:B:201:VAL:HG11	2.09	0.52
1:B:197:GLU:OE2	1:B:197:GLU:HA	2.10	0.52
1:A:343:MET:CA	1:A:347:ILE:HD12	2.31	0.52
1:A:357:PHE:HB3	1:A:359:VAL:HG13	1.92	0.52
1:B:17:ASP:OD1	1:B:18:ILE:HG13	2.10	0.52
1:B:50:PHE:C	1:B:52:ASN:N	2.66	0.52
1:B:290:LYS:HG2	1:B:332:VAL:HB	1.92	0.52
1:B:124:THR:CA	1:B:299:ALA:HA	2.40	0.51
1:A:23:ILE:O	1:A:24:PRO:C	2.50	0.51
1:B:101:ASP:HA	1:B:104:ARG:HH11	1.76	0.51
1:B:279:ASN:O	1:B:280:GLU:C	2.53	0.51
1:A:225:ILE:C	1:A:228:GLU:HG2	2.34	0.50
1:B:204:ASN:HD22	1:B:206:LEU:H	1.57	0.50
1:A:208:GLY:O	1:A:209:ALA:HB2	2.11	0.50
1:B:108:THR:O	1:B:112:ARG:HG3	2.10	0.50
1:B:387:ASP:OD2	1:B:392:LYS:CG	2.54	0.50
1:A:240:ARG:HG2	1:A:240:ARG:HH11	1.77	0.50
1:A:381:GLU:CD	1:A:381:GLU:H	2.19	0.50
1:A:117:TRP:CE2	1:A:312:MET:HE2	2.46	0.49
1:A:129:ILE:HB	1:A:132:ASN:ND2	2.28	0.49
1:B:104:ARG:NH1	1:B:104:ARG:HB3	2.27	0.49
1:B:125:GLU:OE2	1:B:303:ILE:HD11	2.13	0.49
1:B:169:HIS:CG	1:B:170:ASP:H	2.30	0.49
1:B:298:LYS:O	1:B:299:ALA:O	2.31	0.49
1:B:124:THR:C	1:B:299:ALA:HA	2.38	0.49
1:B:169:HIS:HD2	1:B:171:VAL:H	1.57	0.49
1:A:392:LYS:C	1:A:394:ALA:N	2.71	0.49
1:B:204:ASN:HD22	1:B:205:PRO:CD	2.26	0.48
1:B:255:LEU:HD12	1:B:255:LEU:C	2.37	0.48
1:B:378:VAL:HB	1:B:379:PRO:HD3	1.95	0.48
1:B:410:ARG:HH11	1:B:410:ARG:CB	2.12	0.48
1:B:24:PRO:CG	1:B:133:CYS:O	2.61	0.48
1:B:374:ARG:CG	1:B:374:ARG:NH1	2.76	0.48
1:A:404:ASN:HB3	1:A:407:ILE:HB	1.95	0.48
1:B:34:ALA:CB	1:B:44:ILE:HG12	2.43	0.48
1:B:148:LEU:HD23	1:B:148:LEU:H	1.79	0.48
1:A:52:ASN:HD22	1:A:55:GLU:HG3	1.79	0.48
1:B:24:PRO:HG2	1:B:133:CYS:O	2.13	0.48
1:B:36:LYS:HB2	1:B:42:TRP:CE2	2.48	0.48
1:A:97:ILE:O	1:A:103:GLY:HA3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:387:ASP:OD2	1:A:392:LYS:CG	2.44	0.48
1:B:47:ARG:CZ	1:B:58:LEU:HD13	2.44	0.48
1:B:54:GLU:H	1:B:54:GLU:CD	2.21	0.48
1:B:255:LEU:HD11	1:B:366:LEU:CD1	2.44	0.47
1:A:37:ILE:O	1:A:38:HIS:HB2	2.15	0.47
1:A:274:ASP:C	1:A:274:ASP:OD1	2.57	0.47
1:B:398:THR:O	1:B:401:ASN:ND2	2.47	0.47
1:B:101:ASP:OD1	1:B:101:ASP:N	2.41	0.47
1:B:16:VAL:HG12	1:B:17:ASP:N	2.28	0.47
1:B:302:ILE:HD11	1:B:312:MET:HG3	1.96	0.47
1:B:315:VAL:CG2	1:B:316:PHE:H	2.27	0.47
1:A:116:PHE:HE1	1:A:296:LEU:HD21	1.79	0.47
1:A:190:ASP:O	1:A:374:ARG:HD3	2.15	0.47
1:A:143:TYR:CD1	1:A:143:TYR:C	2.92	0.47
1:A:324:GLU:HB2	1:A:330:PHE:HE1	1.78	0.47
1:A:375:ILE:HD12	1:A:377:ILE:HG23	1.95	0.47
1:B:134:ILE:HG23	1:B:148:LEU:CD2	2.44	0.47
1:B:148:LEU:HD23	1:B:148:LEU:N	2.30	0.47
1:A:96:ARG:HA	1:A:385:ILE:HG23	1.97	0.47
1:A:225:ILE:HG21	1:A:264:THR:HG23	1.96	0.47
1:B:13:VAL:HG11	1:B:20:TYR:HD1	1.78	0.47
1:B:96:ARG:CA	1:B:385:ILE:HG23	2.44	0.47
1:B:36:LYS:HE2	1:B:39:ASN:O	2.15	0.46
1:B:124:THR:O	1:B:299:ALA:HA	2.14	0.46
1:B:265:PHE:CE2	1:B:365:TYR:HA	2.50	0.46
1:B:350:GLU:O	1:B:354:VAL:HG23	2.15	0.46
1:A:7:PHE:HB3	1:A:87:LEU:HD21	1.98	0.46
1:A:24:PRO:HD2	1:A:133:CYS:O	2.16	0.46
1:B:180:GLY:HA3	1:B:231:LEU:O	2.15	0.46
1:B:288:LYS:O	1:B:292:VAL:HG23	2.15	0.46
1:B:304:GLY:O	1:B:306:THR:N	2.48	0.46
1:A:4:ASN:O	1:A:5:LYS:CB	2.63	0.46
1:A:134:ILE:CD1	1:A:148:LEU:HD13	2.44	0.46
1:A:255:LEU:HD23	1:A:256:GLU:H	1.81	0.46
1:B:98:TYR:HD1	1:B:107:LEU:HD12	1.81	0.46
1:A:116:PHE:HA	1:A:316:PHE:CE1	2.50	0.46
1:B:3:VAL:HG13	1:B:37:ILE:HB	1.96	0.46
1:A:48:ASP:OD1	1:A:51:THR:HG23	2.15	0.46
1:B:293:ALA:O	1:B:297:ASN:ND2	2.49	0.46
1:A:52:ASN:ND2	1:A:55:GLU:HG3	2.31	0.46
1:B:176:ARG:HD2	1:B:237:ASN:HA	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:MET:HA	1:A:4:ASN:OD1	2.16	0.45
1:A:228:GLU:CG	1:A:229:HIS:N	2.75	0.45
1:B:265:PHE:CE2	1:B:362:ARG:NH1	2.79	0.45
1:B:371:ALA:HB1	1:B:373:PHE:HE1	1.80	0.45
1:A:378:VAL:HB	1:A:379:PRO:HD3	1.97	0.45
1:B:114:ILE:O	1:B:115:PRO:C	2.60	0.45
1:A:24:PRO:O	1:A:25:ASN:HB2	2.16	0.45
1:B:100:THR:O	1:B:104:ARG:N	2.42	0.45
1:A:208:GLY:HA3	1:A:404:ASN:ND2	2.32	0.45
1:A:1:MET:O	1:A:4:ASN:OD1	2.34	0.45
1:A:86:TYR:CD1	1:A:86:TYR:C	2.93	0.45
1:B:324:GLU:HA	1:B:329:LYS:O	2.16	0.45
1:A:47:ARG:NH1	1:A:76:TYR:HB3	2.32	0.45
1:B:120:SER:HG	1:B:125:GLU:HB2	1.81	0.45
1:B:302:ILE:HB	1:B:309:LEU:CD1	2.46	0.45
1:A:239:ASN:ND2	1:A:240:ARG:NH1	2.65	0.44
1:B:292:VAL:C	1:B:294:SER:N	2.73	0.44
1:A:370:LYS:HB2	1:A:370:LYS:NZ	2.32	0.44
1:A:237:ASN:OD1	1:A:238:PRO:HD2	2.18	0.44
1:A:52:ASN:HA	1:A:53:PRO:HD3	1.85	0.44
1:A:277:GLN:HE21	1:A:277:GLN:HB2	1.65	0.44
1:B:236:ILE:O	1:B:237:ASN:C	2.60	0.44
1:A:122:ILE:CG2	1:A:124:THR:HG22	2.47	0.44
1:A:363:LYS:HE2	1:A:363:LYS:HA	2.00	0.44
1:B:204:ASN:HD21	1:B:206:LEU:HB2	1.82	0.44
1:B:79:THR:O	1:B:83:LYS:HG3	2.18	0.44
1:B:2:PHE:HB2	1:B:98:TYR:CG	2.53	0.43
1:B:48:ASP:OD1	1:B:48:ASP:C	2.61	0.43
1:B:225:ILE:CG2	1:B:264:THR:HG23	2.48	0.43
1:A:335:LEU:CD1	1:A:339:LYS:HE3	2.47	0.43
1:B:29:MET:O	1:B:29:MET:HG3	2.18	0.43
1:A:225:ILE:HD13	1:A:349:THR:HA	2.00	0.43
1:A:362:ARG:HG3	1:A:362:ARG:HH11	1.83	0.43
1:B:128:VAL:HG22	1:B:129:ILE:N	2.33	0.43
1:B:321:LEU:O	1:B:336:LYS:HE3	2.19	0.43
1:B:36:LYS:HB2	1:B:42:TRP:CZ2	2.54	0.43
1:B:362:ARG:HE	1:B:367:ASN:HB2	1.84	0.43
1:B:131:THR:HB	1:B:167:PHE:HB2	2.00	0.43
1:A:244:VAL:HG22	1:A:255:LEU:O	2.19	0.42
1:B:197:GLU:OE2	1:B:360:ILE:HD11	2.18	0.42
1:A:180:GLY:HA3	1:A:231:LEU:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:48:ASP:HA	1:B:153:ILE:HD11	2.02	0.42
1:B:120:SER:HB3	1:B:125:GLU:O	2.19	0.42
1:B:232:TYR:O	1:B:234:ILE:HG23	2.19	0.42
1:B:360:ILE:HG22	1:B:403:GLN:OE1	2.19	0.42
1:A:204:ASN:C	1:A:204:ASN:ND2	2.75	0.42
1:A:325:ASP:OD1	1:A:325:ASP:C	2.62	0.42
1:B:138:GLN:HB3	1:B:139:PRO:HD2	2.02	0.42
1:B:96:ARG:HG3	1:B:385:ILE:O	2.19	0.42
1:A:125:GLU:HG3	1:A:301:SER:OG	2.19	0.42
1:A:243:LYS:HE3	1:A:256:GLU:OE2	2.20	0.42
1:A:225:ILE:HG23	1:A:228:GLU:OE2	2.19	0.42
1:A:271:LYS:HD3	1:A:271:LYS:HA	1.70	0.42
1:A:386:LYS:HB2	1:A:386:LYS:HE2	1.75	0.42
1:B:71:TYR:CE2	1:B:159:ILE:HD12	2.55	0.42
1:B:132:ASN:HA	1:B:182:THR:OG1	2.19	0.42
1:B:409:SER:C	1:B:411:ASN:H	2.28	0.42
1:A:123:ASP:OD2	1:A:298:LYS:HE2	2.20	0.42
1:A:204:ASN:ND2	1:A:206:LEU:N	2.65	0.42
1:A:392:LYS:O	1:A:394:ALA:O	2.38	0.42
1:A:387:ASP:HB3	1:A:390:ASN:O	2.20	0.41
1:B:302:ILE:HG21	1:B:309:LEU:CA	2.50	0.41
1:A:204:ASN:HD21	1:A:206:LEU:HB3	1.85	0.41
1:A:333:ASP:OD2	1:A:336:LYS:HG3	2.19	0.41
1:B:274:ASP:H	1:B:277:GLN:HE21	1.67	0.41
1:B:22:LYS:HB3	1:B:22:LYS:HE3	1.89	0.41
1:B:206:LEU:O	1:B:207:LEU:C	2.63	0.41
1:B:15:GLY:HA3	1:B:139:PRO:HD3	2.02	0.41
1:B:3:VAL:HG21	1:B:91:THR:HG23	2.02	0.41
1:B:96:ARG:HD3	1:B:383:TYR:OH	2.20	0.41
1:B:302:ILE:HG22	1:B:309:LEU:HB2	2.01	0.41
1:A:204:ASN:ND2	1:A:205:PRO:HD2	2.35	0.41
1:A:362:ARG:HG3	1:A:362:ARG:NH1	2.35	0.41
1:B:123:ASP:O	1:B:123:ASP:OD2	2.38	0.41
1:A:305:THR:O	1:A:306:THR:C	2.59	0.41
1:A:377:ILE:HG22	1:A:383:TYR:CD2	2.56	0.41
1:A:98:TYR:HD1	1:A:107:LEU:HD12	1.86	0.41
1:A:207:LEU:O	1:A:208:GLY:C	2.64	0.41
1:A:95:GLU:OE1	1:A:95:GLU:HA	2.19	0.41
1:B:27:GLY:C	1:B:29:MET:H	2.29	0.41
1:B:143:TYR:O	1:B:143:TYR:CD1	2.74	0.41
1:B:392:LYS:C	1:B:394:ALA:N	2.79	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:25:ASN:C	1:A:27:GLY:N	2.77	0.41
1:B:211:LYS:HD3	1:B:371:ALA:HB2	2.03	0.41
1:B:302:ILE:O	1:B:302:ILE:HG12	2.19	0.41
1:A:204:ASN:HD21	1:A:206:LEU:CB	2.34	0.40
1:A:364:THR:HG23	1:A:366:LEU:O	2.21	0.40
1:B:225:ILE:O	1:B:228:GLU:HG2	2.21	0.40
1:B:47:ARG:NH1	1:B:58:LEU:HD13	2.36	0.40
1:B:197:GLU:HG2	1:B:207:LEU:HD23	2.02	0.40
1:B:335:LEU:HG	1:B:339:LYS:HE3	2.03	0.40
1:B:358:LYS:NZ	1:B:358:LYS:CB	2.83	0.40
1:A:24:PRO:O	1:A:25:ASN:CB	2.70	0.40
1:B:35:PHE:CD1	1:B:35:PHE:N	2.89	0.40
1:B:242:PHE:HB2	1:B:259:PHE:HE1	1.87	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	395/425 (93%)	347 (88%)	36 (9%)	12 (3%)	3	12
1	B	393/425 (92%)	339 (86%)	36 (9%)	18 (5%)	2	6
All	All	788/850 (93%)	686 (87%)	72 (9%)	30 (4%)	2	9

All (30) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	LYS
1	A	305	THR
1	A	392	LYS
1	B	299	ALA
1	B	305	THR

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Mol	Chain	Res	Type
1	B	392	LYS
1	A	25	ASN
1	A	168	GLY
1	A	197	GLU
1	A	208	GLY
1	A	393	GLY
1	B	51	THR
1	B	199	LEU
1	B	393	GLY
1	A	123	ASP
1	A	306	THR
1	A	368	PHE
1	A	371	ALA
1	B	25	ASN
1	B	131	THR
1	B	156	SER
1	B	73	ASP
1	B	130	ASP
1	B	159	ILE
1	B	394	ALA
1	B	28	GLN
1	B	45	PRO
1	B	207	LEU
1	B	304	GLY
1	B	171	VAL

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	360/381 (94%)	345 (96%)	15 (4%)	26	61
1	B	358/381 (94%)	341 (95%)	17 (5%)	23	57
All	All	718/762 (94%)	686 (96%)	32 (4%)	24	58

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	PRO
1	A	32	VAL
1	A	128	VAL
1	A	172	LEU
1	A	245	ASN
1	A	255	LEU
1	A	277	GLN
1	A	283	LEU
1	A	295	THR
1	A	335	LEU
1	A	362	ARG
1	A	367	ASN
1	A	370	LYS
1	A	398	THR
1	A	410	ARG
1	B	6	GLN
1	B	23	ILE
1	B	28	GLN
1	B	101	ASP
1	B	130	ASP
1	B	172	LEU
1	B	243	LYS
1	B	278	GLU
1	B	302	ILE
1	B	310	GLN
1	B	315	VAL
1	B	358	LYS
1	B	362	ARG
1	B	364	THR
1	B	381	GLU
1	B	386	LYS
1	B	410	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	GLN
1	A	39	ASN
1	A	59	ASN
1	A	135	ASN
1	A	138	GLN
1	A	204	ASN
1	A	239	ASN

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Mol	Chain	Res	Type
1	A	245	ASN
1	A	268	HIS
1	A	277	GLN
1	A	352	ASN
1	A	390	ASN
1	A	399	ASN
1	A	404	ASN
1	B	6	GLN
1	B	28	GLN
1	B	59	ASN
1	B	138	GLN
1	B	169	HIS
1	B	204	ASN
1	B	277	GLN
1	B	287	ASN
1	B	355	ASN
1	B	390	ASN
1	B	399	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	401/425 (94%)	-0.00	28 (6%) 22 16	9, 25, 70, 89	0
1	B	399/425 (93%)	0.64	52 (13%) 7 6	16, 44, 85, 95	0
All	All	800/850 (94%)	0.32	80 (10%) 12 9	9, 36, 81, 95	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	306	THR	7.0
1	A	305	THR	6.9
1	A	24	PRO	6.5
1	B	143	TYR	6.5
1	A	368	PHE	6.4
1	A	253	SER	5.2
1	A	69	VAL	4.7
1	B	368	PHE	4.6
1	B	228	GLU	4.6
1	B	123	ASP	4.4
1	A	304	GLY	4.4
1	B	305	THR	4.3
1	A	208	GLY	4.3
1	A	209	ALA	4.2
1	B	301	SER	4.0
1	B	246	THR	4.0
1	A	393	GLY	3.9
1	A	197	GLU	3.9
1	B	303	ILE	3.9
1	B	141	GLY	3.8
1	B	306	THR	3.6
1	B	307	ALA	3.6
1	B	142	SER	3.6
1	B	59	ASN	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	246	THR	3.4
1	A	27	GLY	3.3
1	B	416	LYS	3.3
1	A	59	ASN	3.2
1	A	210	GLY	3.2
1	B	304	GLY	3.2
1	B	398	THR	3.2
1	B	171	VAL	3.2
1	B	339	LYS	3.1
1	A	228	GLU	3.1
1	B	7	PHE	3.0
1	A	381	GLU	3.0
1	B	139	PRO	3.0
1	A	26	ALA	2.9
1	B	199	LEU	2.9
1	B	27	GLY	2.8
1	B	327	SER	2.7
1	B	397	SER	2.7
1	B	308	SER	2.7
1	B	311	TYR	2.6
1	A	366	LEU	2.6
1	A	198	SER	2.6
1	A	370	LYS	2.6
1	B	198	SER	2.6
1	B	6	GLN	2.6
1	B	125	GLU	2.6
1	B	366	LEU	2.5
1	B	168	GLY	2.5
1	B	121	THR	2.5
1	B	138	GLN	2.5
1	A	416	LYS	2.5
1	B	25	ASN	2.4
1	B	116	PHE	2.4
1	B	309	LEU	2.3
1	B	26	ALA	2.3
1	A	397	SER	2.3
1	B	23	ILE	2.3
1	A	25	ASN	2.2
1	B	317	LYS	2.2
1	B	131	THR	2.2
1	A	170	ASP	2.2
1	B	326	THR	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	329	LYS	2.2
1	A	1	MET	2.1
1	B	254	GLY	2.1
1	B	298	LYS	2.1
1	B	28	GLN	2.1
1	A	254	GLY	2.1
1	B	15	GLY	2.1
1	B	291	ASP	2.0
1	B	24	PRO	2.0
1	B	126	LEU	2.0
1	B	314	ASN	2.0
1	A	398	THR	2.0
1	B	140	ASP	2.0
1	B	334	LYS	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.