



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 17, 2024 – 04:19 PM EDT

PDB ID : 3HZJ
Title : Crystal structure of the RabGAP domain of the RABGAP1L protein
Authors : Nedyalkova, L.; Tempel, W.; Tong, Y.; Zhong, N.; MacKenzie, F.; Arrowsmith, C.H.; Edwards, A.M.; Bountra, C.; Weigelt, J.; Bochkarev, A.; Park, H.; Structural Genomics Consortium (SGC)
Deposited on : 2009-06-23
Resolution : 2.30 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

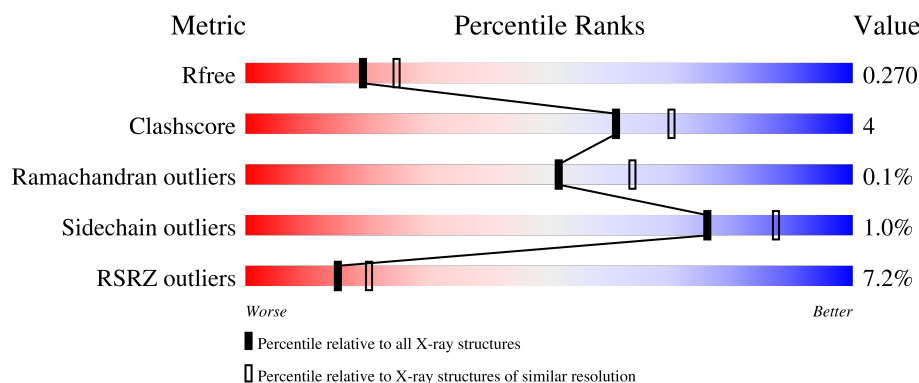
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	310	 2% 81% 11% • 7%
1	B	310	 12% 73% 9% 17%
1	C	310	 5% 84% 9% • 7%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	UNX	A	2	-	-	-	X
2	UNX	A	4	-	-	-	X
2	UNX	A	901	-	-	-	X
2	UNX	A	902	-	-	-	X
2	UNX	A	903	-	-	-	X
2	UNX	A	904	-	-	-	X
2	UNX	A	905	-	-	-	X
2	UNX	A	906	-	-	-	X
2	UNX	A	907	-	-	-	X
2	UNX	A	908	-	-	-	X
2	UNX	A	909	-	-	-	X
2	UNX	A	910	-	-	-	X
2	UNX	A	911	-	-	-	X
2	UNX	B	901	-	-	-	X
2	UNX	B	902	-	-	-	X
2	UNX	B	908	-	-	-	X
2	UNX	B	910	-	-	-	X
2	UNX	C	5	-	-	-	X
2	UNX	C	6	-	-	-	X
2	UNX	C	901	-	-	-	X
2	UNX	C	902	-	-	-	X
2	UNX	C	903	-	-	-	X
2	UNX	C	904	-	-	-	X
2	UNX	C	905	-	-	-	X
2	UNX	C	906	-	-	-	X
2	UNX	C	907	-	-	-	X
2	UNX	C	908	-	-	-	X
2	UNX	C	909	-	-	-	X
2	UNX	C	910	-	-	-	X
2	UNX	C	911	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6473 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 RAB GTPase-activating protein 1-like.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	287	Total	C	N	O	S	Se	0	0	0
			2270	1466	378	410	8	8			
1	B	256	Total	C	N	O	S	Se	0	0	0
			1887	1231	312	330	7	7			
1	C	288	Total	C	N	O	S	Se	0	0	0
			2271	1467	382	406	8	8			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	506	GLY	-	EXPRESSION TAG	UNP Q5R372
B	506	GLY	-	EXPRESSION TAG	UNP Q5R372
C	506	GLY	-	EXPRESSION TAG	UNP Q5R372

- Molecule 2 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	14	Total	X	0	0
			14	14		
2	B	4	Total	X	0	0
			4	4		
2	C	14	Total	X	0	0
			14	14		

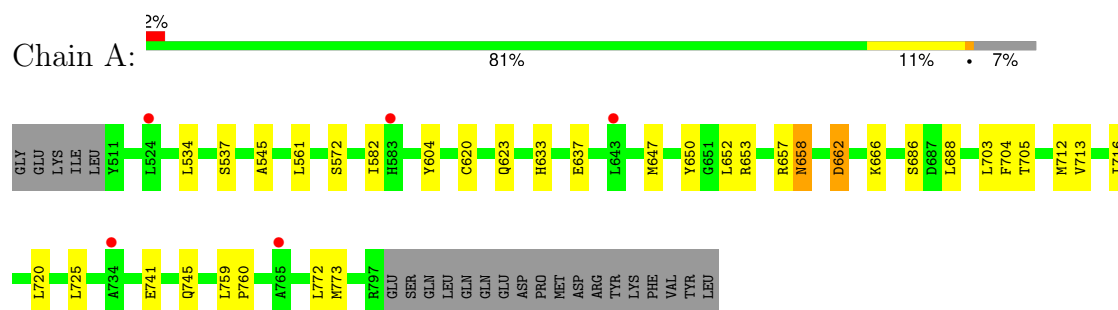
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	O	0	0
			3	3		
3	C	10	Total	O	0	0
			10	10		

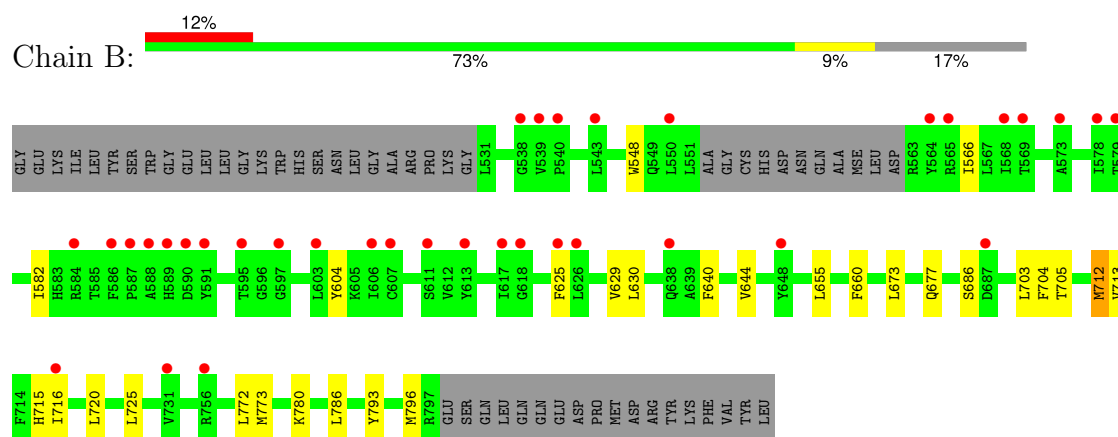
3 Residue-property plots [i](#)

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.

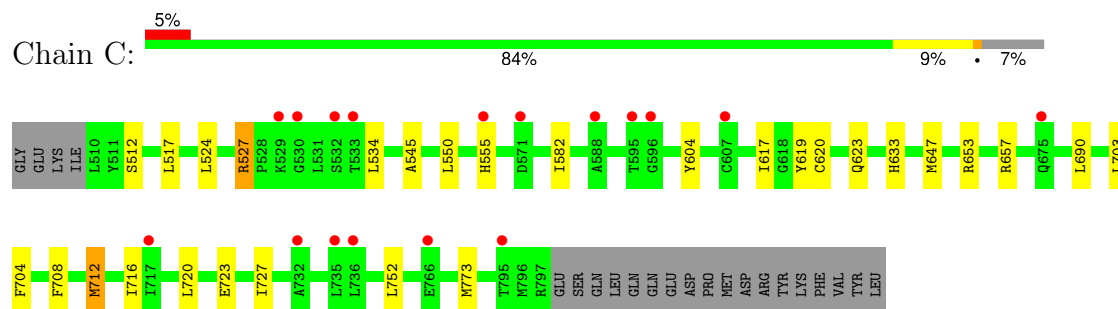
- Molecule 1: RAB GTPase-activating protein 1-like



- Molecule 1: RAB GTPase-activating protein 1-like



- Molecule 1: RAB GTPase-activating protein 1-like



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	48.09Å 64.57Å 290.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.30 19.80 – 2.30	Depositor EDS
% Data completeness (in resolution range)	92.3 (20.00-2.30) 92.3 (19.80-2.30)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.89 (at 2.30Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.244 , 0.274 0.240 , 0.270	Depositor DCC
R_{free} test set	1191 reflections (3.13%)	wwPDB-VP
Wilson B-factor (Å ²)	49.4	Xtriage
Anisotropy	0.106	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 57.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6473	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.56% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: UNX

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	0.57	0/2317	0.59	1/3130 (0.0%)
1	B	0.50	0/1923	0.53	0/2609
1	C	0.61	0/2318	0.63	3/3132 (0.1%)
All	All	0.57	0/6558	0.59	4/8871 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	712	MSE	CG-SE-CE	-8.85	79.43	98.90
1	C	527	ARG	NE-CZ-NH2	6.17	123.39	120.30
1	C	527	ARG	NE-CZ-NH1	-5.35	117.62	120.30
1	A	688	LEU	CA-CB-CG	5.28	127.45	115.30

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	2270	0	2159	22	0
1	B	1887	0	1686	17	0
1	C	2271	0	2159	18	0
2	A	14	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	4	0	0	0	0
2	C	14	0	0	0	0
3	A	3	0	0	0	0
3	C	10	0	0	0	0
All	All	6473	0	6004	56	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 4.

All (56) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:703:LEU:HD13	1:A:720:LEU:HD22	1.62	0.81
1:C:712:MSE:SE	1:C:716:ILE:HD11	2.33	0.77
1:C:712:MSE:SE	1:C:716:ILE:CD1	2.90	0.69
1:C:708:PHE:CD2	1:C:712:MSE:HE1	2.28	0.68
1:A:712:MSE:SE	1:A:716:ILE:HD11	2.52	0.59
1:C:617:ILE:HD12	1:C:620:CYS:SG	2.42	0.59
1:B:715:HIS:HB3	1:B:773:MSE:HG3	1.85	0.58
1:B:793:TYR:CE1	1:B:796:MSE:HE1	2.38	0.58
1:B:793:TYR:CZ	1:B:796:MSE:HE1	2.38	0.57
1:B:703:LEU:HD13	1:B:720:LEU:HD22	1.86	0.56
1:C:524:LEU:O	1:C:527:ARG:NH1	2.38	0.56
1:A:686:SER:HB3	1:B:686:SER:HB3	1.88	0.56
1:C:703:LEU:HD13	1:C:720:LEU:HD22	1.87	0.56
1:B:793:TYR:CE1	1:B:796:MSE:CE	2.89	0.54
1:B:673:LEU:HD11	1:B:786:LEU:HD21	1.88	0.54
1:A:704:PHE:CD1	1:A:716:ILE:HD13	2.43	0.54
1:B:582:ILE:HD11	1:B:604:TYR:HA	1.91	0.52
1:B:704:PHE:CD1	1:B:716:ILE:HD13	2.43	0.52
1:A:650:TYR:O	1:A:725:LEU:HD12	2.10	0.51
1:C:712:MSE:SE	1:C:716:ILE:HD12	2.61	0.51
1:B:548:TRP:CZ3	1:B:630:LEU:HD23	2.47	0.50
1:A:582:ILE:HD11	1:A:604:TYR:HA	1.92	0.49
1:A:712:MSE:SE	1:A:716:ILE:CD1	3.10	0.49
1:A:741:GLU:O	1:A:745:GLN:HG2	2.12	0.49
1:A:772:LEU:HD23	1:A:773:MSE:HE2	1.94	0.49
1:C:712:MSE:HG2	1:C:773:MSE:HE3	1.94	0.49
1:A:657:ARG:HG2	1:A:658:ASN:ND2	2.27	0.48
1:A:647:MSE:HE3	1:A:653:ARG:HB3	1.95	0.48
1:A:657:ARG:HG2	1:A:658:ASN:CG	2.34	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:704:PHE:HD1	1:A:716:ILE:HD13	1.80	0.47
1:A:620:CYS:O	1:A:623:GLN:HB2	2.14	0.47
1:B:677:GLN:NE2	1:B:780:LYS:O	2.48	0.45
1:B:712:MSE:HE2	1:B:772:LEU:CD2	2.47	0.45
1:C:555:HIS:N	1:C:555:HIS:ND1	2.65	0.45
1:C:723:GLU:OE1	1:C:727:ILE:HD11	2.17	0.44
1:A:662:ASP:O	1:A:666:LYS:HG3	2.18	0.44
1:A:652:LEU:HD13	1:A:725:LEU:HD21	2.00	0.43
1:C:704:PHE:CD1	1:C:716:ILE:HD13	2.54	0.43
1:C:517:LEU:HD23	1:C:550:LEU:HD12	2.01	0.43
1:B:705:THR:HA	1:B:713:VAL:HG11	2.01	0.43
1:C:545:ALA:HB2	1:C:633:HIS:O	2.19	0.43
1:A:704:PHE:CD1	1:A:716:ILE:CD1	3.03	0.42
1:A:545:ALA:HB2	1:A:633:HIS:O	2.20	0.42
1:A:561:LEU:HD12	1:A:637:GLU:HG3	2.01	0.42
1:C:582:ILE:HD11	1:C:604:TYR:HA	2.02	0.42
1:A:534:LEU:HD23	1:A:534:LEU:HA	1.90	0.41
1:B:566:ILE:HG22	1:B:566:ILE:O	2.19	0.41
1:C:690:LEU:HD11	1:C:752:LEU:HD21	2.02	0.41
1:C:512:SER:HB3	1:C:534:LEU:HD11	2.01	0.41
1:A:705:THR:HA	1:A:713:VAL:HG11	2.02	0.41
1:C:619:TYR:CE1	1:C:623:GLN:HB3	2.56	0.41
1:B:625:PHE:O	1:B:629:VAL:HG23	2.21	0.41
1:B:640:PHE:O	1:B:644:VAL:HG23	2.22	0.40
1:A:759:LEU:HB3	1:A:760:PRO:HD3	2.04	0.40
1:B:655:LEU:O	1:B:660:PHE:HA	2.21	0.40
1:C:647:MSE:HE3	1:C:653:ARG:HB3	2.04	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	285/310 (92%)	278 (98%)	7 (2%)	0	100	100
1	B	252/310 (81%)	242 (96%)	10 (4%)	0	100	100
1	C	286/310 (92%)	280 (98%)	5 (2%)	1 (0%)	41	50
All	All	823/930 (88%)	800 (97%)	22 (3%)	1 (0%)	51	64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	657	ARG

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	229/266 (86%)	225 (98%)	4 (2%)	60	76
1	B	164/266 (62%)	162 (99%)	2 (1%)	71	84
1	C	227/266 (85%)	227 (100%)	0	100	100
All	All	620/798 (78%)	614 (99%)	6 (1%)	76	87

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	537	SER
1	A	572	SER
1	A	658	ASN
1	A	662	ASP
1	B	712	MSE
1	B	725	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 32 ligands modelled in this entry, 32 are unknown - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [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	279/310 (90%)	0.09	5 (1%) 68 74	28, 47, 67, 83	0
1	B	249/310 (80%)	0.69	36 (14%) 2 3	35, 68, 114, 157	0
1	C	280/310 (90%)	0.23	17 (6%) 21 27	30, 46, 68, 83	0
All	All	808/930 (86%)	0.32	58 (7%) 15 20	28, 50, 94, 157	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	564	TYR	7.7
1	B	648	TYR	6.3
1	B	590	ASP	5.5
1	B	569	THR	5.3
1	B	579	THR	4.9
1	B	573	ALA	4.7
1	B	607	CYS	4.7
1	B	591	TYR	4.3
1	B	568	ILE	4.3
1	B	540	PRO	4.2
1	C	555	HIS	4.0
1	C	532	SER	3.9
1	B	550	LEU	3.7
1	B	613	TYR	3.6
1	C	732	ALA	3.5
1	B	588	ALA	3.4
1	B	589	HIS	3.2
1	C	735	LEU	3.2
1	B	587	PRO	3.1
1	C	795	THR	3.1
1	B	539	VAL	3.1
1	C	596	GLY	2.9
1	C	736	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	611	SER	2.8
1	C	530	GLY	2.8
1	B	731	VAL	2.8
1	B	584	ARG	2.8
1	C	766	GLU	2.7
1	B	603	LEU	2.7
1	B	578	ILE	2.7
1	B	543	LEU	2.6
1	B	538	GLY	2.5
1	C	571	ASP	2.5
1	B	606	ILE	2.5
1	A	643	LEU	2.4
1	B	618	GLY	2.4
1	C	529	LYS	2.4
1	B	638	GLN	2.4
1	A	524	LEU	2.3
1	B	626	LEU	2.3
1	B	595	THR	2.3
1	B	597	GLY	2.3
1	A	765	ALA	2.3
1	C	595	THR	2.3
1	B	617	ILE	2.2
1	C	533	THR	2.2
1	B	586	PHE	2.2
1	C	717	ILE	2.2
1	A	583	HIS	2.1
1	B	716	ILE	2.1
1	C	588	ALA	2.1
1	B	687	ASP	2.1
1	C	675	GLN	2.1
1	B	625	PHE	2.1
1	B	756	ARG	2.1
1	B	565	ARG	2.0
1	A	734	ALA	2.0
1	C	607	CYS	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 monosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	UNX	A	905	1/1	-0.65	1.71	2,2,2,2	1
2	UNX	C	908	1/1	-0.56	2.71	2,2,2,2	1
2	UNX	C	3	1/1	-0.45	0.33	2,2,2,2	1
2	UNX	C	904	1/1	-0.28	2.03	2,2,2,2	1
2	UNX	A	4	1/1	-0.27	0.90	2,2,2,2	1
2	UNX	A	907	1/1	-0.22	3.61	2,2,2,2	1
2	UNX	B	908	1/1	-0.17	2.43	2,2,2,2	1
2	UNX	A	909	1/1	-0.07	2.59	2,2,2,2	1
2	UNX	C	907	1/1	-0.07	3.01	2,2,2,2	1
2	UNX	A	906	1/1	0.03	1.77	2,2,2,2	1
2	UNX	A	2	1/1	0.04	2.54	2,2,2,2	1
2	UNX	A	911	1/1	0.05	1.57	2,2,2,2	1
2	UNX	C	903	1/1	0.05	3.33	2,2,2,2	1
2	UNX	C	909	1/1	0.07	1.59	2,2,2,2	1
2	UNX	A	902	1/1	0.10	1.76	2,2,2,2	1
2	UNX	A	910	1/1	0.13	1.80	2,2,2,2	1
2	UNX	A	904	1/1	0.22	1.16	2,2,2,2	1
2	UNX	A	908	1/1	0.25	2.59	2,2,2,2	1
2	UNX	C	6	1/1	0.25	1.40	2,2,2,2	1
2	UNX	C	906	1/1	0.28	2.62	2,2,2,2	1
2	UNX	B	910	1/1	0.30	3.78	2,2,2,2	1
2	UNX	A	901	1/1	0.33	1.41	2,2,2,2	1
2	UNX	C	5	1/1	0.35	2.57	2,2,2,2	1
2	UNX	C	902	1/1	0.46	0.81	2,2,2,2	1
2	UNX	A	903	1/1	0.48	2.33	2,2,2,2	1
2	UNX	B	902	1/1	0.49	1.66	2,2,2,2	1
2	UNX	C	911	1/1	0.56	1.55	2,2,2,2	1
2	UNX	C	905	1/1	0.66	3.31	2,2,2,2	1
2	UNX	C	910	1/1	0.67	1.35	2,2,2,2	1
2	UNX	A	1	1/1	0.69	0.37	2,2,2,2	1
2	UNX	B	901	1/1	0.77	1.71	2,2,2,2	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	UNX	C	901	1/1	0.79	1.76	2,2,2,2	1

6.5 Other polymers [i](#)

There are no such residues in this entry.