



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:55 PM UTC

PDB ID : 6X02 / pdb_00006x02
Title : Nup84-Nup133 (aa521-1157) from *S. cerevisiae* bound by VHH-SAN8
Authors : Nordeen, S.A.; Schwartz, T.U.
Deposited on : 2020-05-15
Resolution : 6.38 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

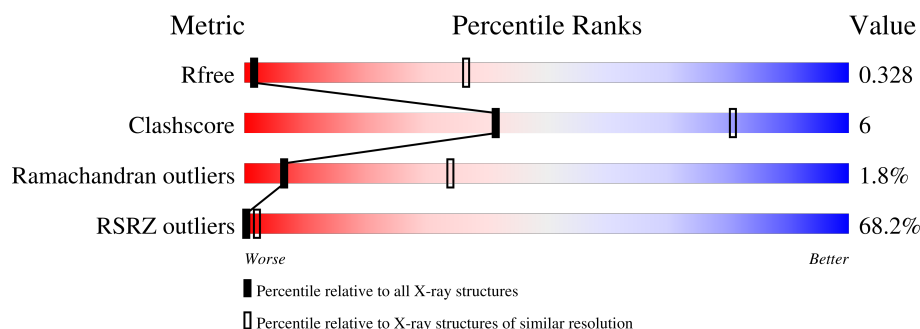
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 6.38 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	1156 (8.70-4.00)
Clashscore	190562	1018 (8.70-4.02)
Ramachandran outliers	187476	1044 (8.70-4.00)
RSRZ outliers	180081	1149 (8.70-4.00)

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	726	55% 84% 5% 10%
2	B	643	70% 84% 9% 6%
3	C	131	50% 55% 11% • 31%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6667 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 Nucleoporin NUP84.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	650	Total	C	N	O	0	0	0
			3234	1934	650	650			

- Molecule 2 is a protein called Nucleoporin NUP133.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	602	Total	C	N	O	0	0	0
			2993	1789	602	602			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	515	MET	-	expression tag	UNP P36161
B	516	ALA	-	expression tag	UNP P36161
B	517	ASP	-	expression tag	UNP P36161
B	518	PRO	-	expression tag	UNP P36161
B	519	GLY	-	expression tag	UNP P36161
B	520	PHE	-	expression tag	UNP P36161
B	1021	ILE	LEU	conflict	UNP P36161
B	1027	ASP	ASN	conflict	UNP P36161

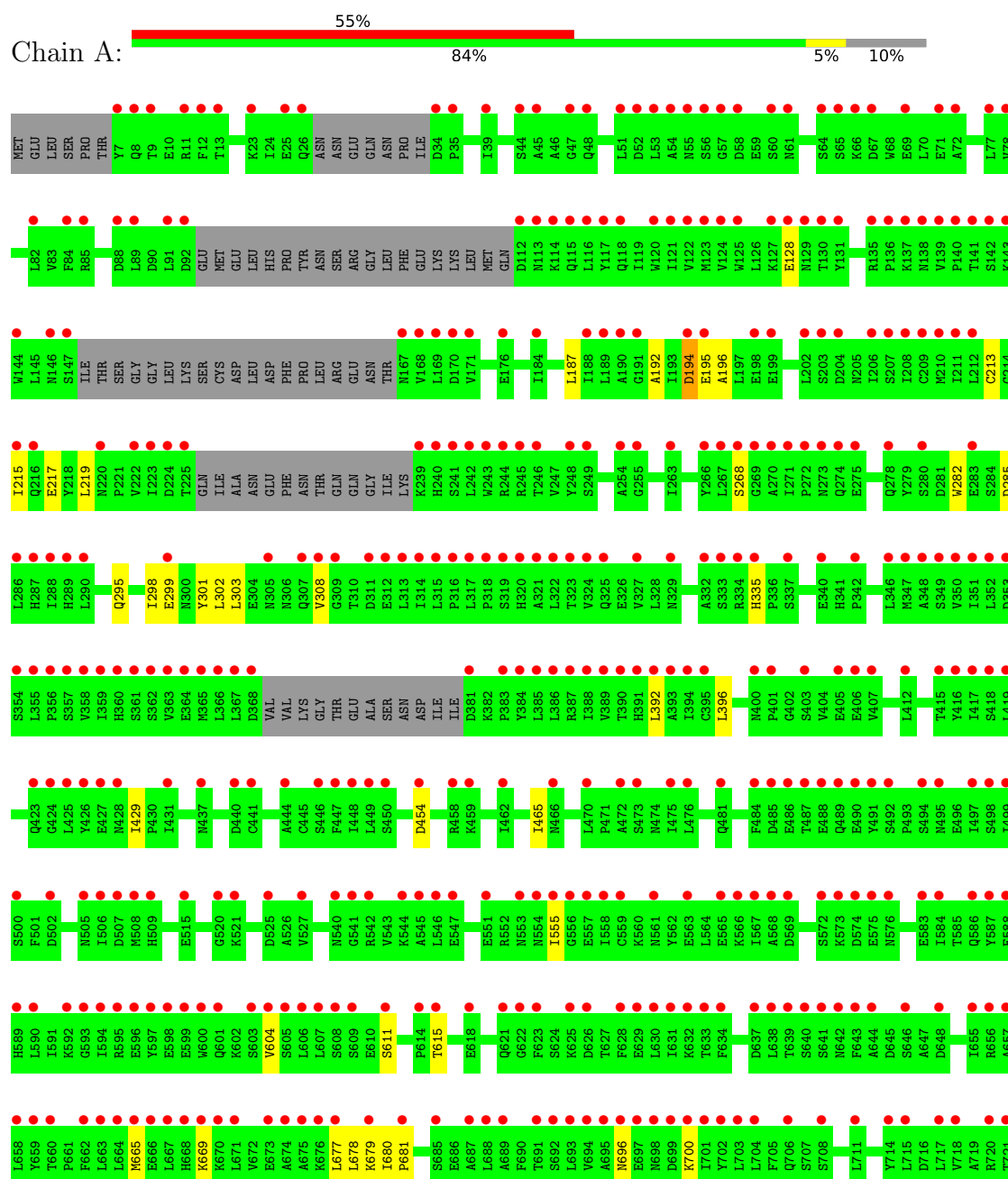
- Molecule 3 is a protein called VHH-SAN8.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	90	Total	C	N	O	0	0	0
			440	260	90	90			

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.

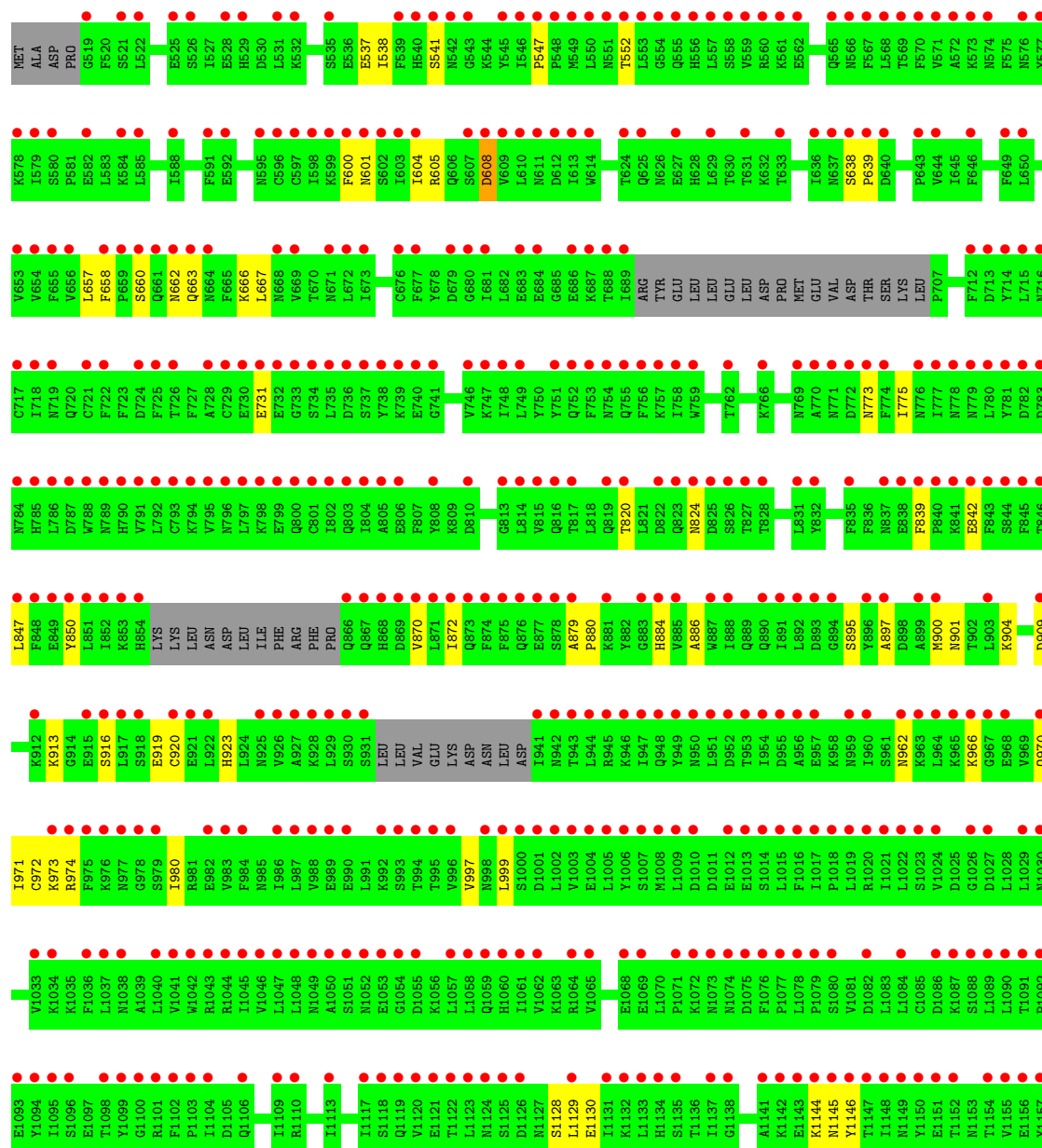
• Molecule 1: Nucleoporin NUP84



A722
 T723
 L724
 S725
 M726

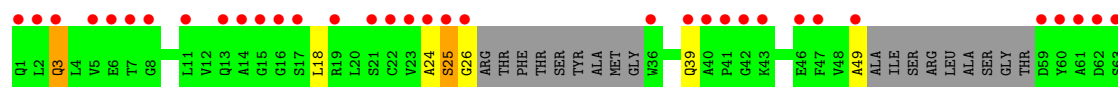
• Molecule 2: Nucleoporin NUP133

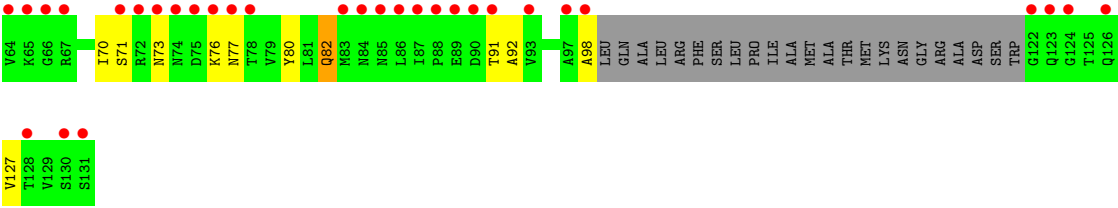
Chain B: 70% 84% 9% 6%



• Molecule 3: VHH-SAN8

Chain C: 50% 55% 11% 31%





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.26Å 287.65Å 297.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	103.38 – 6.38 103.38 – 6.38	Depositor EDS
% Data completeness (in resolution range)	98.5 (103.38-6.38) 98.5 (103.38-6.38)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 6.19Å)	Xtriage
Refinement program	PHENIX 1.18_3845	Depositor
R, R_{free}	0.314 , 0.324 0.313 , 0.328	Depositor DCC
R_{free} test set	1354 reflections (9.91%)	wwPDB-VP
Wilson B-factor (Å ²)	614.5	Xtriage
Anisotropy	0.136	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.47 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.018 for -h,l,k	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	6667	wwPDB-VP
Average B, all atoms (Å ²)	574.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.41% 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 [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	0.16	0/3228	0.43	2/4500 (0.0%)
2	B	0.25	0/2989	1.00	12/4168 (0.3%)
3	C	0.26	0/436	0.73	3/598 (0.5%)
All	All	0.21	0/6653	0.76	17/9266 (0.2%)

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	658	PHE	CA-C-N	34.34	154.24	119.56
2	B	658	PHE	C-N-CA	34.34	154.24	119.56
3	C	82	GLN	N-CA-C	9.09	123.17	109.63
2	B	971	ILE	CB-CA-C	-8.80	103.47	111.74
2	B	971	ILE	N-CA-C	8.42	117.98	107.70
2	B	970	GLN	N-CA-C	8.36	120.16	111.14
2	B	973	LYS	N-CA-C	7.83	119.82	111.28
2	B	972	CYS	N-CA-C	-6.63	97.73	108.41
2	B	974	ARG	N-CA-C	5.92	117.74	111.28
2	B	839	PHE	CA-C-N	5.85	125.71	119.28
2	B	839	PHE	C-N-CA	5.85	125.71	119.28
1	A	301	TYR	N-CA-C	-5.46	104.98	111.69
1	A	194	ASP	N-CA-C	-5.44	105.46	111.71
3	C	82	GLN	CA-C-N	5.38	130.51	122.86
3	C	82	GLN	C-N-CA	5.38	130.51	122.86
2	B	547	PRO	CA-C-N	5.22	124.84	119.05
2	B	547	PRO	C-N-CA	5.22	124.84	119.05

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	3234	0	1392	18	0
2	B	2993	0	1244	32	0
3	C	440	0	211	14	0
All	All	6667	0	2847	61	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 6.

All (61) 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:B:662:ASN:O	2:B:666:LYS:CB	1.83	1.25
3:C:73:ASN:CB	3:C:77:ASN:O	1.84	1.25
1:A:298:ILE:O	1:A:302:LEU:CB	1.99	1.10
2:B:662:ASN:O	2:B:666:LYS:N	1.97	0.97
3:C:18:LEU:O	3:C:82:GLN:CB	2.18	0.91
3:C:3:GLN:O	3:C:25:SER:CB	2.24	0.86
2:B:663:GLN:O	2:B:667:LEU:N	2.08	0.86
2:B:537:GLU:O	2:B:541:SER:O	1.94	0.85
1:A:282:TRP:CB	1:A:335:HIS:CB	2.57	0.82
1:A:696:ASN:HA	1:A:700:LYS:HA	1.61	0.80
2:B:662:ASN:O	2:B:666:LYS:CA	2.30	0.79
1:A:195:GLU:CB	3:C:26:GLY:O	2.32	0.78
2:B:601:ASN:O	2:B:605:ARG:N	2.18	0.75
1:A:268:SER:O	1:A:295:GLN:CB	2.34	0.75
1:A:192:ALA:O	1:A:196:ALA:N	2.20	0.73
1:A:299:GLU:O	1:A:303:LEU:CB	2.42	0.67
2:B:962:ASN:O	2:B:966:LYS:CB	2.45	0.65
3:C:49:ALA:HB1	3:C:70:ILE:CB	2.30	0.62
2:B:657:LEU:O	2:B:660:SER:O	2.18	0.61
2:B:662:ASN:CB	2:B:731:GLU:CB	2.79	0.61
3:C:3:GLN:O	3:C:25:SER:N	2.33	0.61
2:B:604:ILE:O	2:B:608:ASP:N	2.27	0.60
2:B:847:LEU:O	2:B:850:TYR:N	2.31	0.60
1:A:298:ILE:O	1:A:302:LEU:N	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:213:CYS:O	1:A:217:GLU:N	2.34	0.58
3:C:3:GLN:CB	3:C:25:SER:CB	2.81	0.58
2:B:847:LEU:O	2:B:850:TYR:CB	2.52	0.58
2:B:919:GLU:O	2:B:923:HIS:N	2.32	0.57
2:B:900:MET:O	2:B:904:LYS:N	2.30	0.56
3:C:24:ALA:O	3:C:26:GLY:N	2.39	0.56
2:B:657:LEU:C	2:B:660:SER:H	2.13	0.56
1:A:392:LEU:O	1:A:396:LEU:N	2.36	0.55
2:B:886:ALA:HB1	2:B:901:ASN:CB	2.37	0.54
2:B:897:ALA:O	2:B:901:ASN:N	2.39	0.54
1:A:194:ASP:HA	3:C:76:LYS:HA	1.90	0.54
2:B:1144:LYS:O	2:B:1146:TYR:N	2.43	0.51
1:A:215:ILE:O	1:A:219:LEU:N	2.44	0.51
2:B:820:THR:O	2:B:824:ASN:N	2.44	0.50
2:B:916:SER:O	2:B:920:CYS:N	2.28	0.50
2:B:600:PHE:O	2:B:604:ILE:N	2.37	0.50
2:B:663:GLN:O	2:B:667:LEU:CB	2.61	0.49
2:B:847:LEU:C	2:B:850:TYR:H	2.21	0.48
1:A:665:MET:O	1:A:669:LYS:N	2.46	0.48
2:B:884:HIS:C	2:B:886:ALA:H	2.21	0.47
2:B:538:ILE:HA	2:B:541:SER:O	2.14	0.47
2:B:909:ASP:HA	2:B:913:LYS:CB	2.46	0.46
3:C:91:THR:HA	3:C:127:VAL:O	2.16	0.46
1:A:677:LEU:O	1:A:679:LYS:N	2.45	0.45
3:C:3:GLN:O	3:C:25:SER:CA	2.63	0.45
1:A:128:GLU:CB	3:C:98:ALA:O	2.65	0.45
1:A:611:SER:O	1:A:615:THR:N	2.44	0.44
2:B:1128:SER:O	2:B:1129:LEU:C	2.61	0.43
3:C:71:SER:CB	3:C:80:TYR:HA	2.48	0.43
2:B:870:VAL:C	2:B:872:ILE:H	2.26	0.43
2:B:657:LEU:O	2:B:660:SER:N	2.43	0.43
2:B:997:VAL:C	2:B:999:LEU:H	2.25	0.43
2:B:1129:LEU:O	2:B:1130:GLU:C	2.60	0.42
1:A:187:LEU:O	1:A:192:ALA:HB3	2.20	0.42
2:B:884:HIS:C	2:B:886:ALA:N	2.77	0.41
3:C:39:GLN:O	3:C:92:ALA:HB1	2.21	0.41
1:A:298:ILE:O	1:A:302:LEU:CA	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	638/726 (88%)	576 (90%)	52 (8%)	10 (2%)	7	37
2	B	594/643 (92%)	520 (88%)	62 (10%)	12 (2%)	6	31
3	C	82/131 (63%)	73 (89%)	7 (8%)	2 (2%)	4	27
All	All	1314/1500 (88%)	1169 (89%)	121 (9%)	24 (2%)	6	34

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	638	SER
2	B	639	PRO
2	B	773	ASN
2	B	879	ALA
2	B	880	PRO
1	A	285	ASP
1	A	308	VAL
1	A	604	VAL
2	B	552	THR
2	B	980	ILE
2	B	1145	ASN
3	C	3	GLN
3	C	25	SER
2	B	775	ILE
2	B	895	SER
1	A	429	ILE
1	A	678	LEU
2	B	608	ASP
2	B	842	GLU
1	A	465	ILE
1	A	555	ILE
1	A	454	ASP
1	A	681	PRO
1	A	680	ILE

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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

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	650/726 (89%)	3.03	397 (61%) 0 2	253, 616, 917, 1137	0
2	B	602/643 (93%)	3.79	453 (75%) 0 1	269, 473, 656, 818	0
3	C	90/131 (68%)	4.07	65 (72%) 0 2	492, 922, 1078, 1159	0
All	All	1342/1500 (89%)	3.44	915 (68%) 0 2	253, 556, 945, 1159	0

All (915) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	721	CYS	22.2
2	B	999	LEU	22.2
2	B	925	ASN	19.6
1	A	629	GLU	19.3
2	B	724	ASP	18.3
2	B	1090	LEU	17.3
1	A	622	GLY	16.9
3	C	123	GLN	16.7
2	B	725	PHE	16.0
2	B	1042	TRP	15.6
2	B	1046	VAL	15.5
2	B	1018	PRO	14.4
1	A	691	THR	14.2
1	A	112	ASP	13.8
1	A	618	GLU	13.7
2	B	565	GLN	13.3
2	B	1098	THR	13.1
3	C	63	SER	13.0
1	A	223	ILE	12.8
2	B	1045	ILE	12.5
2	B	1089	LEU	12.5
3	C	89	GLU	12.4
2	B	752	GLN	12.4

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Mol	Chain	Res	Type	RSRZ
2	B	1006	TYR	12.4
2	B	556	HIS	12.2
1	A	633	THR	12.2
2	B	823	GLN	12.2
1	A	225	THR	12.1
1	A	615	THR	11.3
1	A	605	SER	11.3
2	B	751	TYR	11.2
1	A	625	LYS	11.0
2	B	1005	LEU	10.8
2	B	1075	ASP	10.7
2	B	1099	TYR	10.6
2	B	1120	VAL	10.3
2	B	676	CYS	10.2
2	B	956	ALA	10.2
1	A	663	LEU	10.1
1	A	692	SER	10.1
1	A	626	ASP	10.1
2	B	998	ASN	10.1
1	A	621	GLN	10.0
2	B	1044	ARG	9.9
2	B	837	ASN	9.7
1	A	189	LEU	9.6
1	A	395	CYS	9.5
2	B	1003	VAL	9.4
1	A	385	LEU	9.3
1	A	659	TYR	9.3
2	B	1147	THR	9.1
1	A	246	THR	9.0
3	C	122	GLY	8.9
1	A	666	GLU	8.9
2	B	669	VAL	8.9
1	A	389	VAL	8.8
2	B	729	CYS	8.8
2	B	542	ASN	8.8
2	B	1037	LEU	8.8
1	A	718	VAL	8.7
2	B	1079	PRO	8.6
2	B	866	GLN	8.6
2	B	552	THR	8.6
1	A	545	ALA	8.6
2	B	668	ASN	8.6

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Mol	Chain	Res	Type	RSRZ
2	B	728	ALA	8.5
2	B	568	LEU	8.5
2	B	672	LEU	8.5
1	A	606	LEU	8.4
2	B	1043	ARG	8.4
2	B	808	TYR	8.4
2	B	1041	VAL	8.3
3	C	23	VAL	8.2
2	B	754	ASN	8.2
2	B	1054	GLY	8.2
1	A	699	ASP	8.1
3	C	131	SER	8.1
2	B	987	LEU	8.0
1	A	614	PRO	8.0
1	A	9	THR	7.8
2	B	762	THR	7.8
3	C	14	ALA	7.8
2	B	722	PHE	7.8
1	A	390	THR	7.8
2	B	977	ASN	7.7
1	A	224	ASP	7.7
2	B	791	VAL	7.7
2	B	827	THR	7.7
1	A	641	SER	7.7
2	B	1095	ILE	7.7
1	A	721	THR	7.7
1	A	388	ILE	7.7
3	C	87	ILE	7.6
2	B	592	GLU	7.6
2	B	1092	PRO	7.6
1	A	391	HIS	7.5
1	A	211	ILE	7.5
3	C	59	ASP	7.4
2	B	718	ILE	7.4
1	A	600	TRP	7.4
2	B	755	GLN	7.4
3	C	74	ASN	7.4
1	A	307	GLN	7.3
2	B	1000	SER	7.3
2	B	1058	LEU	7.3
3	C	22	CYS	7.3
3	C	21	SER	7.3

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Mol	Chain	Res	Type	RSRZ
2	B	1002	LEU	7.3
2	B	888	ILE	7.3
1	A	604	VAL	7.2
3	C	1	GLN	7.2
1	A	723	THR	7.2
2	B	528	GLU	7.1
2	B	960	ILE	7.1
2	B	1103	PRO	7.0
1	A	355	LEU	7.0
2	B	554	GLY	7.0
1	A	363	VAL	6.9
2	B	787	ASP	6.9
2	B	569	THR	6.9
1	A	603	SER	6.8
2	B	555	GLN	6.8
1	A	289	HIS	6.8
1	A	689	ALA	6.8
3	C	2	LEU	6.8
2	B	789	ASN	6.8
2	B	1137	ILE	6.8
1	A	416	TYR	6.8
2	B	1087	LYS	6.7
2	B	1016	PHE	6.7
2	B	1102	PHE	6.7
2	B	784	ASN	6.7
2	B	854	HIS	6.6
1	A	239	LYS	6.6
2	B	887	TRP	6.6
2	B	1004	GLU	6.5
1	A	714	TYR	6.5
3	C	97	ALA	6.5
2	B	558	SER	6.5
1	A	113	ASN	6.5
2	B	1001	ASP	6.4
2	B	1084	LEU	6.4
2	B	1133	LEU	6.4
1	A	417	ILE	6.4
1	A	8	GLN	6.4
1	A	593	GLY	6.4
2	B	1007	SER	6.4
3	C	130	SER	6.4
3	C	7	THR	6.3

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Mol	Chain	Res	Type	RSRZ
2	B	770	ALA	6.3
2	B	1148	ILE	6.3
1	A	350	VAL	6.3
3	C	98	ALA	6.3
1	A	92	ASP	6.2
1	A	353	ASP	6.2
1	A	632	LYS	6.2
2	B	595	ASN	6.2
1	A	188	ILE	6.2
1	A	423	GLN	6.1
1	A	556	GLY	6.1
1	A	427	GLU	6.1
2	B	1129	LEU	6.1
1	A	394	ILE	6.1
3	C	72	ARG	6.1
1	A	392	LEU	6.1
2	B	929	LEU	6.1
1	A	34	ASP	6.1
2	B	1073	ASN	6.0
1	A	122	VAL	6.0
1	A	26	GLN	6.0
3	C	76	LYS	6.0
2	B	1123	LEU	6.0
1	A	204	ASP	6.0
2	B	852	ILE	6.0
1	A	381	ASP	5.9
1	A	642	ASN	5.9
2	B	1053	GLU	5.9
2	B	967	GLY	5.9
1	A	567	ILE	5.9
2	B	1012	GLU	5.9
2	B	588	ILE	5.9
2	B	1157	TYR	5.9
3	C	73	ASN	5.9
2	B	885	VAL	5.9
2	B	1019	LEU	5.9
2	B	548	PRO	5.8
2	B	869	ASP	5.8
1	A	129	ASN	5.8
1	A	140	PRO	5.8
2	B	561	LYS	5.8
1	A	628	PHE	5.8

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Mol	Chain	Res	Type	RSRZ
1	A	130	THR	5.8
2	B	1074	ASN	5.8
2	B	782	ASP	5.8
3	C	85	ASN	5.8
2	B	820	THR	5.8
2	B	610	LEU	5.7
2	B	689	ILE	5.7
2	B	793	CYS	5.7
1	A	640	SER	5.7
1	A	124	VAL	5.7
1	A	368	ASP	5.7
1	A	167	ASN	5.7
2	B	1038	ASN	5.7
1	A	317	LEU	5.7
1	A	324	VAL	5.7
2	B	545	TYR	5.6
1	A	590	LEU	5.6
2	B	943	THR	5.6
2	B	788	TRP	5.6
1	A	267	LEU	5.6
1	A	660	THR	5.6
1	A	85	ARG	5.6
1	A	360	HIS	5.6
1	A	569	ASP	5.6
2	B	688	THR	5.5
2	B	1145	ASN	5.5
1	A	263	ILE	5.5
2	B	717	CYS	5.5
2	B	562	GLU	5.5
1	A	208	ILE	5.5
2	B	1050	ALA	5.4
2	B	1091	THR	5.4
3	C	126	GLN	5.4
1	A	354	SER	5.4
1	A	697	GLU	5.4
1	A	630	LEU	5.4
2	B	953	THR	5.4
2	B	1008	MET	5.4
1	A	121	ILE	5.3
1	A	696	ASN	5.3
1	A	673	GLU	5.3
2	B	1143	GLU	5.3

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Mol	Chain	Res	Type	RSRZ
1	A	51	LEU	5.3
2	B	1106	GLN	5.3
2	B	1150	TYR	5.3
2	B	1017	ILE	5.3
2	B	853	LYS	5.3
1	A	366	LEU	5.3
1	A	384	TYR	5.2
3	C	47	PHE	5.2
1	A	356	PRO	5.2
2	B	604	ILE	5.2
1	A	319	SER	5.2
3	C	5	VAL	5.2
1	A	47	GLY	5.2
2	B	871	LEU	5.2
2	B	772	ASP	5.2
1	A	120	TRP	5.2
1	A	244	ARG	5.1
1	A	485	ASP	5.1
2	B	602	SER	5.1
2	B	736	ASP	5.1
2	B	771	ASN	5.1
2	B	930	SER	5.1
2	B	1109	ILE	5.1
2	B	646	PHE	5.1
1	A	687	ALA	5.1
2	B	1052	ASN	5.0
1	A	78	VAL	5.0
2	B	983	VAL	5.0
1	A	255	GLY	5.0
2	B	838	GLU	5.0
3	C	90	ASP	5.0
2	B	1113	ILE	5.0
1	A	57	GLY	5.0
2	B	1015	LEU	5.0
2	B	928	LYS	5.0
1	A	243	TRP	4.9
1	A	559	CYS	4.9
1	A	611	SER	4.9
2	B	549	MET	4.9
2	B	872	ILE	4.9
1	A	207	SER	4.9
2	B	815	VAL	4.9

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Mol	Chain	Res	Type	RSRZ
2	B	633	THR	4.9
2	B	920	CYS	4.9
2	B	918	SER	4.9
2	B	1094	TYR	4.9
1	A	115	GLN	4.9
1	A	674	ALA	4.8
1	A	48	GLN	4.8
2	B	681	ILE	4.8
2	B	732	GLU	4.8
2	B	790	HIS	4.8
2	B	893	ASP	4.8
1	A	198	GLU	4.8
1	A	220	ASN	4.8
1	A	698	ASN	4.8
2	B	671	ASN	4.8
2	B	571	VAL	4.8
2	B	591	PHE	4.8
1	A	358	VAL	4.8
2	B	737	SER	4.7
2	B	1138	GLY	4.7
2	B	551	ASN	4.7
1	A	135	ARG	4.7
2	B	731	GLU	4.7
1	A	333	SER	4.7
1	A	364	GLU	4.7
1	A	386	LEU	4.7
3	C	43	LYS	4.7
1	A	314	ILE	4.7
1	A	450	SER	4.7
1	A	323	THR	4.6
3	C	75	ASP	4.6
2	B	946	LYS	4.6
3	C	77	ASN	4.6
2	B	804	ILE	4.6
1	A	12	PHE	4.6
1	A	286	LEU	4.6
1	A	271	ILE	4.6
2	B	1061	ILE	4.6
2	B	814	LEU	4.6
1	A	55	ASN	4.6
1	A	346	LEU	4.6
1	A	88	ASP	4.6

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Mol	Chain	Res	Type	RSRZ
1	A	631	ILE	4.6
1	A	7	TYR	4.5
1	A	639	THR	4.5
1	A	315	LEU	4.5
2	B	942	ASN	4.5
2	B	1118	SER	4.5
2	B	1065	VAL	4.5
2	B	959	ASN	4.5
1	A	245	ARG	4.5
2	B	650	LEU	4.5
1	A	270	ALA	4.5
2	B	870	VAL	4.5
2	B	896	TYR	4.5
2	B	1080	SER	4.5
2	B	570	PHE	4.5
2	B	1048	LEU	4.5
3	C	46	GLU	4.5
1	A	321	ALA	4.5
1	A	362	SER	4.5
2	B	828	THR	4.4
3	C	61	ALA	4.4
1	A	724	LEU	4.4
3	C	25	SER	4.4
2	B	598	ILE	4.4
2	B	663	GLN	4.4
2	B	780	LEU	4.4
1	A	320	HIS	4.4
2	B	758	ILE	4.4
1	A	568	ALA	4.4
2	B	799	GLU	4.4
3	C	36	TRP	4.4
2	B	550	LEU	4.4
1	A	190	ALA	4.3
1	A	194	ASP	4.3
1	A	170	ASP	4.3
2	B	738	TYR	4.3
2	B	1021	ILE	4.3
1	A	668	HIS	4.3
1	A	52	ASP	4.3
1	A	426	TYR	4.3
1	A	316	PRO	4.2
2	B	673	ILE	4.2

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Mol	Chain	Res	Type	RSRZ
2	B	931	SER	4.2
2	B	525	GLU	4.2
2	B	1126	ASP	4.2
1	A	347	MET	4.2
3	C	19	ARG	4.2
1	A	498	SER	4.2
1	A	725	SER	4.2
1	A	424	GLY	4.2
2	B	656	VAL	4.2
1	A	695	ALA	4.2
3	C	24	ALA	4.2
2	B	796	ASN	4.2
2	B	824	ASN	4.1
1	A	203	SER	4.1
1	A	407	VAL	4.1
1	A	418	SER	4.1
1	A	597	TYR	4.1
2	B	1055	ASP	4.1
1	A	44	SER	4.1
2	B	747	LYS	4.1
2	B	603	ILE	4.1
1	A	589	HIS	4.1
3	C	11	LEU	4.1
1	A	215	ILE	4.1
2	B	795	VAL	4.1
1	A	643	PHE	4.0
1	A	671	LEU	4.0
2	B	899	ALA	4.0
2	B	577	TYR	4.0
2	B	607	SER	4.0
1	A	679	LYS	4.0
1	A	11	ARG	4.0
2	B	733	GLY	4.0
2	B	867	GLN	4.0
1	A	64	SER	4.0
1	A	594	ILE	4.0
2	B	660	SER	4.0
2	B	1033	VAL	4.0
1	A	722	ALA	4.0
2	B	560	ARG	4.0
2	B	816	GLN	3.9
2	B	778	ASN	3.9

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Mol	Chain	Res	Type	RSRZ
2	B	831	LEU	3.9
2	B	687	LYS	3.9
2	B	1082	ASP	3.9
1	A	700	LYS	3.9
2	B	806	GLU	3.9
1	A	702	TYR	3.9
1	A	91	LEU	3.9
1	A	139	VAL	3.9
2	B	1124	ASN	3.9
2	B	1023	SER	3.9
1	A	25	GLU	3.9
2	B	683	GLU	3.9
2	B	1047	LEU	3.9
2	B	802	ILE	3.9
2	B	1146	TYR	3.9
1	A	487	THR	3.9
2	B	759	TRP	3.9
3	C	8	GLY	3.9
2	B	535	SER	3.9
3	C	93	VAL	3.9
1	A	583	GLU	3.8
1	A	318	PRO	3.8
2	B	748	ILE	3.8
2	B	713	ASP	3.8
2	B	964	LEU	3.8
3	C	62	ASP	3.8
2	B	1101	ARG	3.8
2	B	584	LYS	3.8
2	B	572	ALA	3.8
1	A	541	GLY	3.8
2	B	612	ASP	3.8
1	A	138	ASN	3.8
1	A	428	ASN	3.8
1	A	56	SER	3.8
1	A	278	GLN	3.8
1	A	667	LEU	3.8
1	A	547	GLU	3.8
1	A	357	SER	3.8
2	B	1024	VAL	3.8
1	A	448	ILE	3.8
1	A	322	LEU	3.7
1	A	701	ILE	3.7

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Mol	Chain	Res	Type	RSRZ
2	B	922	LEU	3.7
1	A	565	GLU	3.7
2	B	1110	ARG	3.7
2	B	844	SER	3.7
2	B	909	ASP	3.7
2	B	803	GLN	3.7
2	B	734	SER	3.7
2	B	609	VAL	3.7
2	B	1022	LEU	3.7
2	B	1096	SER	3.7
2	B	785	HIS	3.7
2	B	519	GLY	3.7
2	B	921	GLU	3.7
2	B	679	ASP	3.7
2	B	539	PHE	3.7
2	B	776	ASN	3.7
1	A	61	ASN	3.6
2	B	868	HIS	3.6
3	C	41	PRO	3.6
3	C	15	GLY	3.6
2	B	756	PHE	3.6
2	B	715	LEU	3.6
2	B	753	PHE	3.6
3	C	17	SER	3.6
2	B	540	HIS	3.6
2	B	968	GLU	3.6
3	C	49	ALA	3.6
1	A	367	LEU	3.6
2	B	543	GLY	3.6
2	B	1100	GLY	3.6
1	A	287	HIS	3.6
2	B	810	ASP	3.6
1	A	171	VAL	3.6
1	A	553	ASN	3.6
2	B	529	HIS	3.6
1	A	406	GLU	3.6
2	B	842	GLU	3.6
2	B	1152	THR	3.6
3	C	6	GLU	3.6
1	A	184	ILE	3.6
2	B	976	LYS	3.6
1	A	717	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	365	MET	3.5
1	A	572	SER	3.5
2	B	664	ASN	3.5
2	B	739	LYS	3.5
1	A	334	ARG	3.5
2	B	839	PHE	3.5
2	B	927	ALA	3.5
1	A	144	TRP	3.5
1	A	677	LEU	3.5
1	A	147	SER	3.5
1	A	349	SER	3.5
1	A	596	GLU	3.5
1	A	191	GLY	3.5
1	A	141	THR	3.5
2	B	576	ASN	3.5
2	B	716	ASN	3.5
1	A	274	GLN	3.5
3	C	40	ALA	3.5
2	B	1013	GLU	3.5
2	B	1121	GLU	3.5
1	A	592	LYS	3.5
1	A	488	GLU	3.5
1	A	495	ASN	3.5
1	A	558	ILE	3.5
3	C	60	TYR	3.5
1	A	290	LEU	3.4
1	A	637	ASP	3.4
2	B	640	ASP	3.4
2	B	840	PRO	3.4
3	C	128	THR	3.4
2	B	557	LEU	3.4
2	B	955	ASP	3.4
1	A	142	SER	3.4
1	A	472	ALA	3.4
1	A	694	VAL	3.4
2	B	1068	GLU	3.4
1	A	715	LEU	3.4
2	B	876	GLN	3.4
2	B	1071	PRO	3.4
2	B	916	SER	3.4
1	A	561	ASN	3.4
3	C	42	GLY	3.4

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Mol	Chain	Res	Type	RSRZ
2	B	777	ILE	3.4
1	A	575	GLU	3.4
1	A	266	TYR	3.4
1	A	527	VAL	3.4
2	B	559	VAL	3.4
3	C	67	ARG	3.4
1	A	437	ASN	3.4
1	A	383	PRO	3.4
2	B	1119	GLN	3.4
1	A	66	LYS	3.3
2	B	659	PRO	3.3
2	B	1142	LYS	3.3
1	A	720	ARG	3.3
2	B	1057	LEU	3.3
2	B	990	GLU	3.3
2	B	579	ILE	3.3
2	B	891	ILE	3.3
2	B	826	SER	3.3
1	A	117	TYR	3.3
1	A	481	GLN	3.3
2	B	680	GLY	3.3
1	A	114	LYS	3.3
2	B	978	GLY	3.3
1	A	168	VAL	3.3
1	A	542	ARG	3.3
1	A	125	TRP	3.3
2	B	611	ASN	3.3
1	A	665	MET	3.3
1	A	494	SER	3.3
1	A	607	LEU	3.2
2	B	851	LEU	3.2
1	A	551	GLU	3.2
2	B	874	PHE	3.2
2	B	974	ARG	3.2
3	C	64	VAL	3.2
1	A	143	LYS	3.2
2	B	1072	LYS	3.2
1	A	308	VAL	3.2
1	A	470	LEU	3.2
2	B	1078	LEU	3.2
2	B	1132	LYS	3.2
3	C	88	PRO	3.2

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Mol	Chain	Res	Type	RSRZ
2	B	541	SER	3.2
2	B	712	PHE	3.2
2	B	970	GLN	3.2
1	A	327	VAL	3.2
1	A	45	ALA	3.2
2	B	546	ILE	3.2
2	B	638	SER	3.1
2	B	963	LYS	3.1
2	B	965	LYS	3.1
2	B	661	GLN	3.1
2	B	714	TYR	3.1
1	A	458	ARG	3.1
1	A	486	GLU	3.1
2	B	1051	SER	3.1
2	B	873	GLN	3.1
1	A	305	ASN	3.1
2	B	774	PHE	3.1
3	C	84	ASN	3.1
1	A	137	LYS	3.1
2	B	897	ALA	3.1
2	B	915	GLU	3.1
1	A	489	GLN	3.1
3	C	78	THR	3.1
2	B	1036	PHE	3.1
1	A	521	LYS	3.1
1	A	449	LEU	3.1
3	C	3	GLN	3.1
1	A	401	PRO	3.1
1	A	123	MET	3.1
2	B	849	GLU	3.1
2	B	614	TRP	3.1
1	A	35	PRO	3.1
2	B	1049	ASN	3.1
1	A	351	ILE	3.1
1	A	359	ILE	3.1
2	B	947	ILE	3.1
3	C	124	GLY	3.0
1	A	254	ALA	3.0
2	B	841	LYS	3.0
2	B	900	MET	3.0
1	A	212	LEU	3.0
2	B	817	THR	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	623	PHE	3.0
2	B	649	PHE	3.0
2	B	986	ILE	3.0
2	B	786	LEU	3.0
2	B	726	THR	3.0
2	B	843	PHE	3.0
2	B	1122	THR	3.0
2	B	719	ASN	3.0
1	A	206	ILE	3.0
2	B	601	ASN	3.0
2	B	1029	LEU	3.0
2	B	766	LYS	3.0
1	A	65	SER	3.0
1	A	273	ASN	3.0
2	B	631	THR	2.9
1	A	248	TYR	2.9
2	B	547	PRO	2.9
2	B	644	VAL	2.9
2	B	813	GLY	2.9
1	A	662	PHE	2.9
2	B	835	PHE	2.9
1	A	199	GLU	2.9
1	A	242	LEU	2.9
1	A	688	LEU	2.9
2	B	613	ILE	2.9
2	B	662	ASN	2.9
1	A	118	GLN	2.9
2	B	781	TYR	2.9
1	A	240	HIS	2.9
2	B	1131	ILE	2.9
1	A	176	GLU	2.9
2	B	1020	ARG	2.9
2	B	1151	GLU	2.9
2	B	926	VAL	2.9
2	B	996	VAL	2.9
1	A	507	ASP	2.9
3	C	26	GLY	2.9
1	A	337	SER	2.9
2	B	1134	HIS	2.9
1	A	573	LYS	2.9
1	A	574	ASP	2.9
2	B	800	GLN	2.9

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Mol	Chain	Res	Type	RSRZ
2	B	950	ASN	2.9
2	B	654	VAL	2.8
1	A	313	LEU	2.8
2	B	655	PHE	2.8
2	B	890	GLN	2.8
2	B	850	TYR	2.8
2	B	639	PRO	2.8
1	A	415	THR	2.8
1	A	658	LEU	2.8
2	B	1069	GLU	2.8
3	C	13	GLN	2.8
1	A	72	ALA	2.8
2	B	879	ALA	2.8
2	B	599	LYS	2.8
2	B	966	LYS	2.8
1	A	128	GLU	2.8
1	A	500	SER	2.8
1	A	708	SER	2.8
2	B	1062	VAL	2.8
2	B	1149	ASN	2.8
2	B	1064	ARG	2.8
1	A	608	SER	2.8
2	B	740	GLU	2.8
2	B	1135	SER	2.8
1	A	352	LEU	2.8
1	A	506	ILE	2.8
1	A	446	SER	2.8
1	A	332	ALA	2.8
2	B	892	LEU	2.8
2	B	1030	ASN	2.8
1	A	497	ILE	2.8
3	C	16	GLY	2.8
2	B	979	SER	2.8
3	C	91	THR	2.8
1	A	272	PRO	2.8
1	A	146	ASN	2.7
1	A	576	ASN	2.7
2	B	773	ASN	2.7
2	B	995	THR	2.7
2	B	578	LYS	2.7
1	A	412	LEU	2.7
3	C	86	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	706	GLN	2.7
1	A	136	PRO	2.7
1	A	563	GLU	2.7
1	A	466	ASN	2.7
2	B	1077	PRO	2.7
1	A	131	TYR	2.7
1	A	595	ARG	2.7
2	B	1155	VAL	2.7
2	B	580	SER	2.7
1	A	67	ASP	2.7
2	B	952	ASP	2.7
2	B	643	PRO	2.7
3	C	66	GLY	2.7
1	A	566	LYS	2.6
2	B	582	GLU	2.6
3	C	39	GLN	2.6
1	A	473	SER	2.6
2	B	1014	SER	2.6
1	A	440	ASP	2.6
1	A	216	GLN	2.6
1	A	447	PHE	2.6
1	A	675	ALA	2.6
2	B	526	SER	2.6
1	A	342	PRO	2.6
2	B	847	LEU	2.6
2	B	1086	ASP	2.6
1	A	195	GLU	2.6
2	B	625	GLN	2.6
2	B	684	GLU	2.6
2	B	686	GLU	2.6
2	B	757	LYS	2.6
1	A	656	ARG	2.6
2	B	878	SER	2.6
2	B	608	ASP	2.6
2	B	962	ASN	2.6
2	B	1088	SER	2.6
1	A	454	ASP	2.6
1	A	655	ILE	2.6
2	B	637	ASN	2.6
2	B	797	LEU	2.6
3	C	71	SER	2.6
2	B	822	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
2	B	730	GLU	2.6
1	A	540	ASN	2.6
1	A	609	SER	2.5
2	B	954	ILE	2.5
2	B	1027	ASP	2.5
1	A	222	VAL	2.5
2	B	792	LEU	2.5
1	A	669	LYS	2.5
2	B	848	PHE	2.5
2	B	574	ASN	2.5
2	B	798	LYS	2.5
2	B	1104	ILE	2.5
2	B	945	ARG	2.5
1	A	241	SER	2.5
1	A	268	SER	2.5
1	A	71	GLU	2.5
1	A	84	PHE	2.5
1	A	546	LEU	2.5
1	A	335	HIS	2.5
3	C	65	LYS	2.5
1	A	77	LEU	2.5
1	A	425	LEU	2.5
1	A	693	LEU	2.5
1	A	703	LEU	2.5
2	B	825	ASP	2.5
1	A	681	PRO	2.5
1	A	387	ARG	2.5
1	A	459	LYS	2.5
1	A	69	GLU	2.5
2	B	975	PHE	2.5
1	A	505	ASN	2.5
2	B	805	ALA	2.5
2	B	988	VAL	2.4
2	B	881	LYS	2.4
2	B	992	LYS	2.4
1	A	58	ASP	2.4
1	A	502	ASP	2.4
2	B	783	ASP	2.4
1	A	82	LEU	2.4
1	A	202	LEU	2.4
2	B	600	PHE	2.4
2	B	769	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
2	B	746	VAL	2.4
2	B	553	LEU	2.4
1	A	555	ILE	2.4
1	A	441	CYS	2.4
2	B	1093	GLU	2.4
2	B	894	GLY	2.4
1	A	39	ILE	2.4
1	A	554	ASN	2.4
2	B	1034	LYS	2.4
1	A	586	GLN	2.4
2	B	989	GLU	2.4
2	B	883	GLY	2.4
2	B	596	CYS	2.4
2	B	794	LYS	2.4
2	B	877	GLU	2.3
1	A	54	ALA	2.3
1	A	508	MET	2.3
1	A	475	ILE	2.3
1	A	13	THR	2.3
1	A	249	SER	2.3
1	A	89	LEU	2.3
1	A	288	ILE	2.3
2	B	941	ILE	2.3
1	A	405	GLU	2.3
2	B	653	VAL	2.3
1	A	462	ILE	2.3
1	A	657	ALA	2.3
2	B	566	ASN	2.3
2	B	801	CYS	2.3
2	B	521	SER	2.3
2	B	951	LEU	2.3
1	A	525	ASP	2.3
1	A	588	GLU	2.2
2	B	949	TYR	2.2
2	B	636	ILE	2.2
1	A	544	LYS	2.2
1	A	676	LYS	2.2
1	A	169	LEU	2.2
1	A	348	ALA	2.2
1	A	644	ALA	2.2
2	B	1009	LEU	2.2
1	A	598	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	957	GLU	2.2
1	A	634	PHE	2.2
2	B	984	PHE	2.2
1	A	400	ASN	2.2
2	B	1117	ILE	2.2
2	B	624	THR	2.2
1	A	670	LYS	2.2
1	A	116	LEU	2.2
2	B	629	LEU	2.2
1	A	444	ALA	2.2
1	A	520	GLY	2.2
2	B	597	CYS	2.2
2	B	993	SER	2.2
2	B	912	LYS	2.2
1	A	476	LEU	2.2
2	B	779	ASN	2.2
1	A	361	SER	2.2
2	B	1125	SER	2.2
2	B	875	PHE	2.2
2	B	1144	LYS	2.2
2	B	982	GLU	2.2
1	A	311	ASP	2.2
2	B	884	HIS	2.2
1	A	53	LEU	2.2
1	A	209	CYS	2.2
1	A	638	LEU	2.2
2	B	658	PHE	2.2
1	A	23	LYS	2.2
2	B	522	LEU	2.2
1	A	325	GLN	2.2
1	A	491	TYR	2.2
1	A	515	GLU	2.2
2	B	1010	ASP	2.1
2	B	567	PHE	2.1
1	A	664	LEU	2.1
1	A	711	LEU	2.1
2	B	531	LEU	2.1
2	B	994	THR	2.1
1	A	685	SER	2.1
1	A	309	GLY	2.1
1	A	127	LYS	2.1
2	B	845	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	1076	PHE	2.1
1	A	60	SER	2.1
1	A	269	GLY	2.1
1	A	299	GLU	2.1
1	A	340	GLU	2.1
2	B	677	PHE	2.1
1	A	210	MET	2.1
2	B	832	TYR	2.1
1	A	492	SER	2.1
1	A	484	PHE	2.1
1	A	499	ILE	2.1
1	A	704	LEU	2.1
3	C	83	MET	2.1
2	B	1154	THR	2.1
1	A	393	ALA	2.1
1	A	419	LEU	2.1
2	B	741	GLY	2.1
2	B	1026	GLY	2.1
1	A	587	TYR	2.1
2	B	573	LYS	2.1
2	B	973	LYS	2.1
2	B	948	GLN	2.1
1	A	280	SER	2.1
1	A	599	GLU	2.1
1	A	646	SER	2.1
1	A	648	ASP	2.1
1	A	431	ILE	2.1
2	B	846	THR	2.1
2	B	1059	GLN	2.1
1	A	490	GLU	2.1
2	B	1156	GLU	2.1
2	B	749	LEU	2.0
1	A	509	HIS	2.0
2	B	1060	HIS	2.0
1	A	329	ASN	2.0
1	A	283	GLU	2.0
2	B	627	GLU	2.0
2	B	917	LEU	2.0
2	B	1040	LEU	2.0
1	A	312	GLU	2.0
1	A	403	SER	2.0
2	B	585	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
2	B	735	LEU	2.0
2	B	944	LEU	2.0
1	A	584	ILE	2.0
2	B	1141	ALA	2.0
1	A	601	GLN	2.0
2	B	819	GLN	2.0
1	A	275	GLU	2.0
1	A	557	GLU	2.0
2	B	532	LYS	2.0
2	B	903	LEU	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.