



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:02 PM GMT

PDB ID : 4AT6
Title : Fab fragment of antiporphyrin antibody 14H7
Authors : Golinelli-Pimpaneau, B.; Mahy, J.P.
Deposited on : 2012-05-04
Resolution : 2.55 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) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

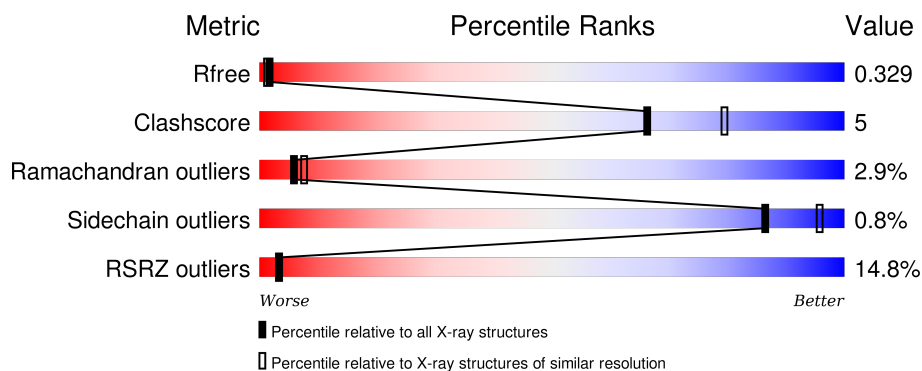
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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}	91344	4549 (2.58-2.50)
Clashscore	102246	5292 (2.58-2.50)
Ramachandran outliers	100387	5194 (2.58-2.50)
Sidechain outliers	100360	5196 (2.58-2.50)
RSRZ outliers	91569	4561 (2.58-2.50)

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.

Mol	Chain	Length	Quality of chain
1	A	217	<div> <div>9%</div> <div>76%</div> <div>18%</div> <div>• •</div> </div>
1	C	217	<div> <div>17%</div> <div>80%</div> <div>15%</div> <div>• •</div> </div>
1	E	217	<div> <div>16%</div> <div>73%</div> <div>21%</div> <div>• •</div> </div>
1	G	217	<div> <div>22%</div> <div>78%</div> <div>15%</div> <div>• 6%</div> </div>
1	H	217	<div> <div>14%</div> <div>79%</div> <div>16%</div> <div>• •</div> </div>

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Mol	Chain	Length	Quality of chain
1	J	217	
1	M	217	
1	O	217	
2	B	212	
2	D	212	
2	F	212	
2	I	212	
2	K	212	
2	L	212	
2	N	212	
2	P	212	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 25238 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 FAB 14H7 HEAVY CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	212	Total	C	N	O	S	0	0	0
			1551	980	255	309	7			
1	C	209	Total	C	N	O	S	0	0	0
			1534	971	252	305	6			
1	E	209	Total	C	N	O	S	0	0	0
			1528	965	252	305	6			
1	G	205	Total	C	N	O	S	0	0	0
			1489	939	247	297	6			
1	H	211	Total	C	N	O	S	0	0	0
			1550	981	255	307	7			
1	J	207	Total	C	N	O	S	0	0	0
			1503	951	250	295	7			
1	M	203	Total	C	N	O	S	0	0	0
			1483	938	244	295	6			
1	O	204	Total	C	N	O	S	0	0	0
			1480	933	244	297	6			

- Molecule 2 is a protein called FAB 14H7 LIGHT CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	212	Total	C	N	O	S	0	0	0
			1596	996	269	325	6			
2	D	212	Total	C	N	O	S	0	0	0
			1594	995	269	324	6			
2	F	212	Total	C	N	O	S	0	0	0
			1596	996	269	325	6			
2	I	212	Total	C	N	O	S	0	0	0
			1596	996	269	325	6			
2	K	212	Total	C	N	O	S	0	0	0
			1596	996	269	325	6			
2	L	212	Total	C	N	O	S	0	0	0
			1591	993	268	324	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	N	212	Total	C	N	O	S	0	0	0
			1596	996	269	325	6			
2	P	212	Total	C	N	O	S	0	0	0
			1596	996	269	325	6			

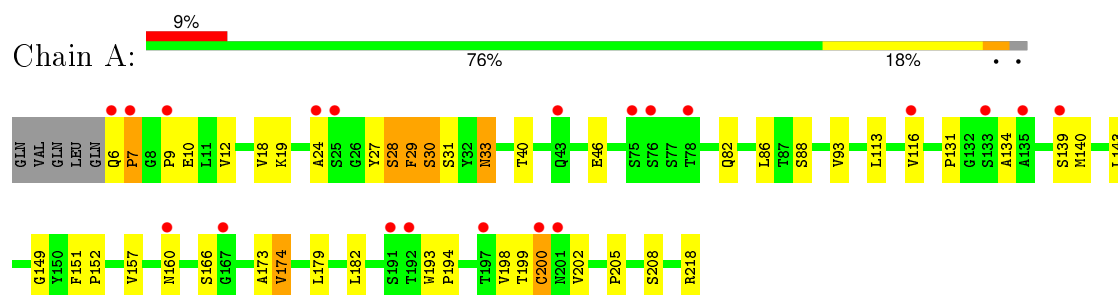
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	19	Total	O	0	0
			19	19		
3	B	31	Total	O	0	0
			31	31		
3	C	25	Total	O	0	0
			25	25		
3	D	26	Total	O	0	0
			26	26		
3	E	24	Total	O	0	0
			24	24		
3	F	23	Total	O	0	0
			23	23		
3	G	16	Total	O	0	0
			16	16		
3	H	15	Total	O	0	0
			15	15		
3	I	23	Total	O	0	0
			23	23		
3	J	22	Total	O	0	0
			22	22		
3	K	27	Total	O	0	0
			27	27		
3	L	21	Total	O	0	0
			21	21		
3	M	12	Total	O	0	0
			12	12		
3	N	24	Total	O	0	0
			24	24		
3	O	16	Total	O	0	0
			16	16		
3	P	35	Total	O	0	0
			35	35		

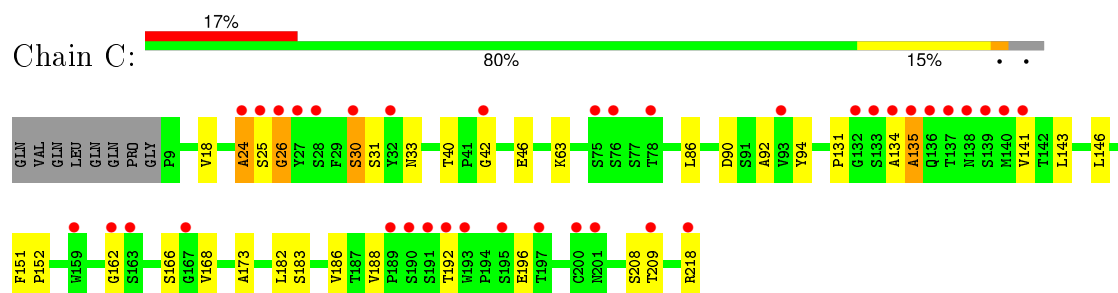
3 Residue-property plots [i](#)

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.

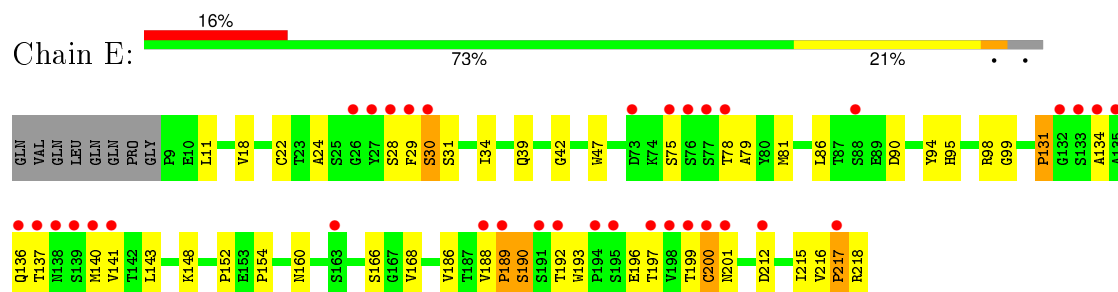
• Molecule 1: FAB 14H7 HEAVY CHAIN



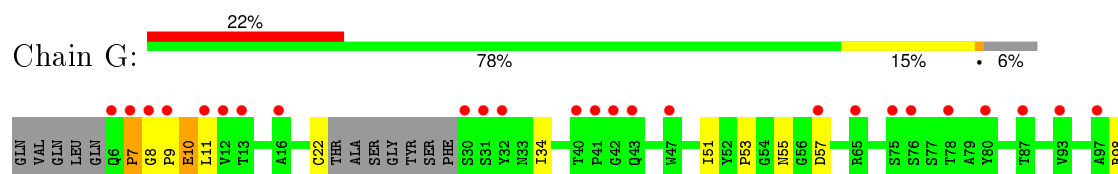
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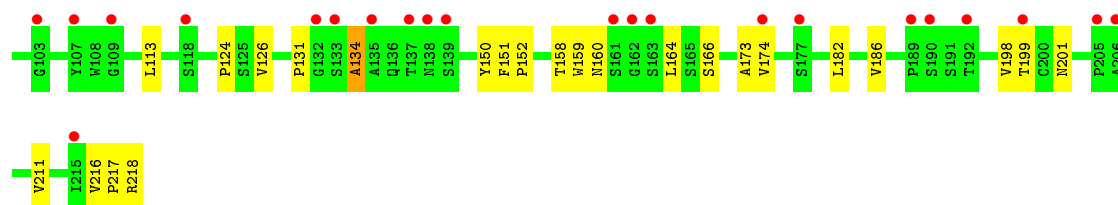


• Molecule 1: FAB 14H7 HEAVY CHAIN

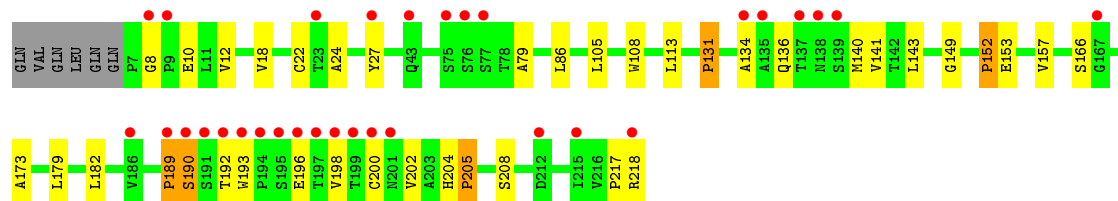
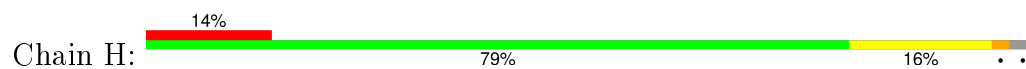


• Molecule 1: FAB 14H7 HEAVY CHAIN

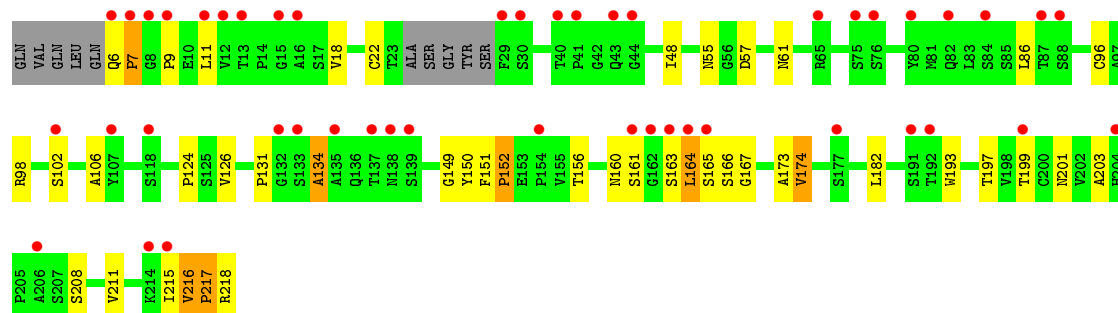
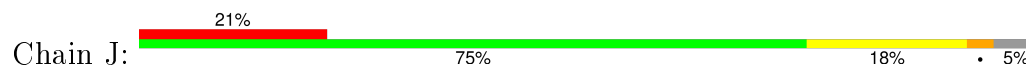




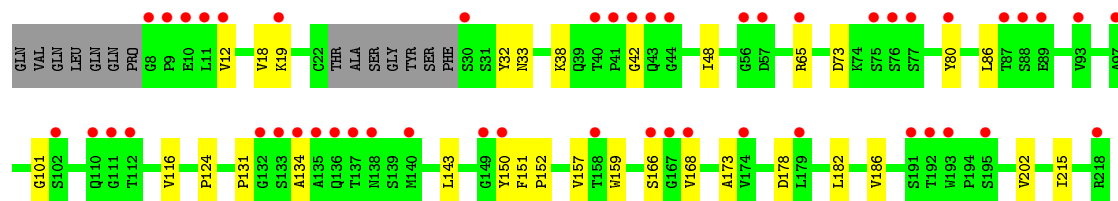
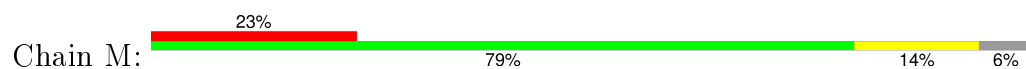
● Molecule 1: FAB 14H7 HEAVY CHAIN



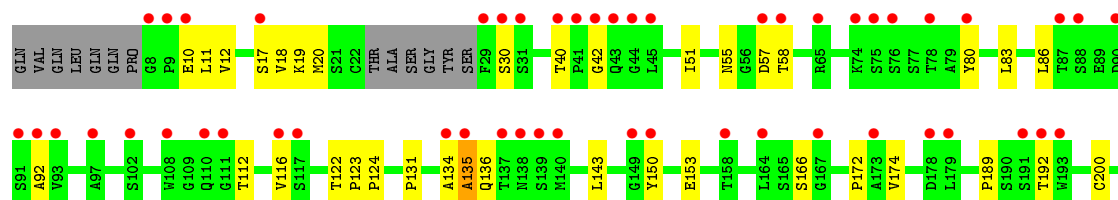
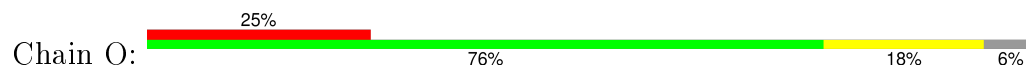
● Molecule 1: FAB 14H7 HEAVY CHAIN

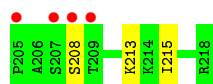


● Molecule 1: FAB 14H7 HEAVY CHAIN

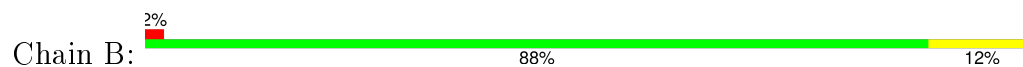


● Molecule 1: FAB 14H7 HEAVY CHAIN

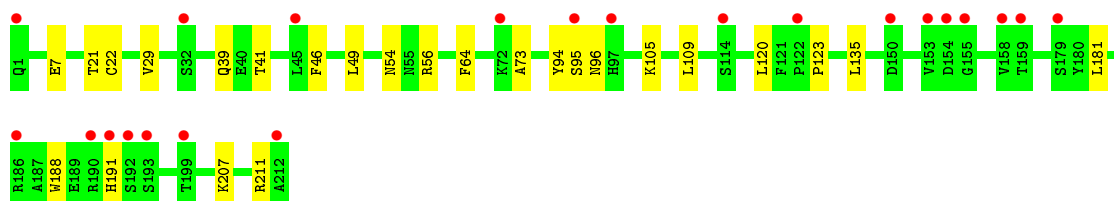
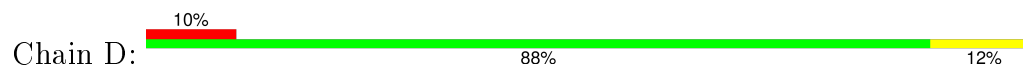




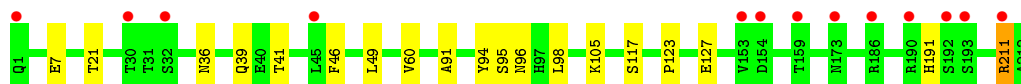
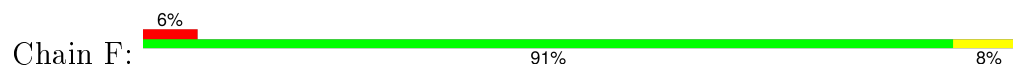
- Molecule 2: FAB 14H7 LIGHT CHAIN



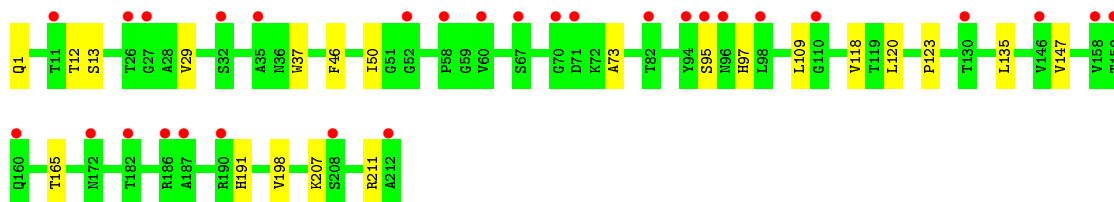
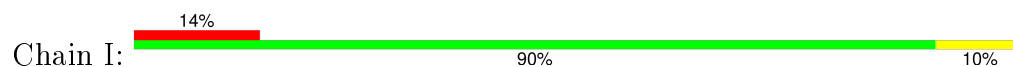
- Molecule 2: FAB 14H7 LIGHT CHAIN



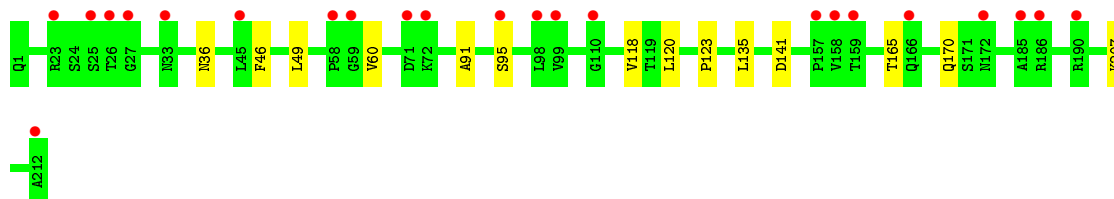
- Molecule 2: FAB 14H7 LIGHT CHAIN



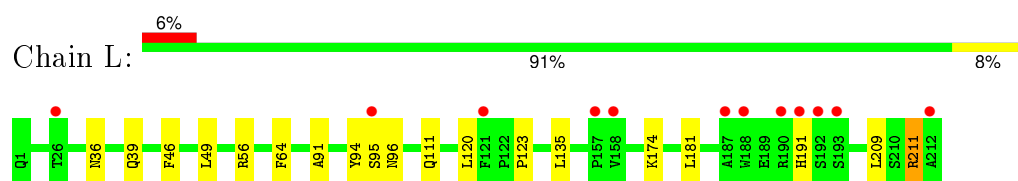
- Molecule 2: FAB 14H7 LIGHT CHAIN



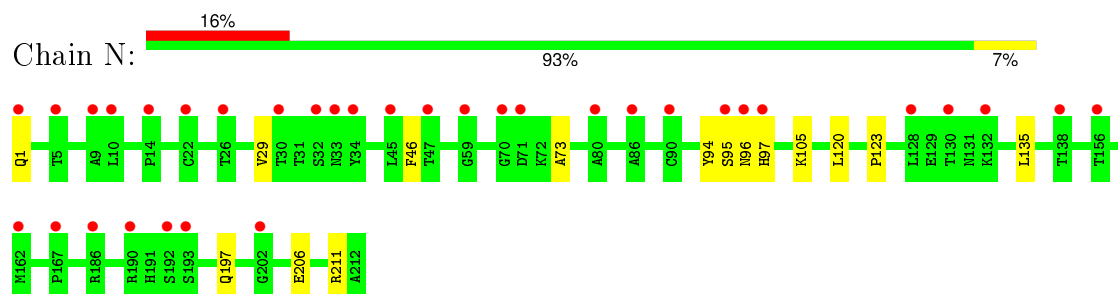
- Molecule 2: FAB 14H7 LIGHT CHAIN



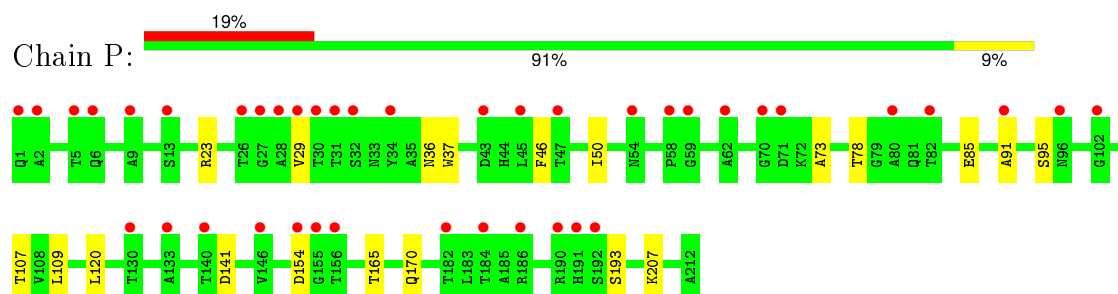
- Molecule 2: FAB 14H7 LIGHT CHAIN



• Molecule 2: FAB 14H7 LIGHT CHAIN



• Molecule 2: FAB 14H7 LIGHT CHAIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	56.20 Å 228.16 Å 146.59 Å 90.00° 90.11° 90.00°	Depositor
Resolution (Å)	16.65 – 2.55 16.65 – 2.55	Depositor EDS
% Data completeness (in resolution range)	93.5 (16.65-2.55) 93.0 (16.65-2.55)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 2.55 Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.279 , 0.328 0.283 , 0.329	Depositor DCC
R_{free} test set	5009 reflections (4.49%)	DCC
Wilson B-factor (Å ²)	36.0	Xtriage
Anisotropy	0.416	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.46 , 75.0	EDS
Estimated twinning fraction	0.499 for H,-K,-L 0.459 for h,-k,-l	Xtriage
Reported twinning fraction	0.499 for H,-K,-L	Depositor
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	3 of 111576 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	25238	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 81.39 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 3.5837e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.24	0/1594	0.50	0/2189
1	C	0.23	0/1576	0.48	1/2163 (0.0%)
1	E	0.23	0/1569	0.50	0/2153
1	G	0.22	0/1529	0.46	0/2100
1	H	0.23	0/1593	0.46	0/2186
1	J	0.24	0/1543	0.49	0/2117
1	M	0.21	0/1522	0.44	0/2090
1	O	0.21	0/1519	0.44	0/2086
2	B	0.23	0/1632	0.42	0/2232
2	D	0.21	0/1630	0.40	0/2229
2	F	0.21	0/1632	0.41	0/2232
2	I	0.21	0/1632	0.41	0/2232
2	K	0.21	0/1632	0.41	0/2232
2	L	0.21	0/1627	0.41	0/2227
2	N	0.21	0/1632	0.40	0/2232
2	P	0.21	0/1632	0.41	0/2232
All	All	0.22	0/25494	0.44	1/34932 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	2
1	J	0	2
All	All	0	4

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	26	GLY	N-CA-C	-6.36	97.19	113.10

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	24	ALA	Peptide
1	C	26	GLY	Peptide
1	J	215	ILE	Peptide
1	J	216	VAL	Peptide

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	1551	0	1483	25	0
1	C	1534	0	1474	15	0
1	E	1528	0	1470	28	0
1	G	1489	0	1413	21	0
1	H	1550	0	1492	22	0
1	J	1503	0	1427	23	0
1	M	1483	0	1422	14	0
1	O	1480	0	1406	19	0
2	B	1596	0	1545	13	0
2	D	1594	0	1540	18	0
2	F	1596	0	1545	13	0
2	I	1596	0	1545	11	0
2	K	1596	0	1545	7	0
2	L	1591	0	1531	12	0
2	N	1596	0	1545	8	0
2	P	1596	0	1545	11	0
3	A	19	0	0	0	0
3	B	31	0	0	1	0
3	C	25	0	0	0	0
3	D	26	0	0	2	0
3	E	24	0	0	0	0
3	F	23	0	0	0	0
3	G	16	0	0	1	0
3	H	15	0	0	1	0
3	I	23	0	0	1	0
3	J	22	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	K	27	0	0	0	0
3	L	21	0	0	0	0
3	M	12	0	0	0	0
3	N	24	0	0	1	0
3	O	16	0	0	1	0
3	P	35	0	0	1	0
All	All	25238	0	23928	238	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 5.

All (238) 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:J:160:ASN:ND2	1:J:197:THR:O	2.23	0.70
1:J:18:VAL:HG13	1:J:86:LEU:HD11	1.74	0.69
1:C:135:ALA:HB3	2:D:207:LYS:HD2	1.74	0.69
1:E:160:ASN:N	1:E:199:THR:O	2.18	0.68
1:H:192:THR:O	1:H:196:GLU:N	2.27	0.68
1:E:143:LEU:HD13	1:E:215:ILE:HG13	1.76	0.68
1:G:160:ASN:HA	1:G:199:THR:HB	1.77	0.67
1:E:28:SER:O	1:E:30:SER:N	2.26	0.67
1:C:192:THR:O	1:C:196:GLU:N	2.27	0.66
1:E:201:ASN:ND2	1:E:212:ASP:OD1	2.29	0.65
1:M:19:LYS:HE3	1:M:80:TYR:HB3	1.79	0.65
2:D:191:HIS:O	2:D:211:ARG:NH1	2.30	0.64
1:C:173:ALA:HB2	1:C:182:LEU:HD23	1.80	0.64
1:A:10:GLU:HG2	1:A:113:LEU:HB3	1.79	0.64
1:G:173:ALA:HB2	1:G:182:LEU:HD23	1.79	0.63
1:C:218:ARG:NH1	2:D:123:PRO:O	2.28	0.63
1:M:134:ALA:HB1	2:N:120:LEU:HB3	1.80	0.63
2:F:191:HIS:O	2:F:211:ARG:NH1	2.30	0.62
1:C:46:GLU:OE2	1:C:63:LYS:NZ	2.32	0.62
1:O:134:ALA:HB1	2:P:120:LEU:HB3	1.80	0.62
1:M:33:ASN:ND2	1:M:101:GLY:O	2.32	0.62
1:M:173:ALA:HB2	1:M:182:LEU:HD23	1.82	0.61
1:H:134:ALA:HB1	2:L:120:LEU:HB3	1.82	0.61
1:J:96:CYS:SG	3:J:2005:HOH:O	2.55	0.61
1:G:55:ASN:ND2	1:G:57:ASP:OD2	2.34	0.60
1:G:218:ARG:NH1	3:G:2016:HOH:O	2.34	0.60
2:L:36:ASN:HB2	2:L:91:ALA:HB3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:160:ASN:HB2	1:G:164:LEU:HB2	1.83	0.60
1:G:126:VAL:HB	1:G:211:VAL:HG11	1.83	0.60
1:H:218:ARG:NH2	2:L:123:PRO:O	2.34	0.60
1:J:55:ASN:ND2	1:J:57:ASP:OD2	2.34	0.60
1:O:19:LYS:HE3	1:O:80:TYR:HB3	1.84	0.59
2:F:36:ASN:HB2	2:F:91:ALA:HB3	1.84	0.59
1:O:124:PRO:HB3	1:O:150:TYR:HB3	1.85	0.59
1:M:18:VAL:HG22	1:M:86:LEU:HD11	1.84	0.59
1:G:22:CYS:O	1:G:98:ARG:NH2	2.35	0.59
2:K:36:ASN:HB2	2:K:91:ALA:HB3	1.85	0.58
1:C:40:THR:HG22	1:C:92:ALA:HB2	1.84	0.58
2:K:141:ASP:OD1	2:K:170:GLN:NE2	2.36	0.58
1:M:38:LYS:HB2	1:M:48:ILE:HD11	1.85	0.58
1:E:143:LEU:HD22	1:E:215:ILE:HG21	1.85	0.57
1:E:11:LEU:HD22	1:E:152:PRO:HG3	1.86	0.57
1:A:173:ALA:HB2	1:A:182:LEU:HD23	1.86	0.57
1:J:165:SER:OG	1:J:166:SER:N	2.37	0.57
2:B:154:ASP:HA	2:B:193:SER:HB2	1.85	0.57
2:D:7:GLU:OE2	2:D:21:THR:OG1	2.21	0.56
1:H:140:MET:HA	1:H:189:PRO:O	2.04	0.56
2:L:191:HIS:O	2:L:211:ARG:NH1	2.39	0.56
1:A:174:VAL:HG13	2:B:165:THR:HG22	1.87	0.56
1:E:196:GLU:HG3	1:E:197:THR:H	1.70	0.56
2:I:118:VAL:HG11	3:I:2014:HOH:O	2.05	0.56
1:M:159:TRP:HZ3	1:M:215:ILE:HD11	1.71	0.55
1:O:150:TYR:OH	1:O:153:GLU:OE1	2.21	0.55
2:I:191:HIS:O	2:I:211:ARG:NH1	2.35	0.55
2:B:29:VAL:HG11	2:B:73:ALA:HB2	1.88	0.54
1:O:55:ASN:ND2	1:O:57:ASP:OD2	2.39	0.54
2:P:154:ASP:HA	2:P:193:SER:HB2	1.89	0.54
2:B:123:PRO:HD3	2:B:135:LEU:HG	1.89	0.54
1:O:189:PRO:O	1:O:192:THR:OG1	2.26	0.54
2:L:56:ARG:NH1	2:L:64:PHE:O	2.37	0.54
1:G:158:THR:OG1	1:G:201:ASN:OD1	2.21	0.54
1:O:174:VAL:HG13	2:P:165:THR:HG22	1.90	0.54
1:J:160:ASN:N	1:J:199:THR:O	2.36	0.53
1:G:10:GLU:HG2	1:G:113:LEU:HB3	1.90	0.53
1:G:164:LEU:HG	1:G:186:VAL:HG21	1.90	0.53
1:A:157:VAL:HG22	1:A:202:VAL:HG22	1.89	0.53
1:E:22:CYS:HB3	1:E:79:ALA:HB3	1.90	0.53
1:O:12:VAL:HG23	1:O:116:VAL:HG22	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:174:VAL:HG13	2:K:165:THR:HG22	1.89	0.53
2:D:22:CYS:HB3	2:D:73:ALA:HB3	1.89	0.53
1:J:6:GLN:N	3:J:2001:HOH:O	2.40	0.53
1:J:134:ALA:HB1	2:K:120:LEU:HB3	1.91	0.52
1:M:168:VAL:HG22	1:M:186:VAL:HG23	1.90	0.52
2:F:7:GLU:OE2	2:F:21:THR:OG1	2.26	0.52
1:E:34:ILE:HG12	1:E:98:ARG:HB3	1.92	0.52
1:J:22:CYS:O	1:J:98:ARG:NH2	2.40	0.52
1:E:39:GLN:OE1	1:E:95:HIS:NE2	2.37	0.52
1:E:141:VAL:HG11	1:E:193:TRP:CE3	2.45	0.52
1:H:12:VAL:HG21	1:H:18:VAL:HG11	1.92	0.52
1:H:157:VAL:HG22	1:H:202:VAL:HG22	1.92	0.51
2:N:197:GLN:HG2	2:N:206:GLU:HG3	1.92	0.51
1:J:173:ALA:HB2	1:J:182:LEU:HD23	1.93	0.51
1:G:9:PRO:O	1:G:11:LEU:N	2.44	0.51
2:D:188:TRP:O	2:D:211:ARG:NH1	2.43	0.51
1:A:160:ASN:N	1:A:199:THR:O	2.22	0.51
1:C:141:VAL:N	1:C:188:VAL:O	2.44	0.50
1:E:30:SER:OG	1:E:31:SER:N	2.44	0.50
2:B:190:ARG:NH2	3:B:2025:HOH:O	2.40	0.50
1:O:20:MET:HG2	1:O:112:THR:HG21	1.94	0.49
1:C:134:ALA:HB1	2:D:120:LEU:HB3	1.94	0.49
2:P:36:ASN:HB2	2:P:91:ALA:HB3	1.94	0.49
1:A:143:LEU:HD12	1:A:198:VAL:HG11	1.94	0.49
1:O:51:ILE:HD12	1:O:58:THR:HG22	1.93	0.49
1:C:30:SER:OG	1:C:31:SER:N	2.44	0.49
1:M:143:LEU:HB3	1:M:215:ILE:HD13	1.94	0.49
1:G:134:ALA:HB1	2:I:120:LEU:HB3	1.93	0.49
1:G:174:VAL:HG13	2:I:165:THR:HG22	1.93	0.49
2:L:94:TYR:O	2:L:96:ASN:N	2.45	0.49
1:G:124:PRO:HB3	1:G:150:TYR:HB3	1.94	0.49
1:H:8:GLY:N	3:H:2001:HOH:O	2.45	0.49
2:N:135:LEU:HD12	3:N:2013:HOH:O	2.12	0.49
2:D:29:VAL:HG11	2:D:73:ALA:HB2	1.95	0.49
1:E:141:VAL:N	1:E:188:VAL:O	2.41	0.48
2:P:37:TRP:HB2	2:P:50:ILE:HB	1.95	0.48
1:E:218:ARG:NH2	2:F:123:PRO:O	2.47	0.48
1:E:18:VAL:HG13	1:E:86:LEU:HD11	1.95	0.48
2:F:39:GLN:HB2	2:F:49:LEU:HD11	1.94	0.48
1:O:135:ALA:HB3	2:P:207:LYS:HD2	1.95	0.48
2:B:56:ARG:NH1	2:B:64:PHE:O	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:SER:OG	1:A:29:PHE:N	2.47	0.48
1:H:204:HIS:HA	1:H:205:PRO:HD2	1.69	0.48
1:E:30:SER:OG	1:E:99:GLY:O	2.32	0.48
1:E:148:LYS:NZ	2:F:127:GLU:OE2	2.44	0.48
1:O:143:LEU:HD13	1:O:215:ILE:HG21	1.95	0.48
2:I:29:VAL:HG11	2:I:73:ALA:HB2	1.96	0.47
1:G:173:ALA:HA	1:G:182:LEU:HB3	1.96	0.47
1:A:6:GLN:HA	1:A:7:PRO:HA	1.55	0.47
1:H:193:TRP:CH2	1:H:217:PRO:HB3	2.49	0.47
1:A:199:THR:HA	1:A:200:CYS:CB	2.45	0.47
1:E:215:ILE:O	1:E:217:PRO:HA	2.14	0.47
1:A:6:GLN:O	1:A:18:VAL:HA	2.14	0.47
1:M:32:TYR:HD2	1:M:33:ASN:HD22	1.62	0.47
1:A:88:SER:HA	1:A:116:VAL:HB	1.96	0.47
1:E:193:TRP:CZ2	1:E:217:PRO:HB3	2.49	0.47
1:M:124:PRO:HB3	1:M:150:TYR:HB3	1.96	0.47
2:I:37:TRP:HB2	2:I:50:ILE:HB	1.97	0.47
1:A:18:VAL:HG22	1:A:86:LEU:HD11	1.97	0.47
2:K:118:VAL:O	2:K:207:LYS:NZ	2.44	0.47
1:J:151:PHE:HA	1:J:152:PRO:HA	1.74	0.47
2:B:141:ASP:OD1	2:B:170:GLN:NE2	2.38	0.46
1:A:93:VAL:HG22	1:A:113:LEU:HD12	1.97	0.46
1:H:173:ALA:HB2	1:H:182:LEU:HD23	1.96	0.46
1:A:134:ALA:HB1	2:B:120:LEU:HB3	1.98	0.46
1:A:193:TRP:CG	1:A:194:PRO:HA	2.51	0.46
1:A:19:LYS:HB2	1:A:82:GLN:HG3	1.97	0.46
2:D:22:CYS:N	2:D:73:ALA:O	2.49	0.46
2:N:123:PRO:HD3	2:N:135:LEU:HG	1.98	0.46
1:H:105:LEU:O	1:H:108:TRP:NE1	2.45	0.46
1:E:24:ALA:HB3	1:E:98:ARG:HH21	1.81	0.46
1:A:199:THR:HA	1:A:200:CYS:HB3	1.97	0.46
1:E:189:PRO:HB2	1:E:190:SER:H	1.55	0.46
2:P:29:VAL:HG11	2:P:73:ALA:HB2	1.98	0.45
1:J:48:ILE:O	1:J:61:ASN:N	2.43	0.45
2:P:23:ARG:NH2	3:P:2006:HOH:O	2.47	0.45
1:E:168:VAL:HG22	1:E:186:VAL:HG23	1.97	0.45
2:K:49:LEU:HA	2:K:60:VAL:HG21	1.99	0.45
1:C:146:LEU:HD12	1:C:183:SER:HB3	1.98	0.45
2:D:56:ARG:NH1	2:D:64:PHE:O	2.45	0.45
1:E:131:PRO:HB3	1:E:136:GLN:HE22	1.82	0.45
1:J:6:GLN:HA	1:J:7:PRO:HD3	1.71	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:12:VAL:HG23	1:M:116:VAL:HG22	1.99	0.45
1:A:30:SER:OG	1:A:31:SER:N	2.49	0.45
2:L:39:GLN:HB2	2:L:49:LEU:HD11	1.98	0.45
2:D:105:LYS:NZ	3:D:2013:HOH:O	2.50	0.45
2:K:123:PRO:HD3	2:K:135:LEU:HG	1.98	0.44
1:J:124:PRO:HB3	1:J:150:TYR:HB3	2.00	0.44
1:J:161:SER:H	1:J:201:ASN:HD21	1.64	0.44
2:B:139:ILE:O	2:B:177:ALA:N	2.41	0.44
1:O:122:THR:HA	1:O:123:PRO:HD3	1.88	0.44
2:D:39:GLN:HB2	2:D:49:LEU:HD11	2.00	0.44
1:A:139:SER:OG	1:A:140:MET:N	2.50	0.44
2:I:12:THR:OG1	2:I:13:SER:N	2.50	0.44
1:J:160:ASN:HD22	1:J:164:LEU:HD13	1.83	0.44
2:F:49:LEU:HA	2:F:60:VAL:HG21	1.99	0.44
1:J:193:TRP:CZ2	1:J:217:PRO:HD3	2.52	0.44
1:G:151:PHE:HA	1:G:152:PRO:HA	1.79	0.44
1:G:34:ILE:HB	1:G:51:ILE:HG23	2.00	0.44
1:J:9:PRO:O	1:J:11:LEU:N	2.51	0.44
2:B:36:ASN:HB2	2:B:91:ALA:HB3	1.99	0.44
2:D:135:LEU:HD13	2:D:181:LEU:HD23	1.99	0.44
2:P:141:ASP:OD1	2:P:170:GLN:NE2	2.37	0.44
1:H:149:GLY:HA2	1:H:179:LEU:HB3	1.98	0.44
1:H:152:PRO:HB2	1:H:153:GLU:H	1.66	0.43
1:E:90:ASP:O	1:E:94:TYR:OH	2.27	0.43
1:H:143:LEU:HD12	1:H:198:VAL:HG11	1.98	0.43
2:D:54:ASN:ND2	3:D:2005:HOH:O	2.49	0.43
1:C:168:VAL:HG22	1:C:186:VAL:HG23	2.00	0.43
1:C:18:VAL:HG22	1:C:86:LEU:HD11	2.00	0.43
1:G:198:VAL:O	1:G:199:THR:OG1	2.34	0.43
2:L:123:PRO:HD3	2:L:135:LEU:HD23	2.00	0.43
1:A:7:PRO:HB2	1:A:9:PRO:HD2	1.99	0.43
1:A:149:GLY:HA2	1:A:179:LEU:HB3	2.01	0.43
2:F:96:ASN:N	2:F:96:ASN:OD1	2.51	0.43
1:E:47:TRP:CG	2:F:98:LEU:HB3	2.53	0.43
1:H:10:GLU:HG2	1:H:113:LEU:HD23	2.01	0.43
1:O:172:PRO:HG2	2:P:165:THR:HB	2.01	0.43
1:H:18:VAL:HG22	1:H:86:LEU:HD11	2.01	0.43
2:F:94:TYR:O	2:F:96:ASN:N	2.52	0.43
2:B:94:TYR:O	2:B:96:ASN:N	2.51	0.43
1:O:18:VAL:HG13	1:O:86:LEU:HD11	2.00	0.43
1:E:199:THR:HA	1:E:200:CYS:CB	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:192:THR:O	1:E:196:GLU:N	2.52	0.42
1:J:156:THR:OG1	1:J:203:ALA:HB3	2.20	0.42
2:I:123:PRO:HD3	2:I:135:LEU:HG	2.02	0.42
2:L:135:LEU:HD12	2:L:181:LEU:HD23	2.01	0.42
2:I:118:VAL:O	2:I:207:LYS:NZ	2.49	0.42
1:O:20:MET:HE1	1:O:83:LEU:HD12	2.00	0.42
1:M:151:PHE:HA	1:M:152:PRO:HA	1.88	0.42
2:D:123:PRO:HD3	2:D:135:LEU:HG	2.01	0.42
1:J:9:PRO:HB2	3:J:2002:HOH:O	2.18	0.42
1:H:131:PRO:HB3	1:H:136:GLN:NE2	2.34	0.42
1:G:159:TRP:HB3	1:G:164:LEU:HD23	2.01	0.42
1:G:51:ILE:O	1:G:53:PRO:HD3	2.19	0.42
1:H:22:CYS:HB3	1:H:79:ALA:HB3	2.02	0.42
1:C:90:ASP:O	1:C:94:TYR:OH	2.26	0.42
2:F:105:LYS:HB2	2:F:105:LYS:HE3	1.81	0.42
2:N:29:VAL:HG11	2:N:73:ALA:HB2	2.01	0.42
1:A:218:ARG:NH2	2:B:123:PRO:O	2.53	0.41
1:C:151:PHE:HA	1:C:152:PRO:HA	1.80	0.41
1:H:134:ALA:HB2	2:L:209:LEU:HB3	2.03	0.41
2:F:91:ALA:HB1	2:F:98:LEU:HD11	2.02	0.41
2:L:96:ASN:N	2:L:96:ASN:OD1	2.53	0.41
1:H:141:VAL:HG11	1:H:193:TRP:CE3	2.56	0.41
1:H:10:GLU:HG2	1:H:113:LEU:HB3	2.01	0.41
2:I:147:VAL:HG13	2:I:198:VAL:HG13	2.02	0.41
1:A:151:PHE:HA	1:A:152:PRO:HA	1.84	0.41
2:D:207:LYS:HD3	2:D:207:LYS:HA	1.81	0.41
2:B:116:PRO:HB3	2:B:142:PHE:HB3	2.01	0.41
2:P:85:GLU:HG3	2:P:107:THR:HA	2.03	0.41
1:O:40:THR:HG22	1:O:92:ALA:HB2	2.03	0.41
1:J:126:VAL:HB	1:J:211:VAL:HG11	2.02	0.41
1:J:160:ASN:HB3	1:J:163:SER:CB	2.51	0.41
2:L:111:GLN:HE22	2:L:174:LYS:HG2	1.85	0.41
2:N:94:TYR:O	2:N:96:ASN:N	2.54	0.41
1:O:17:SER:N	3:O:2001:HOH:O	2.51	0.41
1:M:157:VAL:HG22	1:M:202:VAL:HG22	2.03	0.41
2:N:105:LYS:HB2	2:N:105:LYS:HE3	1.86	0.41
1:H:189:PRO:HB2	1:H:190:SER:H	1.66	0.40
2:D:94:TYR:O	2:D:96:ASN:N	2.54	0.40
1:E:137:THR:OG1	2:F:117:SER:HB2	2.21	0.40
1:C:141:VAL:HG12	1:C:143:LEU:HG	2.03	0.40
1:A:33:ASN:C	1:A:33:ASN:HD22	2.25	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:1:GLN:HG2	2:I:97:HIS:NE2	2.36	0.40
2:D:105:LYS:HB2	2:D:105:LYS:HE3	1.85	0.40
1:O:200:CYS:HB3	1:O:213:LYS:HB2	2.03	0.40
1:A:18:VAL:HG13	1:A:86:LEU:HD11	2.04	0.40
1:G:7:PRO:HB2	1:G:8:GLY:H	1.60	0.40
2:N:1:GLN:HG2	2:N:97:HIS:NE2	2.37	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	210/217 (97%)	173 (82%)	26 (12%)	11 (5%)	2	2
1	C	207/217 (95%)	169 (82%)	28 (14%)	10 (5%)	3	3
1	E	207/217 (95%)	174 (84%)	18 (9%)	15 (7%)	1	1
1	G	201/217 (93%)	167 (83%)	27 (13%)	7 (4%)	4	5
1	H	209/217 (96%)	174 (83%)	27 (13%)	8 (4%)	4	4
1	J	203/217 (94%)	164 (81%)	29 (14%)	10 (5%)	3	2
1	M	199/217 (92%)	173 (87%)	23 (12%)	3 (2%)	13	22
1	O	200/217 (92%)	166 (83%)	26 (13%)	8 (4%)	4	4
2	B	210/212 (99%)	194 (92%)	12 (6%)	4 (2%)	10	15
2	D	210/212 (99%)	198 (94%)	9 (4%)	3 (1%)	14	23
2	F	210/212 (99%)	196 (93%)	11 (5%)	3 (1%)	14	23
2	I	210/212 (99%)	194 (92%)	13 (6%)	3 (1%)	14	23
2	K	210/212 (99%)	194 (92%)	14 (7%)	2 (1%)	19	33
2	L	210/212 (99%)	192 (91%)	15 (7%)	3 (1%)	14	23
2	N	210/212 (99%)	194 (92%)	13 (6%)	3 (1%)	14	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	P	210/212 (99%)	194 (92%)	13 (6%)	3 (1%)	14	23
All	All	3316/3432 (97%)	2916 (88%)	304 (9%)	96 (3%)	6	7

All (96) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	27	TYR
1	A	28	SER
1	A	131	PRO
1	A	200	CYS
1	C	25	SER
1	E	29	PHE
1	E	78	THR
1	E	131	PRO
1	E	189	PRO
1	E	200	CYS
1	E	216	VAL
1	E	217	PRO
1	G	217	PRO
1	H	131	PRO
1	H	189	PRO
1	H	190	SER
1	J	134	ALA
1	J	217	PRO
1	A	29	PHE
2	B	95	SER
1	C	24	ALA
1	C	131	PRO
1	C	208	SER
2	D	95	SER
2	D	109	LEU
2	F	95	SER
2	I	95	SER
1	J	7	PRO
2	K	95	SER
2	L	95	SER
1	M	131	PRO
2	N	95	SER
1	O	10	GLU
1	O	135	ALA
1	A	24	ALA
1	A	30	SER

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Mol	Chain	Res	Type
1	A	166	SER
1	A	208	SER
1	C	42	GLY
1	C	135	ALA
1	C	166	SER
1	C	209	THR
2	D	46	PHE
1	E	30	SER
1	E	75	SER
1	E	134	ALA
1	E	166	SER
2	F	46	PHE
1	G	7	PRO
1	G	10	GLU
1	H	166	SER
2	I	46	PHE
1	J	102	SER
1	J	106	ALA
1	J	167	GLY
1	J	208	SER
2	K	46	PHE
2	L	46	PHE
1	M	166	SER
2	N	46	PHE
2	N	211	ARG
1	O	11	LEU
1	O	42	GLY
1	O	166	SER
2	P	46	PHE
2	P	95	SER
2	B	46	PHE
1	C	30	SER
1	E	42	GLY
1	G	134	ALA
1	G	166	SER
1	H	208	SER
1	J	131	PRO
1	O	30	SER
1	O	131	PRO
1	O	208	SER
1	E	190	SER
2	F	211	ARG

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Mol	Chain	Res	Type
1	G	131	PRO
1	G	216	VAL
1	H	24	ALA
1	H	205	PRO
2	I	109	LEU
1	M	42	GLY
1	A	205	PRO
2	B	109	LEU
2	B	211	ARG
1	C	162	GLY
1	E	140	MET
2	L	211	ARG
2	P	109	LEU
1	E	154	PRO
1	J	149	GLY
1	A	7	PRO
1	H	152	PRO
1	J	152	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	172/184 (94%)	167 (97%)	5 (3%)	50	75
1	C	170/184 (92%)	169 (99%)	1 (1%)	90	97
1	E	170/184 (92%)	169 (99%)	1 (1%)	90	97
1	G	163/184 (89%)	163 (100%)	0	100	100
1	H	172/184 (94%)	170 (99%)	2 (1%)	78	92
1	J	162/184 (88%)	158 (98%)	4 (2%)	55	80
1	M	164/184 (89%)	161 (98%)	3 (2%)	66	87
1	O	163/184 (89%)	162 (99%)	1 (1%)	90	97
2	B	179/179 (100%)	178 (99%)	1 (1%)	90	97
2	D	178/179 (99%)	177 (99%)	1 (1%)	90	97

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	F	179/179 (100%)	178 (99%)	1 (1%)	90	97
2	I	179/179 (100%)	179 (100%)	0	100	100
2	K	179/179 (100%)	179 (100%)	0	100	100
2	L	177/179 (99%)	177 (100%)	0	100	100
2	N	179/179 (100%)	179 (100%)	0	100	100
2	P	179/179 (100%)	178 (99%)	1 (1%)	90	97
All	All	2765/2904 (95%)	2744 (99%)	21 (1%)	86	96

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	VAL
1	A	33	ASN
1	A	40	THR
1	A	46	GLU
1	A	174	VAL
2	B	189	GLU
1	C	33	ASN
2	D	41	THR
1	E	81	MET
2	F	41	THR
1	H	27	TYR
1	H	200	CYS
1	J	164	LEU
1	J	174	VAL
1	J	216	VAL
1	J	218	ARG
1	M	65	ARG
1	M	73	ASP
1	M	178	ASP
1	O	136	GLN
2	P	78	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	J	201	ASN
2	L	97	HIS
2	P	1	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	212/217 (97%)	0.74	20 (9%) 11 12	20, 38, 71, 84	0
1	C	209/217 (96%)	1.10	37 (17%) 2 2	26, 44, 84, 107	0
1	E	209/217 (96%)	0.96	35 (16%) 2 2	22, 39, 83, 116	0
1	G	205/217 (94%)	1.37	47 (22%) 1 1	28, 52, 84, 109	0
1	H	211/217 (97%)	0.97	31 (14%) 3 3	23, 45, 81, 93	0
1	J	207/217 (95%)	1.41	46 (22%) 1 1	32, 52, 89, 102	0
1	M	203/217 (93%)	1.37	49 (24%) 1 1	27, 51, 82, 105	0
1	O	204/217 (94%)	1.51	55 (26%) 1 0	30, 56, 85, 103	0
2	B	212/212 (100%)	0.29	4 (1%) 70 74	20, 31, 58, 76	0
2	D	212/212 (100%)	0.66	22 (10%) 8 9	24, 38, 70, 89	0
2	F	212/212 (100%)	0.37	13 (6%) 25 28	20, 31, 64, 86	0
2	I	212/212 (100%)	0.94	29 (13%) 4 4	28, 48, 72, 92	0
2	K	212/212 (100%)	0.82	23 (10%) 8 8	34, 48, 72, 90	0
2	L	212/212 (100%)	0.51	12 (5%) 27 32	21, 39, 67, 80	0
2	N	212/212 (100%)	0.96	34 (16%) 3 2	29, 50, 71, 80	0
2	P	212/212 (100%)	1.10	41 (19%) 2 1	31, 50, 72, 82	0
All	All	3356/3432 (97%)	0.94	498 (14%) 3 3	20, 45, 78, 116	0

All (498) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	163	SER	14.4
1	G	162	GLY	12.5
1	O	9	PRO	11.5
1	M	9	PRO	11.1
1	H	200	CYS	10.5

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Mol	Chain	Res	Type	RSRZ
1	A	75	SER	10.2
1	J	161	SER	9.6
1	M	77	SER	9.5
1	H	9	PRO	9.0
1	G	8	GLY	8.8
1	G	6	GLN	8.7
1	E	135	ALA	8.2
1	A	76	SER	7.8
2	I	159	THR	7.7
1	C	27	TYR	7.7
1	C	133	SER	7.3
1	A	9	PRO	7.3
1	C	75	SER	7.1
1	G	7	PRO	7.0
2	D	192	SER	7.0
1	J	7	PRO	6.9
1	C	138	ASN	6.9
2	I	26	THR	6.8
1	G	13	THR	6.8
1	H	76	SER	6.8
1	J	41	PRO	6.7
1	M	88	SER	6.6
1	O	137	THR	6.6
2	I	27	GLY	6.5
1	J	40	THR	6.5
1	E	191	SER	6.5
1	M	75	SER	6.3
2	N	26	THR	6.3
1	M	76	SER	6.2
1	M	135	ALA	6.2
1	O	138	ASN	6.1
1	C	139	SER	6.0
2	I	190	ARG	5.9
1	C	135	ALA	5.9
1	H	75	SER	5.9
1	C	26	GLY	5.8
1	E	137	THR	5.8
1	G	132	GLY	5.7
1	O	135	ALA	5.7
1	H	189	PRO	5.7
1	E	136	GLN	5.6
1	O	192	THR	5.6

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Mol	Chain	Res	Type	RSRZ
1	C	191	SER	5.6
2	K	110	GLY	5.6
1	J	132	GLY	5.4
1	E	140	MET	5.3
1	M	192	THR	5.3
1	A	192	THR	5.2
1	G	41	PRO	5.2
1	M	149	GLY	5.2
2	D	190	ARG	5.1
2	P	45	LEU	5.1
1	M	44	GLY	5.1
2	P	156	THR	5.1
1	E	138	ASN	5.1
1	C	76	SER	5.1
1	J	15	GLY	5.1
2	F	192	SER	5.0
1	E	134	ALA	5.0
1	J	9	PRO	5.0
1	J	88	SER	5.0
1	C	195	SER	5.0
1	A	167	GLY	5.0
1	G	78	THR	5.0
1	O	40	THR	4.9
1	E	133	SER	4.9
2	D	193	SER	4.8
2	K	159	THR	4.8
1	G	9	PRO	4.8
1	G	76	SER	4.7
1	J	13	THR	4.7
2	I	172	ASN	4.7
1	E	75	SER	4.7
1	C	137	THR	4.6
1	C	134	ALA	4.6
1	M	57	ASP	4.6
1	G	40	THR	4.5
1	O	88	SER	4.5
1	M	43	GLN	4.5
1	H	23	THR	4.5
1	M	136	GLN	4.4
2	I	186	ARG	4.4
2	L	157	PRO	4.4
1	E	76	SER	4.4

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Mol	Chain	Res	Type	RSRZ
1	H	190	SER	4.4
1	C	132	GLY	4.3
2	P	192	SER	4.3
1	M	8	GLY	4.3
1	G	133	SER	4.3
2	P	30	THR	4.3
1	O	191	SER	4.3
1	M	138	ASN	4.3
1	O	17	SER	4.3
2	K	190	ARG	4.3
2	N	95	SER	4.2
1	C	218	ARG	4.2
1	E	199	THR	4.2
1	O	76	SER	4.2
1	H	192	THR	4.2
1	H	195	SER	4.1
1	O	167	GLY	4.1
1	J	165	SER	4.1
1	J	6	GLN	4.1
1	C	163	SER	4.1
1	M	167	GLY	4.1
1	H	135	ALA	4.1
1	O	134	ALA	4.1
1	J	75	SER	4.1
1	O	30	SER	4.1
2	N	202	GLY	4.1
1	J	164	LEU	4.1
2	F	193	SER	4.1
1	A	7	PRO	4.1
1	J	8	GLY	4.0
1	M	87	THR	4.0
2	K	172	ASN	4.0
2	I	95	SER	4.0
1	E	201	ASN	4.0
1	O	44	GLY	4.0
1	A	133	SER	3.9
2	N	192	SER	3.9
1	J	87	THR	3.9
1	J	76	SER	3.9
1	J	29	PHE	3.9
1	M	140	MET	3.9
1	O	140	MET	3.9

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Mol	Chain	Res	Type	RSRZ
1	J	206	ALA	3.9
1	G	11	LEU	3.9
1	C	190	SER	3.9
1	M	158	THR	3.8
2	N	70	GLY	3.8
1	J	133	SER	3.8
1	E	198	VAL	3.8
1	G	205	PRO	3.8
1	O	41	PRO	3.8
1	J	12	VAL	3.8
2	F	186	ARG	3.8
1	G	93	VAL	3.7
2	N	190	ARG	3.7
1	A	200	CYS	3.7
1	G	192	THR	3.7
2	I	160	GLN	3.7
1	M	133	SER	3.7
2	P	70	GLY	3.7
2	P	9	ALA	3.7
2	N	59	GLY	3.7
2	P	31	THR	3.6
1	O	179	LEU	3.6
2	I	212	ALA	3.6
2	I	70	GLY	3.6
2	K	98	LEU	3.6
2	F	190	ARG	3.6
1	C	141	VAL	3.6
2	N	32	SER	3.6
2	I	58	PRO	3.5
1	C	136	GLN	3.5
1	A	116	VAL	3.5
2	L	192	SER	3.5
1	O	78	THR	3.5
1	C	42	GLY	3.5
1	E	29	PHE	3.5
1	M	102	SER	3.5
1	H	167	GLY	3.5
2	D	32	SER	3.5
2	L	158	VAL	3.5
1	G	12	VAL	3.4
1	G	103	GLY	3.4
2	L	190	ARG	3.4

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Mol	Chain	Res	Type	RSRZ
1	O	42	GLY	3.4
2	I	82	THR	3.4
1	O	102	SER	3.4
2	I	98	LEU	3.4
1	C	189	PRO	3.3
1	C	192	THR	3.3
1	G	138	ASN	3.3
2	N	130	THR	3.3
2	P	26	THR	3.3
1	M	10	GLU	3.3
1	E	28	SER	3.3
1	O	10	GLU	3.3
1	C	201	ASN	3.3
2	P	154	ASP	3.3
1	H	218	ARG	3.3
1	H	201	ASN	3.3
2	D	159	THR	3.3
2	P	130	THR	3.3
2	P	182	THR	3.3
1	G	65	ARG	3.3
2	P	96	ASN	3.3
2	F	1	GLN	3.3
1	E	195	SER	3.2
1	G	161	SER	3.2
2	P	133	ALA	3.2
2	K	71	ASP	3.2
2	P	28	ALA	3.2
1	H	138	ASN	3.2
1	M	111	GLY	3.2
1	J	139	SER	3.2
2	P	146	VAL	3.2
2	I	71	ASP	3.2
1	O	116	VAL	3.2
1	E	200	CYS	3.2
1	M	137	THR	3.2
1	O	111	GLY	3.2
2	L	191	HIS	3.2
1	H	134	ALA	3.2
1	C	197	THR	3.1
1	O	205	PRO	3.1
1	G	215	ILE	3.1
1	J	43	GLN	3.1

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Mol	Chain	Res	Type	RSRZ
2	P	62	ALA	3.1
1	G	80	TYR	3.1
1	J	84	SER	3.1
2	L	187	ALA	3.1
1	O	93	VAL	3.1
1	E	212	ASP	3.1
1	O	208	SER	3.1
1	M	80	TYR	3.1
2	K	186	ARG	3.1
1	G	199	THR	3.1
2	P	71	ASP	3.1
1	A	191	SER	3.1
2	N	10	LEU	3.1
2	K	212	ALA	3.1
2	D	95	SER	3.1
2	N	96	ASN	3.0
2	B	158	VAL	3.0
1	A	135	ALA	3.0
1	C	30	SER	3.0
2	L	212	ALA	3.0
1	M	168	VAL	3.0
1	O	178	ASP	3.0
1	H	137	THR	3.0
1	G	42	GLY	3.0
2	I	158	VAL	3.0
2	F	211	ARG	3.0
2	K	27	GLY	3.0
1	O	150	TYR	3.0
1	G	75	SER	3.0
1	O	139	SER	3.0
1	M	42	GLY	3.0
2	N	14	PRO	3.0
2	B	190	ARG	2.9
1	O	193	TRP	2.9
1	O	91	SER	2.9
1	J	11	LEU	2.9
1	E	197	THR	2.9
2	B	192	SER	2.9
2	P	186	ARG	2.9
1	E	139	SER	2.9
1	J	30	SER	2.9
2	L	95	SER	2.9

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Mol	Chain	Res	Type	RSRZ
2	N	9	ALA	2.9
1	G	139	SER	2.9
2	D	1	GLN	2.9
1	G	16	ALA	2.9
1	M	41	PRO	2.8
1	C	140	MET	2.8
1	E	141	VAL	2.8
2	N	45	LEU	2.8
1	J	215	ILE	2.8
2	I	94	TYR	2.8
1	A	6	GLN	2.8
1	M	179	LEU	2.8
2	P	5	THR	2.8
2	P	47	THR	2.8
1	C	162	GLY	2.8
2	F	30	THR	2.8
1	M	97	ALA	2.8
1	C	32	TYR	2.8
1	H	27	TYR	2.8
2	P	34	TYR	2.8
1	E	30	SER	2.8
2	K	25	SER	2.8
1	J	82	GLN	2.7
2	N	1	GLN	2.7
2	D	97	HIS	2.7
1	M	56	GLY	2.7
1	O	45	LEU	2.7
1	M	150	TYR	2.7
1	A	78	THR	2.7
1	H	194	PRO	2.7
2	D	191	HIS	2.7
1	J	16	ALA	2.7
2	N	86	ALA	2.7
1	O	43	GLN	2.7
1	E	192	THR	2.7
1	M	193	TRP	2.7
1	O	75	SER	2.7
1	H	196	GLU	2.7
2	P	59	GLY	2.7
1	G	43	GLN	2.7
1	E	163	SER	2.7
1	E	189	PRO	2.7

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Mol	Chain	Res	Type	RSRZ
1	G	87	THR	2.7
1	H	198	VAL	2.7
1	M	93	VAL	2.7
1	O	92	ALA	2.7
1	C	78	THR	2.6
1	G	190	SER	2.6
2	P	184	THR	2.6
2	I	208	SER	2.6
2	B	26	THR	2.6
1	A	160	ASN	2.6
1	M	134	ALA	2.6
1	H	215	ILE	2.6
2	N	193	SER	2.6
1	O	58	THR	2.6
2	D	199	THR	2.6
1	G	97	ALA	2.6
2	D	153	VAL	2.6
2	I	52	GLY	2.6
1	O	87	THR	2.6
1	M	174	VAL	2.6
1	A	139	SER	2.6
2	K	95	SER	2.6
2	P	58	PRO	2.6
1	A	201	ASN	2.6
1	M	218	ARG	2.6
2	N	186	ARG	2.6
2	F	32	SER	2.6
2	P	13	SER	2.6
1	E	194	PRO	2.6
1	H	197	THR	2.6
2	P	82	THR	2.6
1	E	73	ASP	2.5
1	C	28	SER	2.5
1	O	158	THR	2.5
1	G	137	THR	2.5
2	L	188	TRP	2.5
2	D	154	ASP	2.5
1	J	138	ASN	2.5
2	D	179	SER	2.5
1	M	110	GLN	2.5
2	F	154	ASP	2.5
2	N	71	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
2	P	2	ALA	2.5
1	G	118	SER	2.5
2	D	150	ASP	2.5
1	J	162	GLY	2.5
2	I	187	ALA	2.5
2	K	157	PRO	2.5
1	M	11	LEU	2.5
1	E	78	THR	2.5
1	J	137	THR	2.5
2	N	90	CYS	2.5
2	P	91	ALA	2.5
1	E	88	SER	2.5
1	H	139	SER	2.5
1	J	154	PRO	2.5
1	G	57	ASP	2.5
2	P	191	HIS	2.5
1	O	8	GLY	2.5
1	J	177	SER	2.5
1	M	195	SER	2.5
2	K	185	ALA	2.5
2	I	182	THR	2.4
2	K	26	THR	2.4
1	A	25	SER	2.4
1	G	107	TYR	2.4
1	O	74	LYS	2.4
1	H	193	TRP	2.4
1	J	44	GLY	2.4
1	O	207	SER	2.4
1	J	107	TYR	2.4
2	N	34	TYR	2.4
2	P	1	GLN	2.4
2	I	146	VAL	2.4
1	O	209	THR	2.4
1	H	191	SER	2.4
1	M	132	GLY	2.4
2	N	138	THR	2.4
2	N	162	MET	2.4
1	G	189	PRO	2.4
1	O	80	TYR	2.4
1	E	132	GLY	2.4
1	M	112	THR	2.4
2	L	193	SER	2.4

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Mol	Chain	Res	Type	RSRZ
2	L	121	PHE	2.4
1	O	65	ARG	2.4
2	N	47	THR	2.4
2	N	156	THR	2.4
1	E	26	GLY	2.3
2	N	132	LYS	2.3
2	P	190	ARG	2.3
2	P	32	SER	2.3
1	J	135	ALA	2.3
2	P	102	GLY	2.3
1	G	163	SER	2.3
1	H	77	SER	2.3
1	J	102	SER	2.3
1	M	12	VAL	2.3
2	F	159	THR	2.3
1	C	25	SER	2.3
1	M	30	SER	2.3
1	C	200	CYS	2.3
2	K	99	VAL	2.3
1	H	8	GLY	2.3
2	F	45	LEU	2.3
1	C	209	THR	2.3
1	G	174	VAL	2.3
2	D	72	LYS	2.3
2	I	35	ALA	2.3
1	M	19	LYS	2.3
2	I	60	VAL	2.3
2	P	43	ASP	2.3
1	C	24	ALA	2.3
1	M	191	SER	2.3
1	G	32	TYR	2.3
1	H	199	THR	2.3
2	K	58	PRO	2.3
2	K	33	ASN	2.2
2	D	186	ARG	2.2
2	K	158	VAL	2.2
1	J	118	SER	2.2
1	M	166	SER	2.2
2	I	32	SER	2.2
2	D	45	LEU	2.2
1	J	204	HIS	2.2
1	O	31	SER	2.2

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Mol	Chain	Res	Type	RSRZ
2	I	67	SER	2.2
2	D	155	GLY	2.2
1	O	164	LEU	2.2
2	K	45	LEU	2.2
1	E	217	PRO	2.2
2	N	167	PRO	2.2
1	O	97	ALA	2.2
2	D	212	ALA	2.2
2	N	80	ALA	2.2
2	L	26	THR	2.2
1	J	214	LYS	2.2
1	H	186	VAL	2.2
1	H	212	ASP	2.2
1	A	24	ALA	2.2
1	G	30	SER	2.2
2	I	110	GLY	2.2
1	H	43	GLN	2.2
1	J	192	THR	2.2
1	G	109	GLY	2.1
1	O	149	GLY	2.1
2	D	114	SER	2.1
2	I	130	THR	2.1
2	N	5	THR	2.1
1	G	177	SER	2.1
2	K	59	GLY	2.1
1	O	173	ALA	2.1
1	E	27	TYR	2.1
2	P	155	GLY	2.1
1	M	89	GLU	2.1
1	O	29	PHE	2.1
1	J	199	THR	2.1
1	O	110	GLN	2.1
2	P	6	GLN	2.1
1	M	65	ARG	2.1
1	C	159	TRP	2.1
1	E	77	SER	2.1
2	N	22	CYS	2.1
2	P	29	VAL	2.1
2	N	33	ASN	2.1
1	A	197	THR	2.1
2	D	122	PRO	2.1
2	I	11	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	193	TRP	2.1
1	G	47	TRP	2.1
1	G	135	ALA	2.1
2	K	166	GLN	2.1
2	I	96	ASN	2.1
1	J	80	TYR	2.1
1	M	40	THR	2.1
1	J	191	SER	2.1
1	O	117	SER	2.1
2	K	23	ARG	2.0
2	P	80	ALA	2.0
1	E	188	VAL	2.0
2	F	153	VAL	2.0
1	C	167	GLY	2.0
2	N	97	HIS	2.0
2	P	27	GLY	2.0
1	G	31	SER	2.0
1	O	57	ASP	2.0
2	P	140	THR	2.0
1	J	65	ARG	2.0
2	D	158	VAL	2.0
1	O	108	TRP	2.0
1	A	43	GLN	2.0
1	O	90	ASP	2.0
2	N	30	THR	2.0
2	F	173	ASN	2.0
1	G	206	ALA	2.0
1	C	93	VAL	2.0
2	N	128	LEU	2.0
2	K	72	LYS	2.0
2	P	54	ASN	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 carbohydrates 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.