



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:16 PM UTC

PDB ID : 7T5F / pdb_00007t5f
Title : Botulinum neurotoxin Type B Light Chain complexed with nanobodies JLJ-G3 and JNE-B10
Authors : Jin, R.; Lam, K.-H.
Deposited on : 2021-12-12
Resolution : 2.60 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

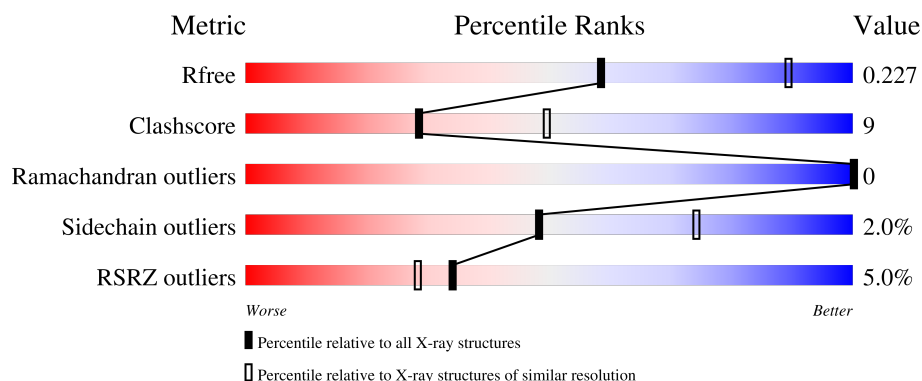
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	430	 2% 80% 16% ..
1	D	430	 3% 81% 15% ..
2	C	130	 5% 59% 28% • 12%
2	F	130	 7% 62% 25% • 12%
3	B	131	 4% 66% 23% • 11%

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Mol	Chain	Length	Quality of chain
3	E	131	18% 60% 21% • 16%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 10467 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 B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	421	Total	C	N	O	S	0	0	0
			3432	2203	565	651	13			
1	D	420	Total	C	N	O	S	6	0	0
			3426	2200	564	649	13			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP P10844
A	-3	PRO	-	expression tag	UNP P10844
A	-2	LEU	-	expression tag	UNP P10844
A	-1	GLY	-	expression tag	UNP P10844
A	0	SER	-	expression tag	UNP P10844
D	-4	GLY	-	expression tag	UNP P10844
D	-3	PRO	-	expression tag	UNP P10844
D	-2	LEU	-	expression tag	UNP P10844
D	-1	GLY	-	expression tag	UNP P10844
D	0	SER	-	expression tag	UNP P10844

- Molecule 2 is a protein called JLJ-G3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	115	Total	C	N	O	S	0	0	0
			868	538	153	172	5			
2	F	114	Total	C	N	O	S	0	0	0
			861	533	152	171	5			

- Molecule 3 is a protein called JNE-B10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	B	117	Total	C	N	O	S	0	0	0
			892	559	159	170	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	110	Total	C	N	O	S	38	0	0
			850	533	151	162	4			

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	0	0
			1	1		
4	D	1	Total	Zn	0	0
			1	1		

- Molecule 5 is IODIDE ION (CCD ID: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	I	0	0
			2	2		
5	D	1	Total	I	0	0
			1	1		
5	C	1	Total	I	0	0
			1	1		
5	B	1	Total	I	0	0
			1	1		
5	E	1	Total	I	0	0
			1	1		

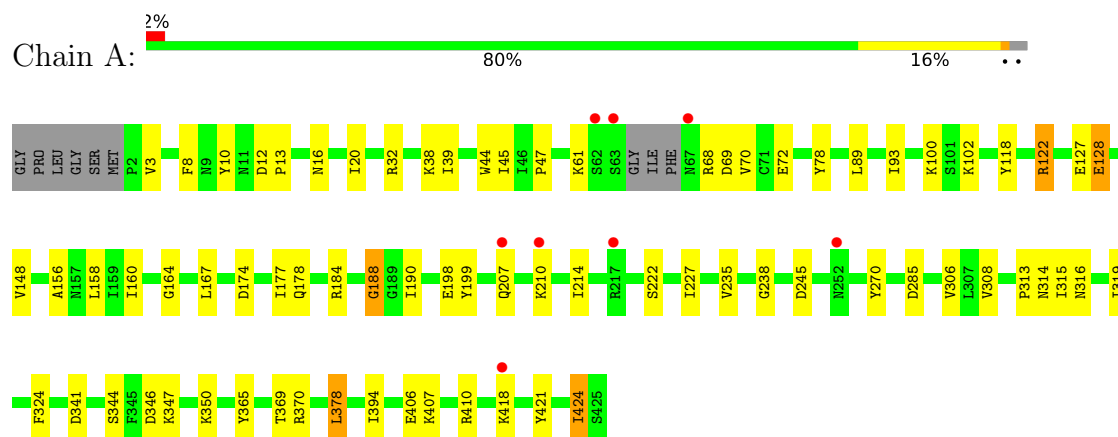
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	65	Total	O	0	0
			65	65		
6	D	49	Total	O	0	0
			49	49		
6	C	3	Total	O	0	0
			3	3		
6	B	7	Total	O	0	0
			7	7		
6	F	6	Total	O	0	0
			6	6		

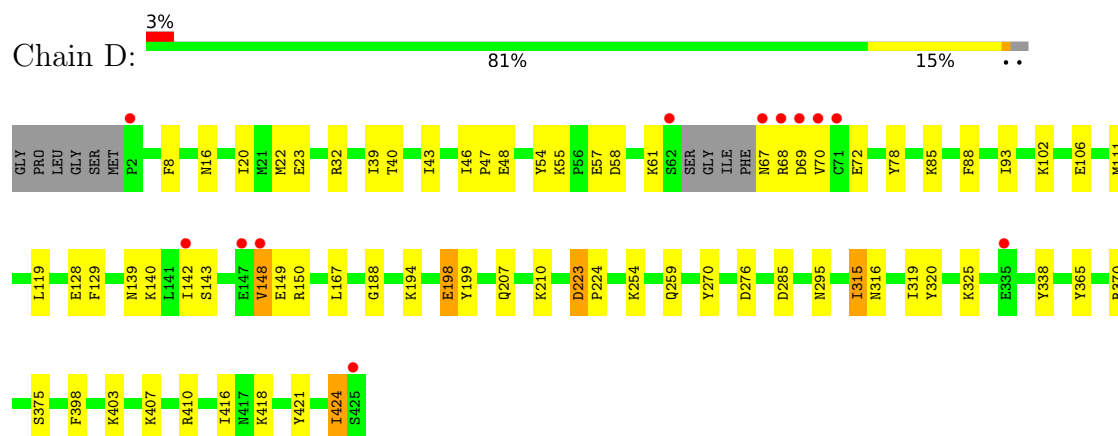
3 Residue-property plots [i](#)

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.

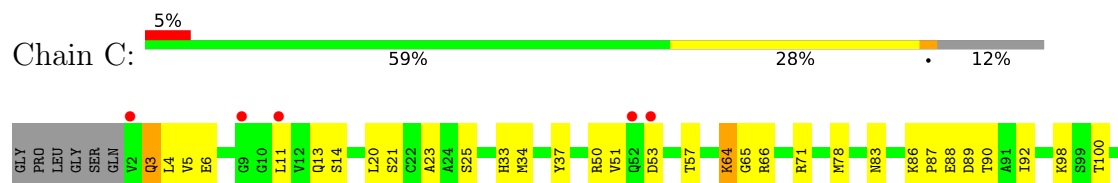
• Molecule 1: Botulinum neurotoxin type B

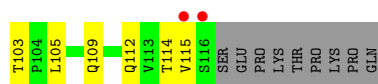


• Molecule 1: Botulinum neurotoxin type B

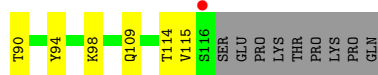
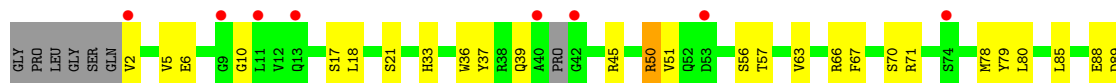


• Molecule 2: JLJ-G3

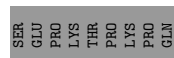




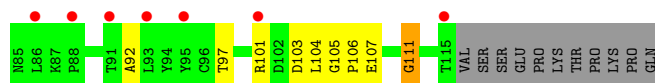
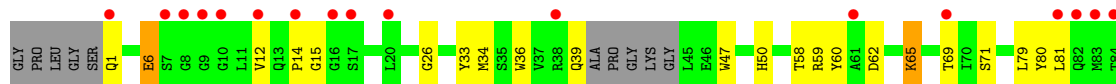
• Molecule 2: JLJ-G3



• Molecule 3: JNE-B10



• Molecule 3: JNE-B10



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	149.32Å 88.28Å 114.48Å 90.00° 97.03° 90.00°	Depositor
Resolution (Å)	75.84 – 2.60 75.84 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.9 (75.84-2.60) 92.4 (75.84-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.64 (at 2.62Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.194 , 0.222 0.201 , 0.227	Depositor DCC
R_{free} test set	2280 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	38.5	Xtriage
Anisotropy	0.703	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 59.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10467	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.47% 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: ZN, IOD

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	0.64	0/3508	0.92	8/4732 (0.2%)
1	D	0.66	0/3502	0.94	7/4724 (0.1%)
2	C	0.57	0/883	0.90	0/1191
2	F	0.53	0/874	0.90	1/1176 (0.1%)
3	B	0.60	0/911	0.96	1/1234 (0.1%)
3	E	0.52	0/867	0.96	3/1173 (0.3%)
All	All	0.62	0/10545	0.93	20/14230 (0.1%)

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	12	ASP	CA-C-N	-7.09	113.36	120.31
1	A	12	ASP	C-N-CA	-7.09	113.36	120.31
1	D	188	GLY	N-CA-C	-7.05	103.80	112.33
1	D	276	ASP	CA-C-N	-6.93	112.66	119.87
1	D	276	ASP	C-N-CA	-6.93	112.66	119.87
3	E	104	LEU	N-CA-C	6.87	121.40	112.89
1	A	128	GLU	N-CA-C	6.27	119.92	109.95
1	A	188	GLY	N-CA-C	-6.26	103.55	112.81
1	D	148	VAL	N-CA-C	6.12	122.06	109.34
2	F	17	SER	N-CA-C	5.73	118.40	109.52
3	E	111	GLY	N-CA-C	5.37	118.75	111.72
1	D	223	ASP	CA-C-N	5.35	125.68	119.47
1	D	223	ASP	C-N-CA	5.35	125.68	119.47
1	A	378	LEU	CA-C-N	-5.32	114.90	120.38
1	A	378	LEU	C-N-CA	-5.32	114.90	120.38
3	E	12	VAL	N-CA-C	-5.21	100.26	108.90
3	B	12	VAL	N-CA-C	-5.20	100.27	108.90
1	A	164	GLY	CA-C-N	5.05	125.07	119.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	164	GLY	C-N-CA	5.05	125.07	119.32
1	D	106	GLU	N-CA-C	-5.04	105.79	111.28

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	3432	0	3395	42	0
1	D	3426	0	3390	49	1
2	C	868	0	851	34	0
2	F	861	0	843	21	0
3	B	892	0	875	19	0
3	E	850	0	829	18	0
4	A	1	0	0	0	0
4	D	1	0	0	0	0
5	A	2	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	1	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
6	A	65	0	0	5	0
6	B	7	0	0	0	0
6	C	3	0	0	1	0
6	D	49	0	0	3	0
6	F	6	0	0	1	0
All	All	10467	0	10183	179	1

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 9.

All (179) 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:C:98:LYS:HG3	2:C:105:LEU:HD23	1.23	1.16
1:D:325:LYS:HD3	1:D:338:TYR:CE2	1.90	1.07
1:A:32:ARG:NH1	6:A:601:HOH:O	1.92	1.00
2:C:11:LEU:O	2:C:11:LEU:HD23	1.66	0.95
3:B:11:LEU:HA	3:B:115:THR:O	1.67	0.92
2:C:98:LYS:HG3	2:C:105:LEU:CD2	2.01	0.91
3:E:6:GLU:OE1	3:E:111:GLY:N	2.06	0.87
2:C:71:ARG:HB2	5:C:201:IOD:I	2.46	0.86
1:D:32:ARG:NH2	3:E:103:ASP:OD2	2.08	0.85
2:C:98:LYS:CG	2:C:105:LEU:HD23	2.08	0.84
3:B:67:ARG:NH2	3:B:90:ASP:OD2	2.12	0.83
3:B:91:THR:HG23	3:B:115:THR:HG22	1.63	0.81
2:C:86:LYS:HD2	2:C:88:GLU:OE2	1.83	0.78
1:A:70:VAL:HG12	1:A:72:GLU:H	1.50	0.77
1:D:70:VAL:HG12	1:D:72:GLU:H	1.50	0.77
2:F:66:ARG:NH2	2:F:89:ASP:OD2	2.18	0.76
1:D:58:ASP:O	1:D:61:LYS:HG2	1.86	0.75
2:C:66:ARG:NH2	2:C:89:ASP:OD2	2.21	0.74
1:D:325:LYS:HD3	1:D:338:TYR:HE2	1.54	0.73
2:F:10:GLY:HA3	2:F:18:LEU:HD11	1.70	0.72
2:C:3:GLN:NE2	6:C:301:HOH:O	2.22	0.72
3:B:83:MET:HB3	3:B:86:LEU:HD21	1.71	0.71
2:C:33:HIS:HB3	2:C:98:LYS:HB2	1.71	0.70
2:F:51:VAL:HG22	2:F:57:THR:HG22	1.75	0.69
1:D:148:VAL:O	1:D:150:ARG:HG3	1.93	0.68
1:D:140:LYS:HE3	1:D:142:ILE:HD13	1.76	0.67
2:C:3:GLN:HG2	2:C:25:SER:HB3	1.77	0.67
2:F:39:GLN:HB2	2:F:45:ARG:HG2	1.76	0.67
2:F:5:VAL:HG13	2:F:109:GLN:HE22	1.61	0.66
1:D:398:PHE:O	6:D:601:HOH:O	2.14	0.65
3:E:58:THR:O	3:E:59:ARG:NH1	2.25	0.65
1:A:78:TYR:OH	1:A:198:GLU:OE2	2.12	0.65
2:C:64:LYS:HD2	2:C:65:GLY:H	1.62	0.65
2:C:92:ILE:HG12	2:C:112:GLN:HG2	1.79	0.64
1:D:16:ASN:HA	1:D:20:ILE:HG22	1.79	0.64
3:B:2:VAL:HG21	3:B:107:GLU:HG2	1.81	0.63
2:C:51:VAL:HG22	2:C:57:THR:HG22	1.81	0.62
1:D:40:THR:HG22	1:D:43:ILE:HB	1.82	0.62
1:A:407:LYS:O	1:A:410:ARG:HG3	1.99	0.61
2:F:33:HIS:HB3	2:F:98:LYS:HB2	1.82	0.61
1:D:407:LYS:O	1:D:410:ARG:HG3	2.00	0.61
1:D:23:GLU:HB3	1:D:139:ASN:HB2	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:50:ARG:NH2	2:F:56:SER:OG	2.35	0.60
2:C:5:VAL:HG13	2:C:109:GLN:NE2	2.17	0.59
3:E:47:TRP:CE3	3:E:101:ARG:HD3	2.37	0.59
1:D:47:PRO:HB3	1:D:88:PHE:HD2	1.67	0.59
2:C:5:VAL:HG13	2:C:109:GLN:HE22	1.67	0.59
1:D:148:VAL:O	1:D:148:VAL:HG12	2.02	0.59
1:D:39:ILE:HD11	1:D:93:ILE:HA	1.86	0.58
1:A:207:GLN:HA	1:A:210:LYS:HG2	1.86	0.57
1:D:410:ARG:HB3	1:D:416:ILE:HG21	1.85	0.57
1:D:325:LYS:HD3	1:D:338:TYR:CD2	2.38	0.57
2:F:85:LEU:HD23	2:F:115:VAL:CG2	2.35	0.57
3:B:86:LEU:HB3	3:B:116:VAL:HG21	1.88	0.56
1:A:38:LYS:HB2	1:A:44:TRP:CZ3	2.40	0.56
3:B:34:MET:SD	3:B:98:LEU:HD23	2.47	0.55
2:C:86:LYS:C	2:C:115:VAL:HG11	2.31	0.55
2:F:90:THR:HG23	2:F:114:THR:HA	1.88	0.55
2:C:86:LYS:CD	2:C:88:GLU:OE2	2.54	0.54
3:E:97:THR:OG1	3:E:107:GLU:O	2.14	0.54
1:A:102:LYS:HD3	1:A:365:TYR:CE2	2.43	0.54
3:E:60:TYR:CE1	3:E:69:THR:HA	2.44	0.53
2:C:109:GLN:H	2:C:109:GLN:CD	2.16	0.53
1:A:68:ARG:HG3	1:A:69:ASP:N	2.24	0.53
1:D:68:ARG:HG3	1:D:69:ASP:N	2.24	0.52
1:A:308:VAL:HG21	2:C:37:TYR:CE1	2.44	0.52
1:A:127:GLU:O	1:A:306:VAL:HA	2.10	0.52
3:E:62:ASP:HA	3:E:65:LYS:HB3	1.92	0.52
2:F:85:LEU:HD23	2:F:115:VAL:HG21	1.91	0.52
1:D:315:ILE:HD12	1:D:320:TYR:CE1	2.44	0.51
2:F:70:SER:HB3	2:F:79:TYR:HB2	1.92	0.51
2:C:100:THR:H	2:C:103:THR:HB	1.74	0.51
1:A:270:TYR:OH	1:A:285:ASP:OD2	2.21	0.51
1:A:13:PRO:O	6:A:602:HOH:O	2.19	0.50
1:A:3:VAL:O	1:A:100:LYS:HD2	2.12	0.50
1:A:341:ASP:HB3	1:A:344:SER:HB3	1.94	0.50
1:A:316:ASN:ND2	1:A:319:ILE:HG12	2.26	0.50
2:C:86:LYS:HB2	2:C:88:GLU:HG2	1.93	0.50
3:E:47:TRP:CE2	3:E:101:ARG:HB2	2.47	0.50
1:D:102:LYS:HB2	1:D:365:TYR:CZ	2.47	0.49
1:D:403:LYS:NZ	6:D:609:HOH:O	2.43	0.49
2:C:11:LEU:O	2:C:11:LEU:CD2	2.49	0.49
1:D:23:GLU:OE1	1:D:139:ASN:ND2	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:45:ILE:HD13	1:A:160:ILE:HB	1.95	0.49
1:A:222:SER:HB2	1:A:227:ILE:HD11	1.94	0.49
1:D:40:THR:CG2	1:D:43:ILE:HB	2.42	0.48
3:B:3:GLN:HB2	3:B:25:SER:OG	2.13	0.48
1:A:118:TYR:HA	1:A:324:PHE:CZ	2.48	0.48
1:A:16:ASN:HA	1:A:20:ILE:HG22	1.96	0.48
1:D:199:TYR:HD1	1:D:424:ILE:HD11	1.78	0.48
3:E:36:TRP:NE1	3:E:81:LEU:HB2	2.28	0.48
2:F:85:LEU:HB3	2:F:115:VAL:HG21	1.96	0.48
3:B:14:PRO:HB3	3:B:116:VAL:CG1	2.43	0.47
2:F:63:VAL:HA	2:F:66:ARG:HH11	1.79	0.47
2:F:88:GLU:OE1	2:F:88:GLU:N	2.34	0.47
1:D:46:ILE:O	1:D:48:GLU:N	2.45	0.47
1:A:199:TYR:CD1	1:A:424:ILE:HD11	2.49	0.47
1:D:32:ARG:HG2	3:E:33:TYR:CD2	2.50	0.47
1:D:270:TYR:OH	1:D:285:ASP:OD2	2.21	0.47
2:C:34:MET:HE2	2:C:78:MET:HE2	1.96	0.47
2:F:71:ARG:NH1	6:F:201:HOH:O	2.48	0.47
1:D:20:ILE:HD11	1:D:22:MET:HE3	1.97	0.47
2:C:115:VAL:O	2:C:115:VAL:HG12	2.15	0.46
1:A:156:ALA:O	1:A:190:ILE:HG12	2.15	0.46
1:A:61:LYS:O	6:A:603:HOH:O	2.20	0.46
1:D:143:SER:HB3	1:D:150:ARG:HB2	1.97	0.46
2:C:98:LYS:CG	2:C:105:LEU:CD2	2.83	0.46
1:D:148:VAL:O	1:D:149:GLU:C	2.58	0.46
2:C:90:THR:HG23	2:C:114:THR:HA	1.97	0.46
1:D:47:PRO:HB3	1:D:88:PHE:CD2	2.49	0.46
1:D:207:GLN:HA	1:D:210:LYS:HG2	1.98	0.46
1:A:10:TYR:HE1	1:A:47:PRO:HG2	1.81	0.46
1:A:214:ILE:H	1:A:214:ILE:HD12	1.81	0.46
2:C:13:GLN:HG3	2:C:14:SER:N	2.30	0.46
1:A:122:ARG:HB3	6:A:633:HOH:O	2.17	0.45
1:D:199:TYR:CD1	1:D:424:ILE:HD11	2.51	0.45
1:A:418:LYS:HA	1:A:421:TYR:CE2	2.52	0.45
3:B:14:PRO:HB3	3:B:116:VAL:HG11	1.97	0.45
3:E:71:SER:HB2	3:E:80:TYR:HB2	1.97	0.45
1:D:254:LYS:HE2	1:D:254:LYS:HB3	1.68	0.45
1:D:316:ASN:ND2	1:D:319:ILE:HG12	2.31	0.45
3:B:62:ASP:OD1	3:B:65:LYS:NZ	2.29	0.45
1:D:223:ASP:HA	1:D:224:PRO:HD2	1.76	0.45
3:B:71:SER:HB2	3:B:80:TYR:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:14:PRO:HA	3:E:15:GLY:HA2	1.62	0.45
1:D:54:TYR:OH	1:D:194:LYS:HE2	2.17	0.45
1:D:111:MET:HE2	1:D:111:MET:HB3	1.84	0.45
2:F:67:PHE:HB3	2:F:80:LEU:HD11	1.97	0.45
1:D:40:THR:HG21	1:D:43:ILE:HD12	1.99	0.44
3:B:51:ILE:HA	3:B:57:ILE:O	2.17	0.44
3:E:47:TRP:CD2	3:E:101:ARG:HB2	2.51	0.44
3:B:60:TYR:OH	3:B:70:ILE:HG22	2.16	0.44
1:A:394:ILE:HG13	6:A:604:HOH:O	2.17	0.44
3:B:110:GLN:HG3	3:B:111:GLY:N	2.33	0.44
1:A:346:ASP:O	1:A:350:LYS:HG2	2.17	0.44
3:B:97:THR:OG1	3:B:107:GLU:O	2.25	0.44
2:F:36:TRP:NE1	2:F:78:MET:HE3	2.33	0.43
1:D:142:ILE:HD12	1:D:142:ILE:HA	1.89	0.43
3:B:36:TRP:HD1	3:B:70:ILE:CD1	2.31	0.43
1:A:207:GLN:OE1	1:A:210:LYS:HE2	2.18	0.43
1:A:89:LEU:O	1:A:93:ILE:HG13	2.19	0.43
1:D:259:GLN:HB3	1:D:375:SER:HA	2.00	0.43
2:C:64:LYS:HD2	2:C:65:GLY:N	2.30	0.43
1:A:177:ILE:HG22	1:A:178:GLN:HG3	2.01	0.43
2:C:53:ASP:O	2:C:53:ASP:OD1	2.35	0.42
3:B:106:PRO:HD2	3:B:107:GLU:OE1	2.19	0.42
1:D:78:TYR:OH	1:D:198:GLU:OE2	2.34	0.42
1:A:313:PRO:O	1:A:314:ASN:HB2	2.19	0.42
1:D:370:ARG:H	1:D:370:ARG:HG2	1.47	0.42
2:C:64:LYS:HD2	2:C:64:LYS:HA	1.65	0.42
2:C:66:ARG:HB3	2:C:83:ASN:O	2.20	0.42
1:A:207:GLN:HA	1:A:210:LYS:CG	2.49	0.42
1:A:347:LYS:HG2	1:D:407:LYS:HE2	2.02	0.42
1:A:406:GLU:OE1	1:A:407:LYS:HD3	2.19	0.42
1:D:85:LYS:NZ	6:D:602:HOH:O	2.24	0.42
1:D:418:LYS:HD3	1:D:421:TYR:CZ	2.55	0.42
1:A:369:THR:OG1	1:A:370:ARG:N	2.53	0.42
2:F:6:GLU:HA	2:F:21:SER:O	2.20	0.42
1:A:39:ILE:HD11	1:A:93:ILE:HA	2.01	0.41
1:D:55:LYS:HD2	1:D:57:GLU:OE2	2.20	0.41
1:A:174:ASP:OD2	1:A:174:ASP:N	2.47	0.41
2:F:67:PHE:N	2:F:67:PHE:CD1	2.89	0.41
1:D:418:LYS:O	1:D:418:LYS:HD2	2.20	0.41
1:A:188:GLY:HA2	1:A:238:GLY:O	2.20	0.41
2:C:87:PRO:HA	2:C:115:VAL:HB	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:34:MET:HB3	3:E:79:LEU:HD22	2.01	0.41
2:F:37:TYR:O	2:F:94:TYR:N	2.40	0.41
1:A:158:LEU:HD22	1:A:235:VAL:HG11	2.02	0.41
1:D:119:LEU:HB2	1:D:129:PHE:CD1	2.55	0.41
2:C:6:GLU:HA	2:C:21:SER:O	2.21	0.41
3:E:105:GLY:HA2	3:E:106:PRO:HD3	1.79	0.41
2:F:85:LEU:HB3	2:F:115:VAL:HG11	2.03	0.41
1:A:184:ARG:HD3	1:A:245:ASP:HA	2.03	0.41
3:B:14:PRO:HA	3:B:15:GLY:HA2	1.48	0.40
1:A:378:LEU:HD23	1:A:378:LEU:HA	1.92	0.40
3:E:39:GLN:C	3:E:92:ALA:HB1	2.47	0.40
3:E:1:GLN:O	3:E:26:GLY:HA3	2.21	0.40
3:E:50:HIS:CD2	3:E:50:HIS:C	2.98	0.40
2:C:4:LEU:HA	2:C:23:ALA:O	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:67:ASN:OD1	1:D:295:ASN:OD1[4_545]	2.08	0.12

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	417/430 (97%)	404 (97%)	13 (3%)	0	100	100
1	D	416/430 (97%)	401 (96%)	15 (4%)	0	100	100
2	C	113/130 (87%)	111 (98%)	2 (2%)	0	100	100
2	F	110/130 (85%)	110 (100%)	0	0	100	100
3	B	115/131 (88%)	110 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	E	106/131 (81%)	102 (96%)	4 (4%)	0	100	100
All	All	1277/1382 (92%)	1238 (97%)	39 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	383/389 (98%)	376 (98%)	7 (2%)	51	76
1	D	382/389 (98%)	376 (98%)	6 (2%)	55	79
2	C	94/107 (88%)	90 (96%)	4 (4%)	26	51
2	F	93/107 (87%)	91 (98%)	2 (2%)	45	72
3	B	94/106 (89%)	92 (98%)	2 (2%)	47	73
3	E	90/106 (85%)	88 (98%)	2 (2%)	45	72
All	All	1136/1204 (94%)	1113 (98%)	23 (2%)	48	74

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	PHE
1	A	122	ARG
1	A	128	GLU
1	A	148	VAL
1	A	167	LEU
1	A	315	ILE
1	A	424	ILE
1	D	8	PHE
1	D	128	GLU
1	D	167	LEU
1	D	198	GLU
1	D	315	ILE
1	D	424	ILE

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Mol	Chain	Res	Type
2	C	3	GLN
2	C	20	LEU
2	C	50	ARG
2	C	64	LYS
3	B	6	GLU
3	B	65	LYS
3	E	6	GLU
3	E	65	LYS
2	F	2	VAL
2	F	50	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	16	ASN
2	C	52	GLN
3	B	82	GLN
2	F	81	GLN

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 ⓘ

Of 8 ligands modelled in this entry, 8 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

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	421/430 (97%)	-0.24	8 (1%) 66 61	23, 41, 71, 105	0
1	D	420/430 (97%)	-0.03	12 (2%) 53 48	26, 49, 78, 106	2 (0%)
2	C	115/130 (88%)	0.30	7 (6%) 27 22	32, 52, 89, 112	0
2	F	114/130 (87%)	0.36	9 (7%) 18 14	36, 61, 99, 120	0
3	B	117/131 (89%)	0.27	5 (4%) 40 34	31, 51, 84, 107	0
3	E	109/131 (83%)	1.36	24 (22%) 2 2	49, 86, 114, 124	10 (9%)
All	All	1296/1382 (93%)	0.11	65 (5%) 34 28	23, 49, 94, 124	12 (0%)

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	2	VAL	4.0
3	E	88	PRO	3.9
2	F	9	GLY	3.8
2	F	11	LEU	3.8
3	E	84	THR	3.8
1	D	148	VAL	3.7
3	E	12	VAL	3.7
2	F	40	ALA	3.6
3	E	17	SER	3.4
2	F	2	VAL	3.4
3	E	38	ARG	3.2
2	C	11	LEU	3.2
2	F	42	GLY	3.1
1	A	63	SER	3.1
2	F	13	GLN	3.0
3	B	12	VAL	3.0
1	A	210	LYS	2.9
3	E	10	GLY	2.9
1	D	70	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
3	E	16	GLY	2.9
3	E	95	TYR	2.9
3	E	61	ALA	2.9
3	E	14	PRO	2.8
1	A	207	GLN	2.8
1	A	67	ASN	2.7
3	E	86	LEU	2.7
2	F	116	SER	2.7
1	A	418	LYS	2.6
1	D	67	ASN	2.6
3	E	1	GLN	2.6
1	D	62	SER	2.5
3	E	8	GLY	2.5
2	C	52	GLN	2.5
3	E	82	GLN	2.5
2	C	116	SER	2.5
3	B	116	VAL	2.5
3	E	115	THR	2.5
3	B	115	THR	2.4
3	E	83	MET	2.4
2	C	9	GLY	2.4
3	E	93	LEU	2.3
1	A	62	SER	2.3
1	D	69	ASP	2.3
3	E	7	SER	2.3
1	D	2	PRO	2.3
2	F	53	ASP	2.3
3	E	20	LEU	2.2
3	E	81	LEU	2.2
1	D	147	GLU	2.2
3	E	91	THR	2.2
1	A	252	ASN	2.2
2	C	53	ASP	2.2
2	C	115	VAL	2.2
1	D	71	CYS	2.2
1	D	68	ARG	2.1
3	B	105	GLY	2.1
3	E	9	GLY	2.1
1	D	335	GLU	2.1
1	D	142	ILE	2.1
1	D	425	SER	2.0
2	F	74	SER	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	217	ARG	2.0
3	E	101	ARG	2.0
3	B	0	SER	2.0
3	E	69	THR	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
5	IOD	E	201	1/1	0.93	0.07	62,62,62,62	1
5	IOD	C	201	1/1	0.95	0.07	93,93,93,93	1
4	ZN	D	501	1/1	0.95	0.06	52,52,52,52	0
4	ZN	A	501	1/1	0.96	0.05	58,58,58,58	1
5	IOD	A	503	1/1	0.97	0.07	85,85,85,85	1
5	IOD	A	502	1/1	0.99	0.04	55,55,55,55	0
5	IOD	B	201	1/1	0.99	0.03	49,49,49,49	1
5	IOD	D	502	1/1	0.99	0.05	60,60,60,60	0

6.5 Other polymers [i](#)

There are no such residues in this entry.