



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:35 PM UTC

PDB ID : 8TH5 / pdb_00008th5
Title : Crystal Structure of the G3BP1 NTF2-like domain bound to the IDR1 of SARS-CoV-2 nucleocapsid protein P13L mutant
Authors : Hughes, M.P.; Taylor, J.P.; Yang, Z.
Deposited on : 2023-07-13
Resolution : 2.62 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

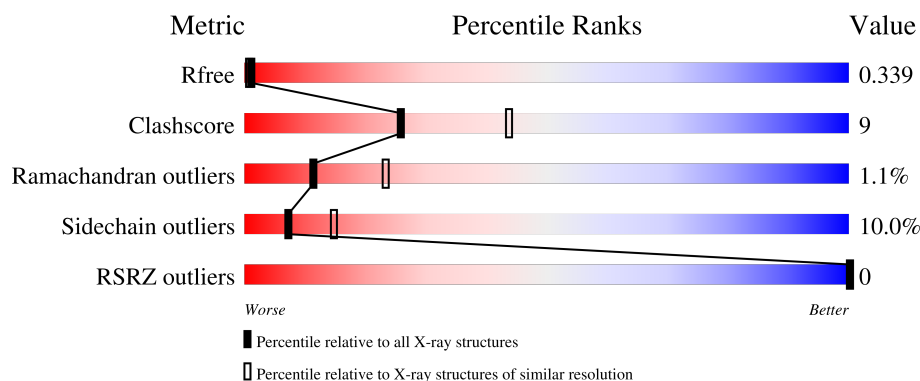
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

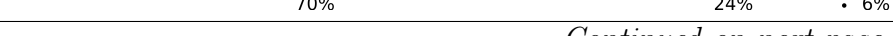
The reported resolution of this entry is 2.62 Å.

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	4951 (2.64-2.60)
Clashscore	190562	5303 (2.64-2.60)
Ramachandran outliers	187476	5217 (2.64-2.60)
Sidechain outliers	187428	5217 (2.64-2.60)
RSRZ outliers	180081	4950 (2.64-2.60)

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	139	
1	B	139	
1	C	139	
1	D	139	
1	E	139	

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Mol	Chain	Length	Quality of chain
1	F	139	
1	G	139	
1	H	139	
1	I	139	
1	J	139	
2	K	25	
2	L	25	
2	M	25	
2	N	25	
2	O	25	
2	P	25	
2	Q	25	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 10350 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 Ras GTPase-activating protein-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	123	Total	C	N	O	S	0	1	0
			1007	639	184	179	5			
1	B	122	Total	C	N	O	S	0	1	0
			995	633	180	177	5			
1	C	125	Total	C	N	O	S	0	1	0
			1023	650	186	182	5			
1	D	129	Total	C	N	O	S	0	0	0
			1045	664	187	187	7			
1	E	131	Total	C	N	O	S	0	0	0
			1055	670	192	189	4			
1	F	130	Total	C	N	O	S	0	2	0
			1063	677	195	186	5			
1	G	125	Total	C	N	O	S	0	0	0
			990	636	177	172	5			
1	H	129	Total	C	N	O	S	0	0	0
			1013	644	182	183	4			
1	I	119	Total	C	N	O	S	0	1	0
			905	578	162	161	4			
1	J	102	Total	C	N	O	S	0	1	0
			798	512	141	141	4			

- Molecule 2 is a protein called Nucleoprotein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	K	9	Total	C	N	O	0	0	0
			65	43	12	10			
2	P	6	Total	C	N	O	0	0	0
			41	28	6	7			
2	L	8	Total	C	N	O	0	0	0
			51	34	8	9			
2	M	9	Total	C	N	O	0	0	0
			62	40	12	10			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	O	9	Total	C	N	O	0	0	0
			59	40	9	10			
2	Q	8	Total	C	N	O	0	0	0
			60	40	11	9			
2	N	9	Total	C	N	O	0	0	0
			54	35	9	10			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	13	LEU	PRO	engineered mutation	UNP P0DTC9
P	13	LEU	PRO	engineered mutation	UNP P0DTC9
L	13	LEU	PRO	engineered mutation	UNP P0DTC9
M	13	LEU	PRO	engineered mutation	UNP P0DTC9
O	13	LEU	PRO	engineered mutation	UNP P0DTC9
Q	13	LEU	PRO	engineered mutation	UNP P0DTC9
N	13	LEU	PRO	engineered mutation	UNP P0DTC9

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	6	Total	O	0	0
			6	6		
3	B	5	Total	O	0	0
			5	5		
3	C	12	Total	O	0	0
			12	12		
3	D	3	Total	O	0	0
			3	3		
3	E	7	Total	O	0	0
			7	7		
3	F	5	Total	O	0	0
			5	5		
3	G	8	Total	O	0	0
			8	8		
3	H	6	Total	O	0	0
			6	6		
3	I	8	Total	O	0	0
			8	8		
3	J	2	Total	O	0	0
			2	2		
3	P	1	Total	O	0	0
			1	1		

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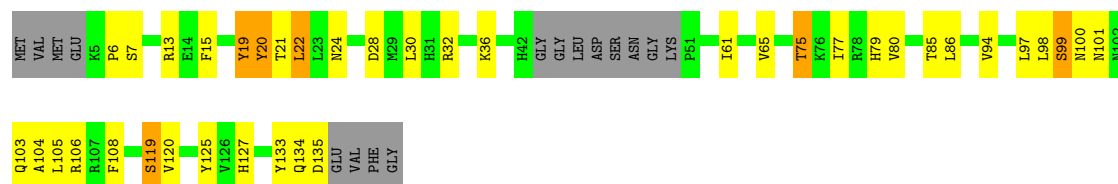
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	O	1	Total	O	0	0
			1	1		

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.

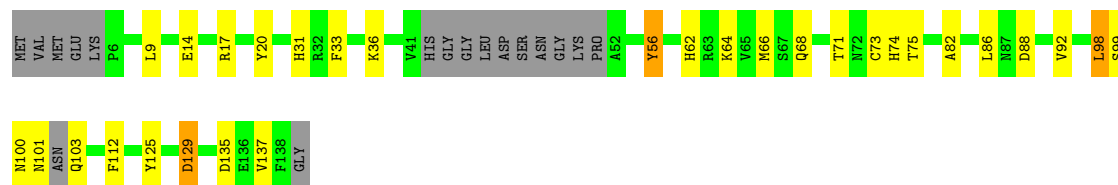
- Molecule 1: Ras GTPase-activating protein-binding protein 1

Chain A: 



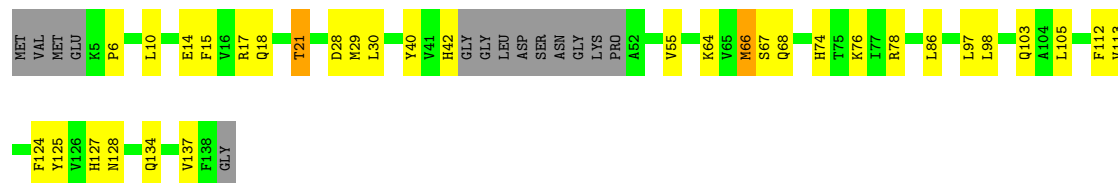
- Molecule 1: Ras GTPase-activating protein-binding protein 1

Chain B: 



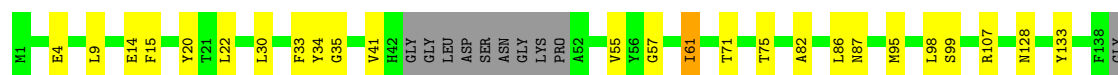
- Molecule 1: Ras GTPase-activating protein-binding protein 1

Chain C: 



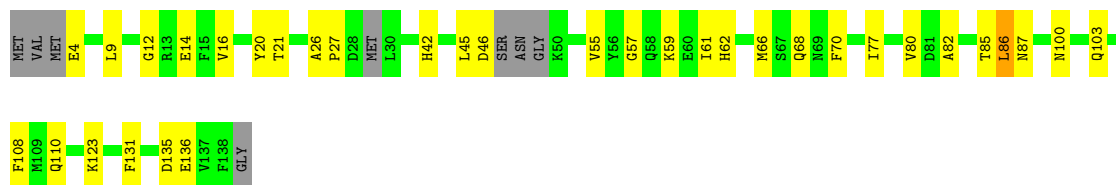
- Molecule 1: Ras GTPase-activating protein-binding protein 1

Chain D: 



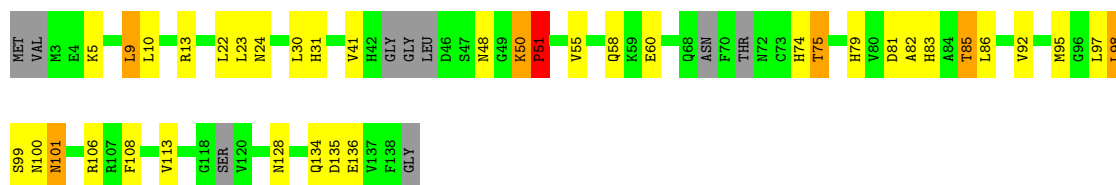
- Molecule 1: Ras GTPase-activating protein-binding protein 1

Chain E:  70% 24% 6%



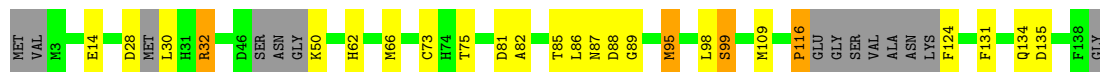
- Molecule 1: Ras GTPase-activating protein-binding protein 1

Chain F:  66% 22% 6%



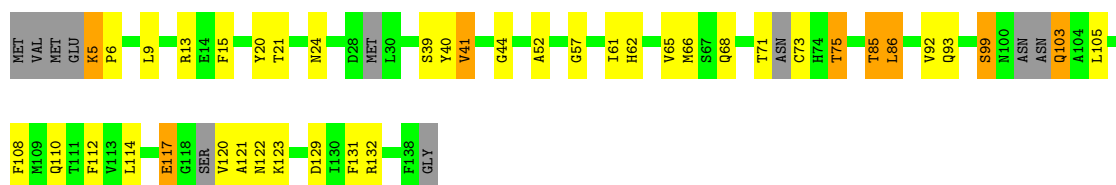
- Molecule 1: Ras GTPase-activating protein-binding protein 1

Chain G:  72% 15% 10%



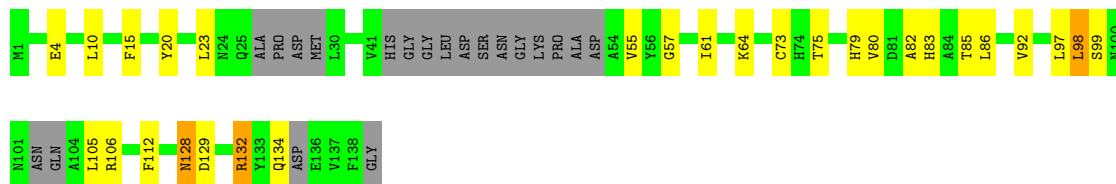
- Molecule 1: Ras GTPase-activating protein-binding protein 1

Chain H:  63% 24% 6% 7%



- Molecule 1: Ras GTPase-activating protein-binding protein 1

Chain I:  65% 18% 14%



- Molecule 1: Ras GTPase-activating protein-binding protein 1

Chain J:  50% 19% 27%



MET	SER	ASP	ASN	GLY	PRO	GLN	ASN	GLN	ARG	ASN	A12	L13	T16	F17	G18	G19	P20	SER	ASP	SER	THR	GLY
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	61.60Å 69.45Å 101.04Å 70.66° 76.86° 88.31°	Depositor
Resolution (Å)	46.70 – 2.62 46.70 – 2.62	Depositor EDS
% Data completeness (in resolution range)	71.4 (46.70-2.62) 71.4 (46.70-2.62)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.91 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.8.0419	Depositor
R, R_{free}	0.226 , 0.336 0.229 , 0.339	Depositor DCC
R_{free} test set	1633 reflections (3.55%)	wwPDB-VP
Wilson B-factor (Å ²)	37.9	Xtriage
Anisotropy	0.073	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 27.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.050 for -h,k,k-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10350	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.87% 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	0.52	0/1032	1.02	4/1397 (0.3%)
1	B	0.51	0/1019	1.00	1/1375 (0.1%)
1	C	0.49	0/1048	0.95	0/1418
1	D	0.52	0/1069	0.89	0/1445
1	E	0.51	0/1079	0.93	0/1457
1	F	0.53	0/1088	0.95	0/1465
1	G	0.52	0/1012	0.92	0/1367
1	H	0.53	0/1035	1.03	0/1398
1	I	0.55	0/924	1.00	1/1251 (0.1%)
1	J	0.53	0/813	1.00	1/1094 (0.1%)
2	K	0.62	0/66	0.96	0/88
2	L	0.68	0/52	0.72	0/70
2	M	0.49	0/63	0.94	0/84
2	N	0.53	0/54	0.89	0/72
2	O	0.51	0/60	0.85	0/81
2	P	0.48	0/41	0.77	0/55
2	Q	0.59	0/61	0.93	0/81
All	All	0.52	0/10516	0.97	7/14198 (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	G	0	1
1	I	0	1
All	All	0	2

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	21	THR	N-CA-C	-5.24	106.61	113.06
1	J	79	HIS	CA-CB-CG	5.24	119.04	113.80
1	A	19	TYR	CB-CA-C	5.13	119.07	110.92
1	A	20[A]	TYR	N-CA-CB	-5.11	101.85	110.49
1	A	20[B]	TYR	N-CA-CB	-5.11	101.85	110.49
1	I	129	ASP	CA-CB-CG	5.07	117.67	112.60
1	B	129	ASP	CA-CB-CG	5.01	117.61	112.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	G	32	ARG	Sidechain
1	I	132	ARG	Sidechain

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	1007	0	967	34	0
1	B	995	0	975	17	0
1	C	1023	0	981	18	0
1	D	1045	0	1011	16	0
1	E	1055	0	1014	19	0
1	F	1063	0	1025	23	0
1	G	990	0	948	15	0
1	H	1013	0	951	23	0
1	I	905	0	834	13	0
1	J	798	0	751	17	0
2	K	65	0	68	1	0
2	L	51	0	43	0	0
2	M	62	0	59	3	0
2	N	54	0	42	3	0
2	O	59	0	57	2	0
2	P	41	0	35	1	0
2	Q	60	0	63	1	0
3	A	6	0	0	0	0
3	B	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	12	0	0	0	0
3	D	3	0	0	0	0
3	E	7	0	0	1	0
3	F	5	0	0	0	0
3	G	8	0	0	0	0
3	H	6	0	0	0	0
3	I	8	0	0	0	0
3	J	2	0	0	0	0
3	O	1	0	0	0	0
3	P	1	0	0	0	0
All	All	10350	0	9824	191	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 9.

All (191) 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:19:TYR:O	1:J:21:THR:N	1.85	1.07
1:E:135:ASP:OD1	1:E:136:GLU:N	2.11	0.83
1:F:9:LEU:HA	1:F:82:ALA:HB3	1.66	0.77
1:F:50:LYS:CB	1:F:51:PRO:HD2	2.19	0.73
1:E:62:HIS:CE1	1:E:66:MET:HE3	2.25	0.71
1:A:20[B]:TYR:CD2	1:A:77:ILE:HD11	2.26	0.70
1:B:100:ASN:O	1:B:103:GLN:HG2	1.91	0.69
1:A:20[B]:TYR:HD2	1:A:77:ILE:HD11	1.55	0.69
1:B:14:GLU:OE2	1:B:17:ARG:NH1	2.26	0.68
1:H:24:ASN:HA	1:H:73:CYS:HB3	1.76	0.68
1:H:44:GLY:O	1:H:52:ALA:N	2.28	0.66
1:D:55:VAL:HG23	1:D:61:ILE:HG22	1.79	0.65
1:B:98[B]:LEU:HD23	1:B:99:SER:N	2.12	0.64
1:A:20[A]:TYR:CD2	1:A:75:THR:HG21	2.34	0.63
1:C:15:PHE:HB2	2:M:17:PHE:CZ	2.36	0.61
1:A:100:ASN:O	1:A:103:GLN:HG2	2.01	0.60
1:C:64:LYS:O	1:C:67:SER:HB3	2.02	0.60
1:B:62:HIS:CE1	1:B:66:MET:HE1	2.35	0.60
1:F:97:LEU:HA	1:F:106:ARG:O	2.03	0.59
1:C:14:GLU:O	1:C:18:GLN:HG3	2.03	0.59
1:E:26:ALA:O	1:E:27:PRO:C	2.44	0.59
1:A:20[B]:TYR:OH	1:A:94:VAL:HG21	2.03	0.58
1:C:14:GLU:OE1	1:C:17:ARG:HD3	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:15:PHE:HB2	2:N:17:PHE:CZ	2.39	0.58
1:B:62:HIS:CE1	1:B:66:MET:CE	2.86	0.58
1:C:17:ARG:O	1:C:21:THR:OG1	2.21	0.57
1:C:125:TYR:OH	1:C:127:HIS:HD2	1.86	0.57
1:H:108:PHE:CD2	1:H:131:PHE:CE2	2.93	0.57
1:E:20:TYR:OH	1:E:110:GLN:NE2	2.37	0.57
1:E:42:HIS:N	3:E:201:HOH:O	2.24	0.56
1:F:100:ASN:O	1:F:101:ASN:C	2.47	0.56
1:I:92:VAL:HB	1:I:112:PHE:HB2	1.86	0.56
1:D:95:MET:HE3	1:G:109:MET:SD	2.46	0.56
1:F:106:ARG:HH21	1:F:135:ASP:CG	2.13	0.56
1:I:98:LEU:O	1:I:105:LEU:HA	2.06	0.56
1:I:57:GLY:O	1:I:61:ILE:CB	2.54	0.56
1:H:57:GLY:O	1:H:61:ILE:HG13	2.05	0.56
1:E:9:LEU:HA	1:E:82:ALA:HB3	1.89	0.55
1:A:15:PHE:HB2	2:K:17:PHE:CZ	2.42	0.54
1:I:15:PHE:HB2	2:Q:17:PHE:CZ	2.43	0.54
1:J:112:PHE:HA	1:J:128:ASN:O	2.07	0.54
1:A:119:SER:HB2	1:A:120:VAL:HG23	1.89	0.54
1:F:75:THR:OG1	1:F:98[B]:LEU:HD12	2.08	0.54
2:O:13:LEU:HD23	2:O:13:LEU:O	2.08	0.54
1:F:135:ASP:OD1	1:F:136:GLU:N	2.41	0.54
1:C:97:LEU:HB3	1:C:105:LEU:HG	1.91	0.53
1:E:77:ILE:CG2	1:E:80:VAL:HG23	2.39	0.53
1:F:98[B]:LEU:HD23	1:F:99:SER:N	2.24	0.53
1:F:50:LYS:CB	1:F:51:PRO:CD	2.87	0.53
1:H:62:HIS:NE2	1:H:66:MET:HE1	2.23	0.53
1:C:124:PHE:O	2:M:17:PHE:HA	2.09	0.52
1:H:120:VAL:HG12	1:H:121:ALA:N	2.24	0.52
1:C:40:TYR:HB3	1:C:55:VAL:HG23	1.92	0.52
1:B:20:TYR:CD1	1:B:75:THR:HG21	2.44	0.52
1:F:50:LYS:O	1:F:51:PRO:C	2.53	0.52
1:C:28:ASP:OD1	1:C:28:ASP:N	2.39	0.51
1:E:14:GLU:HA	1:E:14:GLU:OE1	2.09	0.51
1:A:19:TYR:HB3	1:A:20[B]:TYR:HD1	1.74	0.51
1:C:98:LEU:C	1:C:98:LEU:HD23	2.35	0.51
1:F:55:VAL:HB	1:F:60:GLU:HG3	1.93	0.51
1:J:81:ASP:OD1	1:J:81:ASP:C	2.53	0.51
1:E:135:ASP:OD1	1:E:136:GLU:HG3	2.11	0.51
1:I:97:LEU:HA	1:I:106:ARG:O	2.10	0.51
1:A:20[B]:TYR:N	1:A:20[B]:TYR:CD1	2.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:73:CYS:SG	1:B:98[B]:LEU:HD11	2.51	0.50
1:I:128:ASN:HD22	1:I:128:ASN:N	2.08	0.50
1:A:61:ILE:O	1:A:65:VAL:HG23	2.11	0.50
1:D:107:ARG:HH11	1:G:134:GLN:HE21	1.59	0.50
1:G:73:CYS:SG	1:G:98:LEU:HD21	2.52	0.50
1:B:101:ASN:O	1:B:103:GLN:N	2.44	0.50
1:B:92:VAL:HB	1:B:112:PHE:HB2	1.94	0.50
1:F:98[A]:LEU:HD12	1:F:108:PHE:CE2	2.47	0.50
1:I:55:VAL:HG21	1:I:64:LYS:CB	2.41	0.50
1:F:98[B]:LEU:HG	1:F:99:SER:H	1.77	0.50
1:C:42:HIS:CD2	1:C:68:GLN:HE22	2.30	0.49
1:I:79:HIS:CG	1:I:80:VAL:N	2.80	0.49
1:C:112:PHE:HA	1:C:128:ASN:O	2.12	0.49
1:A:19:TYR:CD2	1:A:20[A]:TYR:CD1	3.01	0.49
1:G:87:ASN:OD1	1:G:88:ASP:N	2.40	0.49
1:J:110:GLN:HA	1:J:130:ILE:O	2.12	0.49
1:A:19:TYR:HD2	1:A:20[B]:TYR:CE1	2.30	0.49
1:A:20[B]:TYR:HD1	1:A:20[B]:TYR:N	2.10	0.49
1:H:15:PHE:CG	1:H:114:LEU:HD21	2.48	0.49
1:A:19:TYR:HD2	1:A:20[B]:TYR:CD1	2.31	0.49
1:B:9:LEU:HA	1:B:82:ALA:HB3	1.95	0.48
1:B:74:HIS:O	1:B:98[B]:LEU:HG	2.13	0.48
1:E:12:GLY:O	1:E:16:VAL:HG23	2.14	0.48
1:G:95:MET:HE3	1:G:109:MET:HG2	1.95	0.48
1:B:75:THR:OG1	1:B:98[B]:LEU:HD12	2.13	0.48
1:F:75:THR:CB	1:F:98[B]:LEU:HD12	2.44	0.48
1:J:24:ASN:OD1	1:J:24:ASN:C	2.56	0.48
1:F:113:VAL:HB	1:F:128:ASN:HD22	1.78	0.48
1:J:52:ALA:O	1:J:53:ASP:C	2.56	0.48
1:G:98:LEU:HD23	1:G:99:SER:N	2.28	0.48
1:A:104:ALA:O	1:A:106:ARG:HG3	2.14	0.47
1:B:64:LYS:O	1:B:68:GLN:HG3	2.14	0.47
1:D:34:TYR:CB	1:D:61:ILE:HD11	2.43	0.47
1:H:24:ASN:HA	1:H:73:CYS:CB	2.43	0.47
1:J:127:HIS:O	1:J:128:ASN:CG	2.58	0.47
1:F:106:ARG:NH2	1:F:135:ASP:OD1	2.44	0.47
1:A:108:PHE:CD1	1:A:108:PHE:C	2.93	0.47
1:F:75:THR:CA	1:F:98[B]:LEU:HD12	2.45	0.47
1:J:108:PHE:C	1:J:108:PHE:CD1	2.93	0.47
1:D:128:ASN:HD21	1:G:85:THR:HA	1.79	0.46
1:G:131:PHE:C	1:G:131:PHE:CD1	2.92	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:62:HIS:NE2	1:H:66:MET:CE	2.78	0.46
1:E:70:PHE:HA	1:E:100:ASN:OD1	2.16	0.46
1:A:19:TYR:HB3	1:A:20[B]:TYR:CD1	2.50	0.45
1:J:108:PHE:CG	1:J:131:PHE:CZ	3.04	0.45
1:H:61:ILE:O	1:H:65:VAL:HG23	2.16	0.45
1:J:135:ASP:OD1	1:J:136:GLU:HG3	2.17	0.45
1:H:20:TYR:CD1	1:H:75:THR:HG21	2.51	0.45
1:F:22:LEU:C	1:F:24:ASN:H	2.25	0.45
1:F:74:HIS:O	1:F:98[B]:LEU:HG	2.17	0.45
1:F:79:HIS:HB3	1:F:95:MET:HB3	1.98	0.45
1:H:40:TYR:HB3	1:H:61:ILE:HG12	1.97	0.45
1:A:135:ASP:C	1:A:135:ASP:OD1	2.60	0.45
1:B:100:ASN:O	1:B:103:GLN:CG	2.63	0.44
1:H:20:TYR:OH	1:H:110:GLN:NE2	2.49	0.44
1:H:85:THR:OG1	1:H:86:LEU:N	2.49	0.44
1:I:20:TYR:HB3	1:I:75:THR:OG1	2.17	0.44
1:E:108:PHE:CB	1:E:131:PHE:CZ	3.01	0.44
1:H:92:VAL:HB	1:H:112:PHE:HB2	2.00	0.44
1:D:20:TYR:CD1	1:D:75:THR:HG21	2.53	0.44
1:G:85:THR:HG22	1:G:89:GLY:O	2.18	0.44
1:H:15:PHE:CD1	1:H:114:LEU:HD21	2.52	0.44
1:C:134:GLN:O	1:C:137:VAL:N	2.50	0.43
1:F:85:THR:HG23	1:F:86:LEU:N	2.33	0.43
1:G:62:HIS:NE2	1:G:66:MET:CE	2.81	0.43
1:J:40:TYR:CD1	1:J:41:VAL:N	2.85	0.43
2:P:13:LEU:HD12	2:P:13:LEU:HA	1.81	0.43
1:B:31:HIS:CD2	1:B:62:HIS:ND1	2.86	0.43
1:D:9:LEU:HA	1:D:82:ALA:HB3	2.01	0.43
1:D:34:TYR:HB2	1:D:61:ILE:HD11	2.00	0.43
1:E:85:THR:O	1:E:86:LEU:C	2.61	0.43
1:G:116:PRO:HA	1:G:124:PHE:CE1	2.52	0.43
1:J:89:GLY:HA2	1:J:116:PRO:HD3	2.00	0.43
1:A:19:TYR:O	1:A:22:LEU:HB2	2.18	0.43
1:D:107:ARG:HH11	1:G:134:GLN:NE2	2.16	0.43
1:E:42:HIS:HB3	1:E:68:GLN:HE22	1.83	0.43
1:H:5:LYS:HB3	1:H:6:PRO:HD3	2.00	0.43
1:H:99:SER:OG	1:H:103:GLN:O	2.37	0.43
1:A:19:TYR:HD2	1:A:20[A]:TYR:CD1	2.37	0.43
1:A:79:HIS:CG	1:A:80:VAL:N	2.87	0.43
1:A:13:ARG:HD2	1:I:10:LEU:HD21	2.00	0.43
1:A:24:ASN:OD1	1:A:24:ASN:C	2.62	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:18:GLN:O	1:J:19:TYR:O	2.37	0.43
1:F:31:HIS:HB2	1:F:58:GLN:HG3	2.01	0.43
1:A:98:LEU:HD22	1:A:133:TYR:OH	2.19	0.43
1:H:57:GLY:O	1:H:61:ILE:CG1	2.67	0.43
1:I:97:LEU:HB3	1:I:105:LEU:HB3	2.00	0.43
1:D:22:LEU:HD23	1:D:30:LEU:HA	2.00	0.42
1:I:82:ALA:C	1:I:83:HIS:CD2	2.97	0.42
1:B:56:TYR:CD1	1:B:56:TYR:N	2.86	0.42
1:D:98:LEU:HD23	1:D:133:TYR:OH	2.19	0.42
1:D:15:PHE:HA	2:N:17:PHE:CE2	2.55	0.42
1:G:62:HIS:CE1	1:G:66:MET:CE	3.02	0.42
1:A:32:ARG:HD3	1:C:74[A]:HIS:CD2	2.55	0.42
1:A:99:SER:HB3	1:A:105:LEU:HD23	2.02	0.42
1:B:33:PHE:O	1:B:125:TYR:HB2	2.20	0.42
1:J:82:ALA:C	1:J:83:HIS:CD2	2.98	0.42
1:C:113:VAL:HB	1:C:128:ASN:HB2	2.02	0.41
1:F:81:ASP:OD1	1:F:83:HIS:NE2	2.52	0.41
1:D:33:PHE:HA	2:N:18:GLY:HA2	2.01	0.41
1:E:62:HIS:CE1	1:E:66:MET:CE	3.02	0.41
1:A:19:TYR:CE1	1:A:30:LEU:HD11	2.55	0.41
1:G:81:ASP:OD1	1:G:82:ALA:N	2.54	0.41
1:A:6:PRO:O	1:A:7:SER:C	2.62	0.41
1:C:6:PRO:HG3	2:M:15:ILE:CD1	2.50	0.41
1:D:14:GLU:OE1	1:D:14:GLU:HA	2.20	0.41
1:E:59:LYS:O	1:E:62:HIS:HB3	2.20	0.41
1:C:66:MET:HA	1:C:66:MET:CE	2.50	0.41
1:I:73:CYS:HA	1:I:99:SER:O	2.21	0.41
1:A:134:GLN:O	1:A:135:ASP:C	2.64	0.41
1:E:57:GLY:O	1:E:61:ILE:HG13	2.20	0.41
1:G:14:GLU:OE1	1:G:14:GLU:HA	2.21	0.41
1:H:92:VAL:HG12	1:H:93:GLN:N	2.36	0.41
1:A:98:LEU:HB2	1:A:108:PHE:CE2	2.56	0.40
1:A:125:TYR:OH	1:A:127:HIS:HD2	2.04	0.40
1:D:35:GLY:O	1:D:57:GLY:HA2	2.22	0.40
1:E:100:ASN:O	1:E:103:GLN:HG2	2.21	0.40
1:E:123:LYS:HA	2:O:16:THR:O	2.21	0.40
1:H:117:GLU:OE2	1:H:120:VAL:HG23	2.21	0.40
1:J:127:HIS:O	1:J:127:HIS:CD2	2.74	0.40
1:H:9:LEU:HD11	1:H:13:ARG:HD2	2.04	0.40
1:A:99:SER:HB2	1:A:103:GLN:O	2.20	0.40
1:A:100:ASN:O	1:A:101:ASN:C	2.64	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:129:ASP:C	1:H:129:ASP:OD1	2.65	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	120/139 (86%)	107 (89%)	13 (11%)	0	100	100
1	B	117/139 (84%)	107 (92%)	10 (8%)	0	100	100
1	C	122/139 (88%)	111 (91%)	11 (9%)	0	100	100
1	D	125/139 (90%)	121 (97%)	4 (3%)	0	100	100
1	E	125/139 (90%)	115 (92%)	9 (7%)	1 (1%)	16	31
1	F	123/139 (88%)	107 (87%)	13 (11%)	3 (2%)	4	8
1	G	117/139 (84%)	99 (85%)	18 (15%)	0	100	100
1	H	119/139 (86%)	111 (93%)	7 (6%)	1 (1%)	16	31
1	I	110/139 (79%)	96 (87%)	13 (12%)	1 (1%)	14	28
1	J	91/139 (66%)	76 (84%)	9 (10%)	6 (7%)	1	1
2	K	7/25 (28%)	7 (100%)	0	0	100	100
2	L	6/25 (24%)	6 (100%)	0	0	100	100
2	M	7/25 (28%)	5 (71%)	1 (14%)	1 (14%)	0	0
2	N	7/25 (28%)	3 (43%)	3 (43%)	1 (14%)	0	0
2	O	7/25 (28%)	7 (100%)	0	0	100	100
2	P	4/25 (16%)	4 (100%)	0	0	100	100
2	Q	6/25 (24%)	6 (100%)	0	0	100	100
All	All	1213/1565 (78%)	1088 (90%)	111 (9%)	14 (1%)	11	21

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	J	19	TYR
1	J	20[A]	TYR
1	J	20[B]	TYR
1	J	137	VAL
2	N	16	THR
1	F	51	PRO
1	I	4	GLU
1	J	53	ASP
1	E	87	ASN
1	F	50	LYS
1	F	101	ASN
2	M	17	PHE
1	J	55	VAL
1	H	41	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	108/121 (89%)	99 (92%)	9 (8%)	10	22
1	B	108/121 (89%)	98 (91%)	10 (9%)	8	17
1	C	110/121 (91%)	101 (92%)	9 (8%)	10	22
1	D	113/121 (93%)	106 (94%)	7 (6%)	16	35
1	E	112/121 (93%)	106 (95%)	6 (5%)	20	40
1	F	112/121 (93%)	96 (86%)	16 (14%)	3	6
1	G	102/121 (84%)	92 (90%)	10 (10%)	7	15
1	H	105/121 (87%)	89 (85%)	16 (15%)	3	4
1	I	89/121 (74%)	82 (92%)	7 (8%)	11	24
1	J	79/121 (65%)	68 (86%)	11 (14%)	3	6
2	K	6/20 (30%)	5 (83%)	1 (17%)	2	3
2	L	4/20 (20%)	4 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	M	5/20 (25%)	3 (60%)	2 (40%)	0	0
2	N	3/20 (15%)	1 (33%)	2 (67%)	0	0
2	O	5/20 (25%)	4 (80%)	1 (20%)	1	2
2	P	3/20 (15%)	2 (67%)	1 (33%)	0	0
2	Q	6/20 (30%)	5 (83%)	1 (17%)	2	3
All	All	1070/1350 (79%)	961 (90%)	109 (10%)	7	14

All (109) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	LEU
1	A	28	ASP
1	A	36	LYS
1	A	75	THR
1	A	85	THR
1	A	86	LEU
1	A	97	LEU
1	A	99	SER
1	A	119	SER
1	B	36	LYS
1	B	56	TYR
1	B	71	THR
1	B	86	LEU
1	B	88	ASP
1	B	98[A]	LEU
1	B	98[B]	LEU
1	B	129	ASP
1	B	135	ASP
1	B	137	VAL
1	C	10	LEU
1	C	21	THR
1	C	29	MET
1	C	30	LEU
1	C	66	MET
1	C	76	LYS
1	C	78	ARG
1	C	86	LEU
1	C	103	GLN
1	D	4	GLU
1	D	41	VAL

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Mol	Chain	Res	Type
1	D	61	ILE
1	D	71	THR
1	D	86	LEU
1	D	87	ASN
1	D	99	SER
1	E	4	GLU
1	E	21	THR
1	E	45	LEU
1	E	46	ASP
1	E	55	VAL
1	E	86	LEU
1	F	5	LYS
1	F	9	LEU
1	F	10	LEU
1	F	13[A]	ARG
1	F	13[B]	ARG
1	F	23	LEU
1	F	30	LEU
1	F	41	VAL
1	F	48	ASN
1	F	51	PRO
1	F	75	THR
1	F	85	THR
1	F	92	VAL
1	F	98[A]	LEU
1	F	98[B]	LEU
1	F	134	GLN
1	G	28	ASP
1	G	30	LEU
1	G	32	ARG
1	G	50	LYS
1	G	75	THR
1	G	86	LEU
1	G	95	MET
1	G	99	SER
1	G	116	PRO
1	G	135	ASP
1	H	5	LYS
1	H	21	THR
1	H	39	SER
1	H	41	VAL
1	H	68	GLN

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Mol	Chain	Res	Type
1	H	71	THR
1	H	75	THR
1	H	85	THR
1	H	86	LEU
1	H	99	SER
1	H	103	GLN
1	H	105	LEU
1	H	117	GLU
1	H	122	ASN
1	H	123	LYS
1	H	132	ARG
1	I	23	LEU
1	I	85	THR
1	I	86	LEU
1	I	98	LEU
1	I	128	ASN
1	I	132	ARG
1	I	134	GLN
1	J	1	MET
1	J	2	VAL
1	J	4	GLU
1	J	7	SER
1	J	21	THR
1	J	24	ASN
1	J	36	LYS
1	J	55	VAL
1	J	81	ASP
1	J	97	LEU
1	J	123	LYS
2	K	13	LEU
2	P	13	LEU
2	M	14	ARG
2	M	16	THR
2	O	16	THR
2	Q	13	LEU
2	N	13	LEU
2	N	16	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (48) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	GLN

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Mol	Chain	Res	Type
1	A	31	HIS
1	A	58	GLN
1	A	72	ASN
1	A	83	HIS
1	A	127	HIS
1	A	128	ASN
1	B	18	GLN
1	B	31	HIS
1	B	69	ASN
1	B	103	GLN
1	B	128	ASN
1	C	68	GLN
1	C	72	ASN
1	C	93	GLN
1	C	103	GLN
1	C	127	HIS
1	C	128	ASN
1	D	42	HIS
1	D	68	GLN
1	D	69	ASN
1	D	72	ASN
1	D	93	GLN
1	D	122	ASN
1	D	128	ASN
1	E	25	GLN
1	E	62	HIS
1	E	68	GLN
1	E	93	GLN
1	E	110	GLN
1	E	127	HIS
1	E	134	GLN
1	F	18	GLN
1	F	110	GLN
1	F	128	ASN
1	G	58	GLN
1	G	128	ASN
1	G	134	GLN
1	H	25	GLN
1	H	93	GLN
1	H	110	GLN
1	H	134	GLN
1	I	18	GLN

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Mol	Chain	Res	Type
1	I	68	GLN
1	I	128	ASN
1	J	18	GLN
1	J	127	HIS
1	J	134	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	123/139 (88%)	-1.66	0 100 100	7, 23, 38, 66	1 (0%)
1	B	122/139 (87%)	-1.62	0 100 100	10, 28, 52, 72	1 (0%)
1	C	125/139 (89%)	-1.62	0 100 100	11, 29, 50, 69	1 (0%)
1	D	129/139 (92%)	-1.64	0 100 100	14, 30, 53, 58	0
1	E	131/139 (94%)	-1.58	0 100 100	12, 29, 57, 68	0
1	F	130/139 (93%)	-1.50	0 100 100	10, 36, 61, 73	2 (1%)
1	G	125/139 (89%)	-1.58	0 100 100	17, 37, 56, 60	0
1	H	129/139 (92%)	-1.43	0 100 100	22, 43, 64, 76	0
1	I	119/139 (85%)	-1.45	0 100 100	20, 48, 75, 96	1 (0%)
1	J	102/139 (73%)	-1.34	0 100 100	23, 51, 77, 88	1 (0%)
2	K	9/25 (36%)	-1.34	0 100 100	18, 25, 50, 57	0
2	L	8/25 (32%)	-1.44	0 100 100	28, 30, 44, 51	0
2	M	9/25 (36%)	-1.46	0 100 100	33, 48, 53, 56	0
2	N	9/25 (36%)	-0.97	0 100 100	35, 51, 65, 66	0
2	O	9/25 (36%)	-1.41	0 100 100	37, 42, 48, 49	0
2	P	6/25 (24%)	-1.52	0 100 100	35, 38, 40, 42	0
2	Q	8/25 (32%)	-1.45	0 100 100	39, 56, 63, 65	0
All	All	1293/1565 (82%)	-1.54	0 100 100	7, 35, 63, 96	7 (0%)

There are no RSRZ outliers to report.

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.