



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:42 PM GMT

PDB ID : 4A9A
Title : Structure of Rbg1 in complex with Tma46 dfrp domain
Authors : Francis, S.M.; Gas, M.; Daugeron, M.; Seraphin, B.; Bravo, J.
Deposited on : 2011-11-25
Resolution : 2.67 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

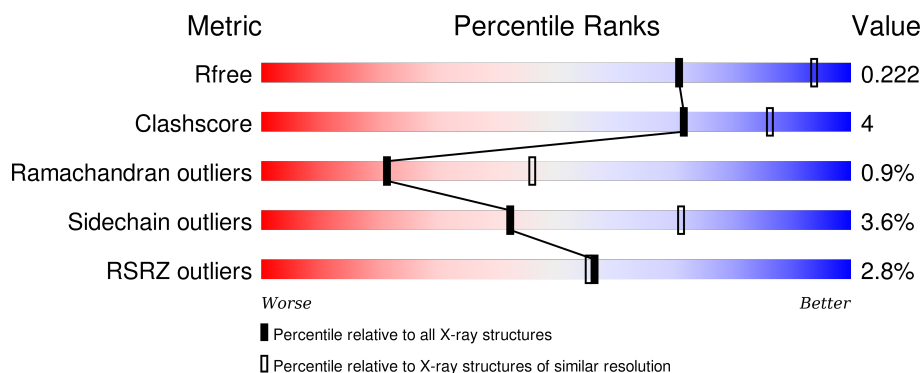
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.67 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	2780 (2.70-2.66)
Clashscore	102246	3138 (2.70-2.66)
Ramachandran outliers	100387	3089 (2.70-2.66)
Sidechain outliers	100360	3089 (2.70-2.66)
RSRZ outliers	91569	2789 (2.70-2.66)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	376	<div> <div>0%</div> <div>81% 13% • 5%</div> </div>
1	B	376	<div> <div>2%</div> <div>82% 11% • 6%</div> </div>
2	C	142	<div> <div>3%</div> <div>68% 7% 25%</div> </div>
2	D	142	<div> <div>5%</div> <div>52% 8% 39%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7107 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 RIBOSOME-INTERACTING GTPASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	356	Total	C	N	O	S	0	0	0
			2776	1764	480	523	9			
1	B	355	Total	C	N	O	S	0	0	0
			2738	1736	476	517	9			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	MET	-	EXPRESSION TAG	UNP P39729
A	-5	HIS	-	EXPRESSION TAG	UNP P39729
A	-4	HIS	-	EXPRESSION TAG	UNP P39729
A	-3	HIS	-	EXPRESSION TAG	UNP P39729
A	-2	HIS	-	EXPRESSION TAG	UNP P39729
A	-1	HIS	-	EXPRESSION TAG	UNP P39729
A	0	HIS	-	EXPRESSION TAG	UNP P39729
B	-6	MET	-	EXPRESSION TAG	UNP P39729
B	-5	HIS	-	EXPRESSION TAG	UNP P39729
B	-4	HIS	-	EXPRESSION TAG	UNP P39729
B	-3	HIS	-	EXPRESSION TAG	UNP P39729
B	-2	HIS	-	EXPRESSION TAG	UNP P39729
B	-1	HIS	-	EXPRESSION TAG	UNP P39729
B	0	HIS	-	EXPRESSION TAG	UNP P39729

- Molecule 2 is a protein called TRANSLATION MACHINERY-ASSOCIATED PROTEIN 46.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	106	Total	C	N	O	S	0	0	0
			844	536	145	162	1			
2	D	86	Total	C	N	O	S	0	0	0
			672	427	117	127	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	204	MET	-	EXPRESSION TAG	UNP Q12000
D	204	MET	-	EXPRESSION TAG	UNP Q12000

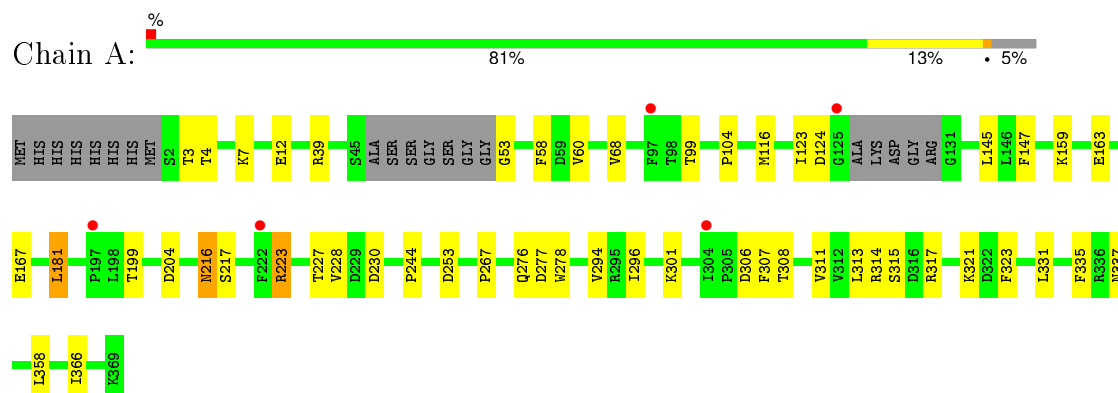
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	36	Total 36	O 36	0	0
3	B	24	Total 24	O 24	0	0
3	C	13	Total 13	O 13	0	0
3	D	4	Total 4	O 4	0	0

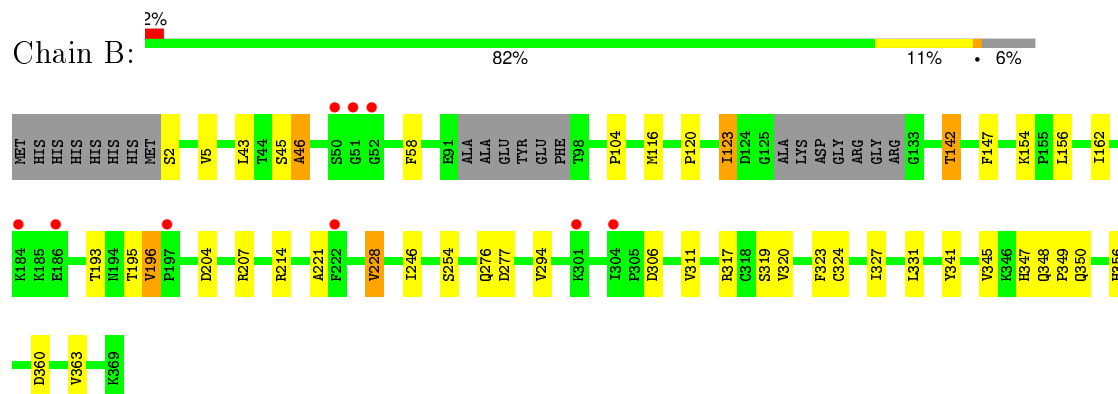
3 Residue-property plots [i](#)

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.

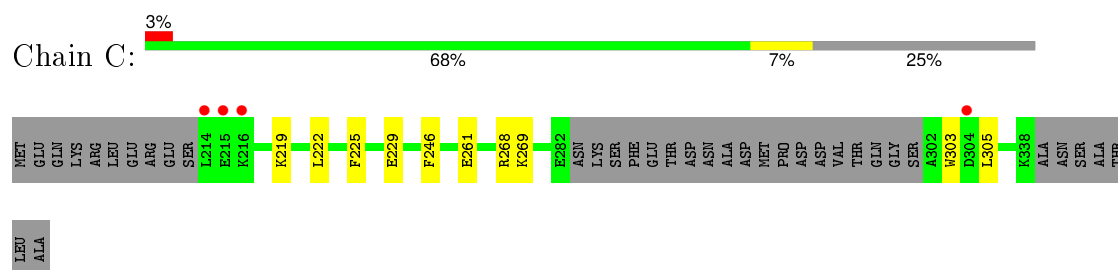
• Molecule 1: RIBOSOME-INTERACTING GTPASE 1



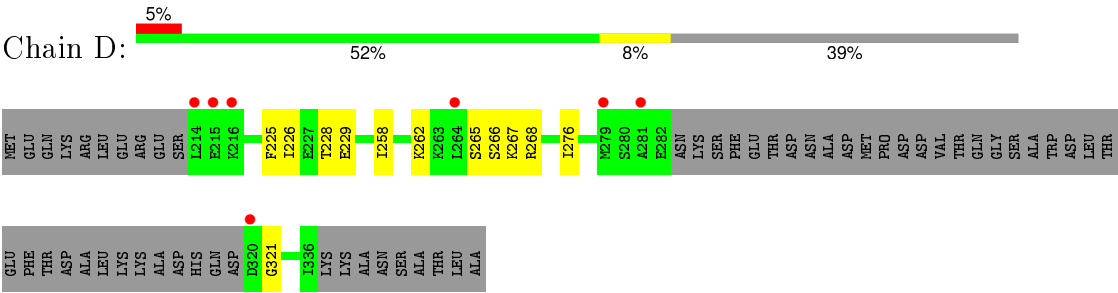
• Molecule 1: RIBOSOME-INTERACTING GTPASE 1



• Molecule 2: TRANSLATION MACHINERY-ASSOCIATED PROTEIN 46



• Molecule 2: TRANSLATION MACHINERY-ASSOCIATED PROTEIN 46



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	86.20Å 224.89Å 84.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	56.22 – 2.67 56.22 – 2.67	Depositor EDS
% Data completeness (in resolution range)	100.0 (56.22-2.67) 100.0 (56.22-2.67)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.68 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.196 , 0.222 0.196 , 0.222	Depositor DCC
R_{free} test set	1200 reflections (2.58%)	DCC
Wilson B-factor (Å ²)	65.8	Xtriage
Anisotropy	0.020	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 43.1	EDS
Estimated twinning fraction	0.025 for l,-k,h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 47658 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7107	wwPDB-VP
Average B, all atoms (Å ²)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.94% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.47	0/2817	0.62	0/3807
1	B	0.45	0/2777	0.60	0/3751
2	C	0.51	1/857 (0.1%)	0.62	0/1146
2	D	0.47	0/681	0.60	0/909
All	All	0.47	1/7132 (0.0%)	0.61	0/9613

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	303	TRP	CD2-CE2	5.03	1.47	1.41

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	2776	0	2869	32	0
1	B	2738	0	2826	23	0
2	C	844	0	865	6	0
2	D	672	0	695	4	0
3	A	36	0	0	0	0
3	B	24	0	0	1	0
3	C	13	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	7107	0	7255	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 4.

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:D:258:ILE:O	2:D:262:LYS:HG2	1.80	0.82
1:B:58:PHE:HB2	1:B:142:THR:HG21	1.64	0.80
1:B:58:PHE:HB2	1:B:142:THR:CG2	2.11	0.80
1:A:68:VAL:HG11	1:A:147:PHE:HE2	1.54	0.73
1:B:147:PHE:HE1	1:B:246:ILE:HD12	1.55	0.69
2:D:225:PHE:HA	2:D:229:GLU:HB2	1.74	0.69
1:B:347:HIS:HB2	1:B:350:GLN:HG2	1.76	0.67
1:B:104:PRO:HD2	1:B:116:MET:O	1.97	0.63
1:A:163:GLU:O	1:A:167:GLU:HG2	2.00	0.62
1:A:104:PRO:HD2	1:A:116:MET:O	1.99	0.61
1:A:181:LEU:HD23	1:A:223:ARG:HH22	1.65	0.60
1:B:123:ILE:HG21	1:B:162:ILE:HG12	1.84	0.60
1:A:68:VAL:CG1	1:A:147:PHE:HE2	2.14	0.60
1:B:193:THR:HB	1:B:221:ALA:HA	1.84	0.59
1:A:216:ASN:HD22	1:A:216:ASN:C	2.06	0.59
2:C:261:GLU:OE2	2:C:268:ARG:NH2	2.35	0.59
1:A:335:PHE:CZ	1:A:337:ASN:HA	2.38	0.58
1:B:323:PHE:CE2	1:B:327:ILE:HD11	2.38	0.58
1:B:58:PHE:HB2	1:B:142:THR:HG23	1.85	0.56
1:A:294:VAL:HG23	1:A:296:ILE:HD12	1.87	0.55
1:B:228:VAL:HG13	3:B:2015:HOH:O	2.07	0.55
1:A:311:VAL:HG21	1:A:323:PHE:CD1	2.42	0.54
1:A:335:PHE:CE2	1:A:337:ASN:HA	2.45	0.52
1:A:68:VAL:CG1	1:A:147:PHE:CE2	2.93	0.51
1:B:195:THR:O	1:B:196:VAL:HB	2.11	0.51
1:A:216:ASN:HD22	1:A:217:SER:HB2	1.77	0.50
1:A:227:THR:HG22	1:A:230:ASP:CG	2.34	0.49
2:C:225:PHE:HA	2:C:229:GLU:HB2	1.95	0.48
1:A:296:ILE:HG12	1:A:358:LEU:HD13	1.96	0.48
1:B:341:TYR:HB2	1:B:363:VAL:HB	1.95	0.48
1:A:159:LYS:HD3	2:C:222:LEU:HD23	1.97	0.47
1:A:216:ASN:ND2	1:A:216:ASN:C	2.69	0.46
1:A:306:ASP:C	1:A:308:THR:H	2.19	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:VAL:HG23	1:A:296:ILE:CD1	2.45	0.46
1:B:324:CYS:HB3	1:B:331:LEU:HB3	1.96	0.46
1:B:147:PHE:CE1	1:B:246:ILE:HD12	2.45	0.46
2:C:268:ARG:HG3	2:C:269:LYS:O	2.17	0.46
1:B:156:LEU:HD13	2:D:226:ILE:HG13	1.98	0.45
1:B:276:GLN:O	1:B:277:ASP:HB2	2.17	0.45
1:A:12:GLU:OE2	1:A:39:ARG:NH2	2.50	0.44
1:A:314:ARG:HH12	1:A:317:ARG:HH11	1.64	0.44
1:B:294:VAL:HG23	1:B:360:ASP:HA	2.00	0.44
2:D:267:LYS:HA	2:D:267:LYS:HE2	2.00	0.44
1:A:3:THR:O	1:A:7:LYS:HG3	2.18	0.44
1:B:320:VAL:O	1:B:323:PHE:HB3	2.17	0.44
1:A:253:ASP:OD1	1:A:253:ASP:N	2.50	0.43
1:A:53:GLY:HA2	1:A:58:PHE:CD1	2.54	0.43
1:A:123:ILE:O	1:A:124:ASP:OD1	2.36	0.42
1:A:296:ILE:HD13	1:A:313:LEU:HD12	2.02	0.42
1:B:2:SER:O	1:B:5:VAL:HG12	2.20	0.42
1:A:276:GLN:O	1:A:277:ASP:HB2	2.20	0.42
1:A:278:TRP:HB3	2:C:246:PHE:CZ	2.55	0.41
1:A:323:PHE:CE2	1:A:366:ILE:HD11	2.56	0.41
1:B:45:SER:N	1:B:46:ALA:CA	2.84	0.41
1:A:267:PRO:HD3	2:C:219:LYS:HG2	2.03	0.41
1:A:216:ASN:ND2	1:A:217:SER:HB2	2.35	0.41
1:B:348:GLN:HA	1:B:349:PRO:HA	1.84	0.41
1:A:145:LEU:HD12	1:A:244:PRO:HB2	2.01	0.40
1:A:311:VAL:HG21	1:A:323:PHE:HD1	1.83	0.40
1:B:43:LEU:C	1:B:45:SER:H	2.25	0.40
1:B:319:SER:HA	1:B:356:HIS:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	350/376 (93%)	337 (96%)	12 (3%)	1 (0%)	46	73
1	B	349/376 (93%)	331 (95%)	14 (4%)	4 (1%)	17	40
2	C	102/142 (72%)	97 (95%)	5 (5%)	0	100	100
2	D	82/142 (58%)	76 (93%)	3 (4%)	3 (4%)	4	8
All	All	883/1036 (85%)	841 (95%)	34 (4%)	8 (1%)	21	46

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	46	ALA
1	B	120	PRO
1	B	204	ASP
2	D	265	SER
1	A	307	PHE
1	B	196	VAL
2	D	266	SER
2	D	321	GLY

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	310/325 (95%)	297 (96%)	13 (4%)	36	65
1	B	305/325 (94%)	294 (96%)	11 (4%)	42	71
2	C	91/123 (74%)	90 (99%)	1 (1%)	80	94
2	D	72/123 (58%)	69 (96%)	3 (4%)	36	65
All	All	778/896 (87%)	750 (96%)	28 (4%)	42	71

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	THR
1	A	60	VAL
1	A	99	THR

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Mol	Chain	Res	Type
1	A	181	LEU
1	A	199	THR
1	A	204	ASP
1	A	216	ASN
1	A	223	ARG
1	A	228	VAL
1	A	301	LYS
1	A	315	SER
1	A	321	LYS
1	A	331	LEU
1	B	123	ILE
1	B	142	THR
1	B	154	LYS
1	B	207	ARG
1	B	214	ARG
1	B	228	VAL
1	B	254	SER
1	B	306	ASP
1	B	311	VAL
1	B	317	ARG
1	B	345	VAL
2	C	305	LEU
2	D	228	THR
2	D	268	ARG
2	D	276	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	158	HIS
1	A	203	ASN
1	A	216	ASN
1	A	325	ASN
1	A	350	GLN
1	B	194	ASN
1	B	325	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	356/376 (94%)	0.28	5 (1%) 78 77	35, 65, 121, 173	0
1	B	355/376 (94%)	0.09	9 (2%) 61 59	42, 71, 127, 186	0
2	C	106/142 (74%)	0.17	4 (3%) 44 43	39, 75, 132, 193	0
2	D	86/142 (60%)	0.55	7 (8%) 15 12	53, 94, 169, 193	0
All	All	903/1036 (87%)	0.22	25 (2%) 56 55	35, 71, 132, 193	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	214	LEU	6.3
2	D	216	LYS	5.9
2	C	215	GLU	4.9
1	B	197	PRO	4.1
1	B	52	GLY	4.0
1	B	50	SER	3.9
2	D	215	GLU	3.8
1	B	304	ILE	3.8
2	C	304	ASP	3.6
2	D	320	ASP	3.2
2	D	264	LEU	3.2
2	C	216	LYS	3.0
1	B	51	GLY	3.0
1	B	184	LYS	2.8
2	D	214	LEU	2.8
1	A	97	PHE	2.8
1	A	222	PHE	2.7
2	D	279	MET	2.5
1	B	301	LYS	2.4
1	A	125	GLY	2.2
1	A	197	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
2	D	281	ALA	2.1
1	B	222	PHE	2.1
1	B	186	GLU	2.1
1	A	304	ILE	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.