



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 10:10 PM GMT

PDB ID : 5CM9  
Title : Structural Basis for the Selectivity of Guanine Nucleotide Exchange Factors for the small G-protein Ral  
Authors : Popovic, M.; Schouten, A.; Rehmann, H.  
Deposited on : 2015-07-16  
Resolution : 2.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : unknown  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026982  
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) : rb-20026982

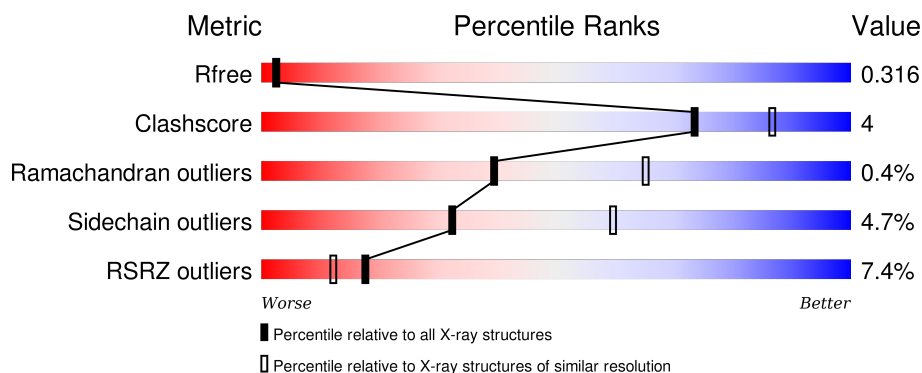
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	473	<div> <div>3%</div> <div>72%</div> <div>13%</div> <div>•</div> <div>14%</div> </div>
1	B	473	<div> <div>3%</div> <div>72%</div> <div>11%</div> <div>16%</div> </div>
2	C	203	<div> <div>13%</div> <div>61%</div> <div>9%</div> <div>•</div> <div>28%</div> </div>
2	D	203	<div> <div>13%</div> <div>67%</div> <div>6%</div> <div>26%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8619 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 Ral guanine nucleotide dissociation stimulator-like 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	405	Total	C	N	O	S	0	0	0
			3162	1994	572	587	9			
1	B	396	Total	C	N	O	S	0	0	0
			3093	1951	557	576	9			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	42	GLY	-	expression tag	UNP Q61193
A	43	PRO	-	expression tag	UNP Q61193
A	44	LEU	-	expression tag	UNP Q61193
A	45	GLY	-	expression tag	UNP Q61193
A	46	SER	-	expression tag	UNP Q61193
A	47	PRO	-	expression tag	UNP Q61193
A	48	ASN	-	expression tag	UNP Q61193
A	49	SER	-	expression tag	UNP Q61193
A	147	TYR	HIS	conflict	UNP Q61193
A	402	THR	MET	conflict	UNP Q61193
B	42	GLY	-	expression tag	UNP Q61193
B	43	PRO	-	expression tag	UNP Q61193
B	44	LEU	-	expression tag	UNP Q61193
B	45	GLY	-	expression tag	UNP Q61193
B	46	SER	-	expression tag	UNP Q61193
B	47	PRO	-	expression tag	UNP Q61193
B	48	ASN	-	expression tag	UNP Q61193
B	49	SER	-	expression tag	UNP Q61193
B	147	TYR	HIS	conflict	UNP Q61193
B	402	THR	MET	conflict	UNP Q61193

- Molecule 2 is a protein called Ras-related protein Ral-a.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	146	Total	C	N	O	S	0	0	0
			1144	725	196	217	6			
2	D	150	Total	C	N	O	S	0	0	0
			1184	747	201	230	6			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	GLY	-	expression tag	UNP P48555
C	0	SER	-	expression tag	UNP P48555
D	-1	GLY	-	expression tag	UNP P48555
D	0	SER	-	expression tag	UNP P48555

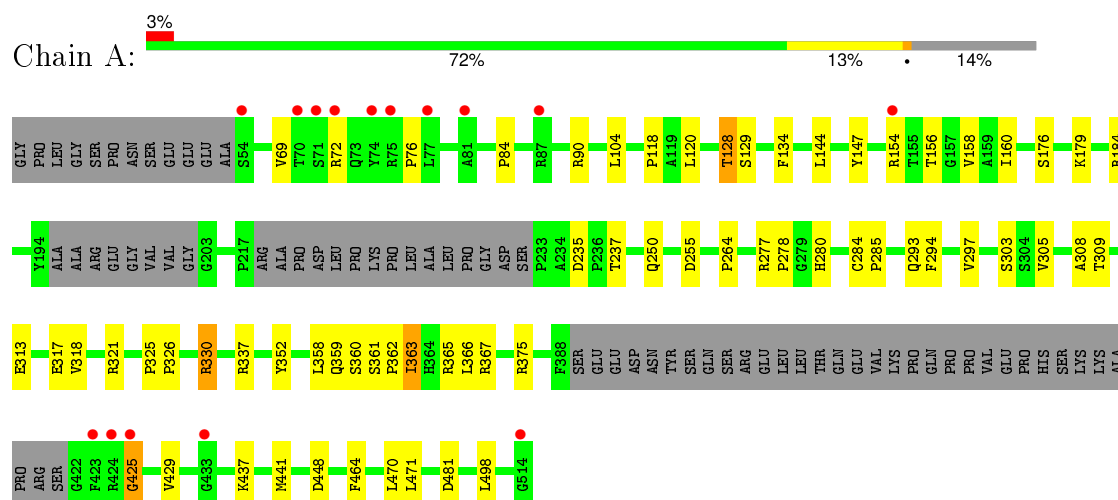
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	14	Total	O	0	0
			14	14		
3	B	16	Total	O	0	0
			16	16		
3	C	2	Total	O	0	0
			2	2		
3	D	4	Total	O	0	0
			4	4		

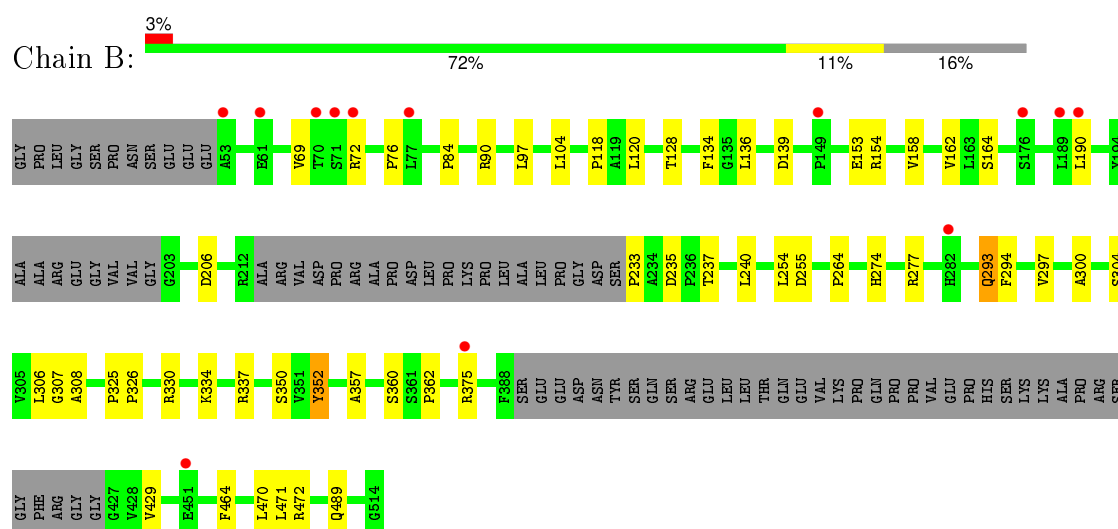
### 3 Residue-property plots [i](#)

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: Ral guanine nucleotide dissociation stimulator-like 2



- Molecule 1: Ral guanine nucleotide dissociation stimulator-like 2



- Molecule 2: Ras-related protein Ral-a





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	169.88Å 99.83Å 111.49Å 90.00° 127.00° 90.00°	Depositor
Resolution (Å)	46.63 – 2.60 46.63 – 2.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.63-2.60) 88.9 (46.63-2.60)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.98 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.273 , 0.320 0.269 , 0.316	Depositor DCC
$R_{free}$ test set	2038 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	49.5	Xtriage
Anisotropy	0.324	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 32.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	3 of 40751 reflections (0.007%)	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	8619	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	58.0	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 40.42 % 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 2.7419e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup> Intensities estimated from amplitudes.

<sup>2</sup> 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

### 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	0.34	0/3229	0.50	0/4384
1	B	0.33	0/3157	0.51	1/4288 (0.0%)
2	C	0.35	0/1160	0.45	0/1561
2	D	0.37	0/1200	0.46	0/1614
All	All	0.34	0/8746	0.49	1/11847 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	233	PRO	N-CA-CB	5.77	110.22	103.30

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	3162	0	3164	32	0
1	B	3093	0	3094	24	0
2	C	1144	0	1120	15	0
2	D	1184	0	1156	7	0
3	A	14	0	0	0	0
3	B	16	0	0	0	0
3	C	2	0	0	0	0
3	D	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	8619	0	8534	70	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 (70) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:119:PHE:HB3	2:C:148:VAL:HG11	1.67	0.75
1:A:425:GLY:HA3	1:A:481:ASP:H	1.53	0.72
1:B:104:LEU:HD11	1:B:162:VAL:HG11	1.73	0.70
1:B:97:LEU:HD22	1:B:128:THR:HG21	1.73	0.68
1:A:264:PRO:HB3	1:A:470:LEU:HD11	1.75	0.67
1:B:235:ASP:OD1	1:B:237:THR:HG22	1.95	0.67
1:A:128:THR:HG22	1:A:129:SER:H	1.63	0.62
1:B:254:LEU:HD11	1:B:489:GLN:HE22	1.64	0.62
2:C:117:ILE:HG13	2:C:118:PRO:HD2	1.82	0.62
1:B:264:PRO:HB3	1:B:470:LEU:HD11	1.83	0.61
1:A:264:PRO:HB3	1:A:470:LEU:CD1	2.31	0.60
2:D:117:ILE:HG13	2:D:118:PRO:HD2	1.83	0.59
1:A:235:ASP:OD1	1:A:237:THR:HG22	2.03	0.58
1:A:176:SER:HB2	1:A:179:LYS:HE2	1.85	0.57
2:D:101:THR:HB	2:D:142:ARG:HH21	1.70	0.57
1:B:97:LEU:CD2	1:B:128:THR:HG21	2.35	0.56
1:B:306:LEU:O	1:B:308:ALA:N	2.39	0.55
2:C:163:LYS:O	2:C:167:ASP:HB2	2.06	0.55
1:A:294:PHE:CZ	2:C:75:ILE:HD11	2.43	0.54
1:A:352:TYR:CE2	2:C:75:ILE:HD12	2.44	0.53
2:C:78:ASN:HD22	2:C:78:ASN:N	2.07	0.52
1:A:359:GLN:O	2:C:81:ARG:NH2	2.41	0.52
2:C:15:ILE:HD11	2:C:83:GLY:HA3	1.92	0.52
1:B:154:ARG:O	1:B:158:VAL:HG23	2.10	0.52
2:C:72:TYR:HB3	2:C:75:ILE:HG12	1.90	0.52
1:A:437:LYS:O	1:A:441:MET:HG3	2.10	0.51
1:B:300:ALA:O	1:B:304:SER:HB2	2.10	0.51
1:A:309:THR:O	1:A:318:VAL:HG23	2.10	0.51
1:A:305:VAL:HG11	1:A:363:ILE:HD12	1.92	0.51
1:B:118:PRO:HB2	1:B:464:PHE:CZ	2.46	0.51
1:A:255:ASP:HB3	1:A:429:VAL:HG11	1.94	0.49
1:A:425:GLY:CA	1:A:481:ASP:H	2.23	0.48
1:A:294:PHE:HZ	2:C:75:ILE:HD11	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:358:LEU:HD23	1:A:363:ILE:HD11	1.95	0.48
1:B:255:ASP:HB3	1:B:429:VAL:HG11	1.95	0.48
1:B:240:LEU:HA	1:B:334:LYS:HE2	1.95	0.47
2:D:162:ASP:O	2:D:166:PHE:HD1	1.98	0.47
1:A:352:TYR:CZ	2:C:75:ILE:HD12	2.50	0.47
1:A:69:VAL:HG22	1:A:90:ARG:HG3	1.97	0.47
1:A:118:PRO:HB2	1:A:464:PHE:CZ	2.50	0.46
1:A:76:PRO:HB3	1:A:84:PRO:HD3	1.97	0.46
2:C:15:ILE:CD1	2:C:83:GLY:HA3	2.45	0.46
1:A:284:CYS:N	1:A:285:PRO:HD3	2.30	0.46
1:B:352:TYR:CE2	2:D:75:ILE:HD12	2.51	0.45
1:A:325:PRO:HB2	1:A:326:PRO:HD3	1.98	0.45
1:B:357:ALA:O	1:B:360:SER:HB3	2.16	0.45
1:B:325:PRO:HB2	1:B:326:PRO:HD3	1.97	0.45
1:A:360:SER:OG	1:A:362:PRO:HD2	2.17	0.45
2:D:119:PHE:HD2	2:D:148:VAL:HG11	1.82	0.45
1:A:365:ARG:O	1:A:367:ARG:N	2.50	0.44
1:A:293:GLN:O	1:A:297:VAL:HG23	2.18	0.44
1:A:156:THR:O	1:A:160:ILE:HG12	2.17	0.44
1:B:69:VAL:HG22	1:B:90:ARG:HG3	2.00	0.43
1:B:255:ASP:OD2	1:B:350:SER:OG	2.31	0.43
1:A:308:ALA:HB3	1:A:498:LEU:HD11	2.01	0.43
2:C:134:VAL:HA	2:C:135:PRO:HD3	1.83	0.43
1:A:277:ARG:HB2	1:A:280:HIS:HD2	1.83	0.43
1:A:144:LEU:HA	1:A:147:TYR:CD1	2.54	0.43
1:A:361:SER:N	1:A:362:PRO:HD2	2.33	0.43
1:A:330:ARG:HA	1:A:330:ARG:HD3	1.92	0.43
1:B:76:PRO:HB3	1:B:84:PRO:HD3	2.00	0.42
2:C:75:ILE:HG22	2:C:79:TYR:HE1	1.84	0.42
1:B:136:LEU:HA	1:B:139:ASP:HB2	2.01	0.42
1:B:360:SER:OG	1:B:362:PRO:HD2	2.20	0.41
1:B:274:HIS:HB3	1:B:277:ARG:HD2	2.03	0.41
1:B:293:GLN:O	1:B:297:VAL:HG23	2.20	0.41
1:B:294:PHE:HZ	2:D:75:ILE:HD11	1.85	0.41
2:C:143:ALA:HB2	2:C:150:TYR:HB2	2.03	0.40
1:B:352:TYR:CZ	2:D:75:ILE:HD12	2.55	0.40
1:A:154:ARG:O	1:A:158:VAL:HG23	2.20	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	397/473 (84%)	386 (97%)	8 (2%)	3 (1%)	24	46
1	B	388/473 (82%)	378 (97%)	9 (2%)	1 (0%)	46	72
2	C	140/203 (69%)	135 (96%)	5 (4%)	0	100	100
2	D	144/203 (71%)	140 (97%)	4 (3%)	0	100	100
All	All	1069/1352 (79%)	1039 (97%)	26 (2%)	4 (0%)	39	65

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	307	GLY
1	A	366	LEU
1	A	425	GLY
1	A	278	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	342/399 (86%)	325 (95%)	17 (5%)	30	56
1	B	335/399 (84%)	321 (96%)	14 (4%)	36	65
2	C	122/178 (68%)	114 (93%)	8 (7%)	21	40
2	D	128/178 (72%)	123 (96%)	5 (4%)	39	68
All	All	927/1154 (80%)	883 (95%)	44 (5%)	32	59

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72	ARG
1	A	104	LEU
1	A	120	LEU
1	A	128	THR
1	A	134	PHE
1	A	184	ARG
1	A	250	GLN
1	A	303	SER
1	A	313	GLU
1	A	317	GLU
1	A	321	ARG
1	A	330	ARG
1	A	337	ARG
1	A	363	ILE
1	A	375	ARG
1	A	448	ASP
1	A	471	LEU
1	B	72	ARG
1	B	120	LEU
1	B	134	PHE
1	B	153	GLU
1	B	164	SER
1	B	190	LEU
1	B	206	ASP
1	B	293	GLN
1	B	330	ARG
1	B	337	ARG
1	B	352	TYR
1	B	375	ARG
1	B	471	LEU
1	B	472	ARG
2	C	17	VAL
2	C	62	ASP
2	C	65	ASP
2	C	78	ASN
2	C	81	ARG
2	C	101	THR
2	C	120	LEU
2	C	167	ASP
2	D	65	ASP
2	D	113	ASN
2	D	117	ILE

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Mol	Chain	Res	Type
2	D	120	LEU
2	D	168	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	280	HIS
1	A	293	GLN
1	A	359	GLN
1	B	489	GLN
2	C	124	ASN
2	D	113	ASN

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	405/473 (85%)	0.26	15 (3%) 45 37	28, 48, 73, 79	0
1	B	396/473 (83%)	0.30	13 (3%) 50 43	30, 51, 71, 81	0
2	C	146/203 (71%)	1.09	27 (18%) 2 1	52, 80, 94, 96	0
2	D	150/203 (73%)	1.04	26 (17%) 2 1	49, 78, 97, 98	0
All	All	1097/1352 (81%)	0.49	81 (7%) 17 12	28, 55, 86, 98	0

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	53	ALA	4.7
2	C	161	VAL	4.5
1	A	424	ARG	4.2
2	C	155	ALA	4.2
2	D	179	ASP	4.2
2	D	34	ASP	4.1
2	D	139	CYS	4.1
2	C	156	LYS	4.0
1	A	77	LEU	4.0
2	D	150	TYR	4.0
2	C	21	GLY	3.5
1	A	514	GLY	3.4
2	D	157	THR	3.4
2	D	148	VAL	3.4
2	C	150	TYR	3.2
2	D	122	VAL	3.2
2	C	33	TYR	3.1
2	D	115	GLU	3.1
1	A	425	GLY	3.1
2	C	113	ASN	3.1
2	C	157	THR	3.1

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Mol	Chain	Res	Type	RSRZ
2	C	167	ASP	3.1
1	B	451	GLU	3.1
2	D	33	TYR	3.0
1	B	282	HIS	3.0
2	D	141	LEU	2.9
2	C	144	GLN	2.9
2	D	143	ALA	2.8
2	C	148	VAL	2.8
2	D	161	VAL	2.8
2	C	142	ARG	2.8
1	B	72	ARG	2.7
2	D	53	VAL	2.7
2	D	121	LEU	2.6
1	A	423	PHE	2.6
2	C	55	ASP	2.5
2	D	93	THR	2.5
2	D	124	ASN	2.5
2	D	145	GLN	2.5
2	C	133	LYS	2.5
2	C	56	GLY	2.5
2	D	137	SER	2.5
2	D	133	LYS	2.4
1	B	77	LEU	2.4
2	D	154	SER	2.4
2	C	109	LEU	2.4
1	A	74	TYR	2.4
2	C	72	TYR	2.4
1	B	176	SER	2.4
1	B	71	SER	2.3
2	C	136	LEU	2.3
1	B	190	LEU	2.3
2	D	116	SER	2.3
1	B	61	GLU	2.3
2	C	146	TRP	2.3
1	A	433	GLY	2.3
1	A	54	SER	2.3
1	A	81	ALA	2.3
2	C	64	LEU	2.3
2	C	172	ILE	2.3
2	D	75	ILE	2.3
2	C	135	PRO	2.2
1	B	70	THR	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	75	ARG	2.2
2	C	30	GLN	2.2
2	C	58	GLU	2.2
1	B	189	LEU	2.2
2	D	152	GLU	2.2
2	D	178	GLU	2.2
1	A	70	THR	2.2
1	B	375	ARG	2.1
2	C	49	ARG	2.1
1	A	72	ARG	2.1
1	A	154	ARG	2.1
2	C	65	ASP	2.1
2	D	177	THR	2.1
2	D	64	LEU	2.1
1	A	71	SER	2.0
1	A	87	ARG	2.0
2	C	116	SER	2.0
1	B	149	PRO	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 carbohydrates 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.