



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:28 PM UTC

PDB ID : 7FMP / pdb_00007fmp
Title : PanDDA analysis group deposition – Aar2/RNaseH in complex with fragment P06E01 from the F2X-Universal Library
Authors : Barthel, T.; Wollenhaupt, J.; Lima, G.M.A.; Wahl, M.C.; Weiss, M.S.
Deposited on : 2022-08-26
Resolution : 1.72 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
Mogul : 2022.3.0, CSD as543be (2022)
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

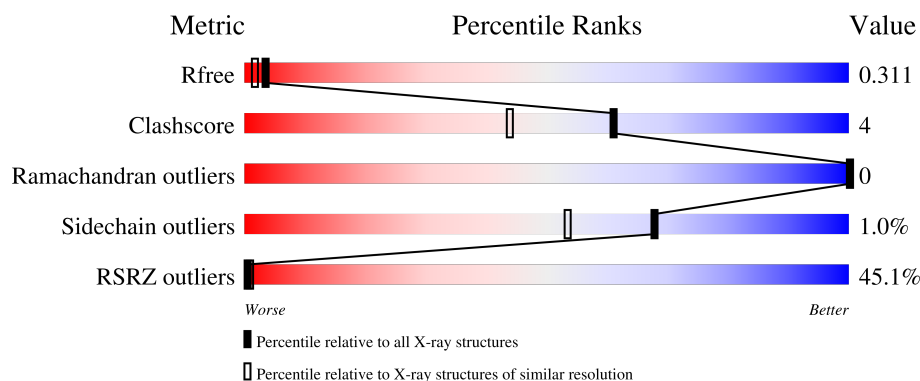
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.72 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	1039 (1.72-1.72)
Clashscore	190562	1049 (1.72-1.72)
Ramachandran outliers	187476	1041 (1.72-1.72)
Sidechain outliers	187428	1041 (1.72-1.72)
RSRZ outliers	180081	1039 (1.72-1.72)

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	258	42% 83% 9% 8%
2	B	308	43% 86% 11% .

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
3	VSQ	B	401	-	X	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9210 atoms, of which 4524 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 Pre-mRNA-splicing factor 8.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	237	4068	1287	2060	336	373	12	18	21	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1833	GLY	-	expression tag	UNP P33334
A	1834	ALA	-	expression tag	UNP P33334
A	1835	MET	-	expression tag	UNP P33334

- Molecule 2 is a protein called A1 cistron-splicing factor AAR2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
2	B	300	5044	1654	2464	421	485	20	0	17	0

There are 20 discrepancies between the modelled and reference sequences:

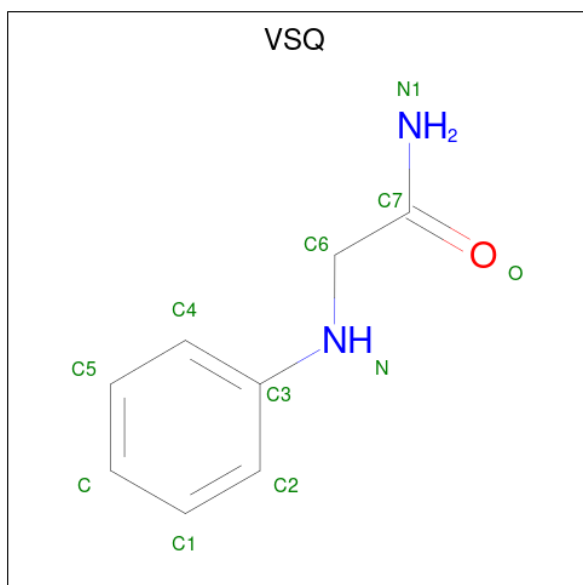
Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	expression tag	UNP P32357
B	-2	ALA	-	expression tag	UNP P32357
B	-1	MET	-	expression tag	UNP P32357
B	0	ALA	-	expression tag	UNP P32357
B	166	SER	LEU	conflict	UNP P32357
B	167	SER	LYS	conflict	UNP P32357
B	?	-	LEU	deletion	UNP P32357
B	?	-	GLN	deletion	UNP P32357
B	?	-	LYS	deletion	UNP P32357
B	?	-	ALA	deletion	UNP P32357
B	?	-	GLY	deletion	UNP P32357
B	?	-	SER	deletion	UNP P32357
B	?	-	LYS	deletion	UNP P32357

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	MET	deletion	UNP P32357
B	?	-	GLU	deletion	UNP P32357
B	?	-	ALA	deletion	UNP P32357
B	?	-	LYS	deletion	UNP P32357
B	?	-	ASN	deletion	UNP P32357
B	?	-	GLU	deletion	UNP P32357
B	170	SER	ASP	conflict	UNP P32357

- Molecule 3 is N 2 -phenylglycinamide (CCD ID: VSQ) (formula: $C_8H_{10}N_2O$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			11	8	2	1		

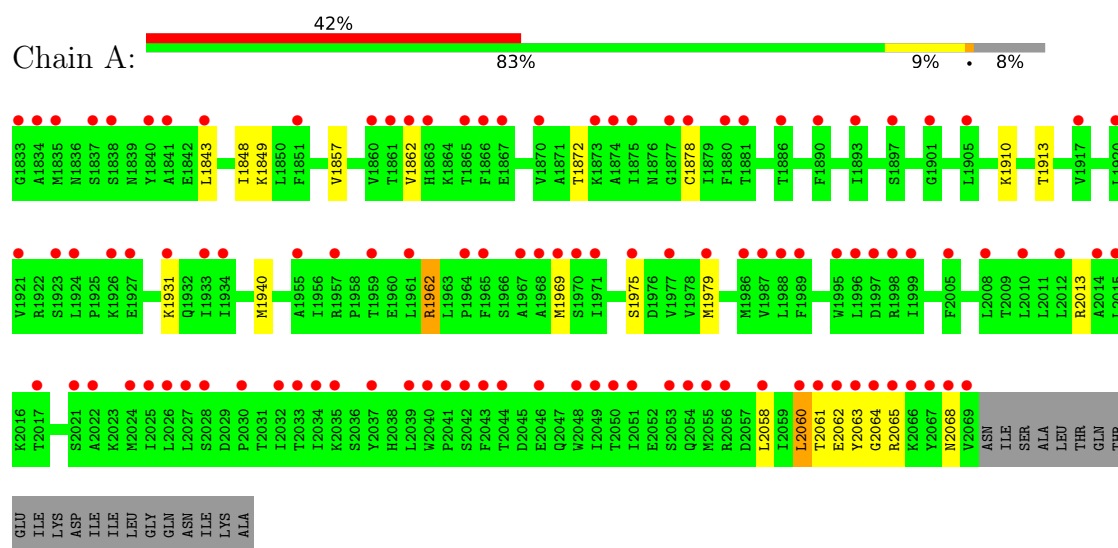
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	37	Total	O	0	0
			37	37		
4	B	50	Total	O	0	0
			50	50		

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: Pre-mRNA-splicing factor 8



• Molecule 2: A1 cistron-splicing factor AAR2



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	87.63Å 81.65Å 93.14Å 90.00° 108.26° 90.00°	Depositor
Resolution (Å)	44.22 – 1.72 44.22 – 1.72	Depositor EDS
% Data completeness (in resolution range)	99.5 (44.22-1.72) 99.9 (44.22-1.72)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.01 (at 1.72Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.263 , 0.310 0.267 , 0.311	Depositor DCC
R_{free} test set	2100 reflections (3.17%)	wwPDB-VP
Wilson B-factor (Å ²)	38.6	Xtriage
Anisotropy	0.373	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 41.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9210	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.58% 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](#)

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

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	0.63	0/2149	0.74	0/2911
2	B	0.70	2/2739 (0.1%)	0.88	4/3699 (0.1%)
All	All	0.67	2/4888 (0.0%)	0.82	4/6610 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	5	PRO	C-O	-6.32	1.16	1.23
2	B	6	PHE	C-O	-5.48	1.17	1.24

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	6	PHE	CA-C-N	6.92	129.55	120.28
2	B	6	PHE	C-N-CA	6.92	129.55	120.28
2	B	6	PHE	CA-CB-CG	6.21	120.01	113.80
2	B	6	PHE	CA-C-O	-6.05	113.82	120.36

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	2008	2060	1974	15	0
2	B	2580	2464	2398	23	0
3	B	11	0	0	0	0
4	A	37	0	0	0	0
4	B	50	0	0	2	0
All	All	4686	4524	4372	38	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 (38) 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:1962:ARG:O	1:A:2013:ARG:NH1	2.15	0.78
1:A:2061:THR:O	1:A:2064:GLY:N	2.19	0.76
2:B:230[B]:ASN:ND2	2:B:239:SER:OG	2.27	0.67
2:B:287:ARG:O	2:B:291:ILE:HD13	1.96	0.66
2:B:50:ASP:OD1	2:B:51:ASN:N	2.32	0.62
1:A:2064:GLY:O	1:A:2068:ASN:N	2.33	0.60
2:B:4:VAL:HG11	2:B:44[B]:ILE:CD1	2.32	0.59
1:A:2062:GLU:OE1	1:A:2065:ARG:NH1	2.38	0.56
1:A:1878:CYS:SG	1:A:1969:MET:HE3	2.47	0.54
1:A:1843:LEU:HA	1:A:1849:LYS:HD2	1.90	0.54
2:B:258:LYS:HD2	2:B:258:LYS:H	1.72	0.53
1:A:1848:ILE:H	1:A:1931[A]:LYS:HZ2	1.57	0.53
2:B:96:PHE:CB	2:B:102:MET:HE3	2.39	0.53
1:A:1975:SER:O	1:A:1979[A]:MET:SD	2.67	0.53
2:B:1:MET:HB3	2:B:35:ASP:HA	1.91	0.52
2:B:1:MET:N	4:B:505:HOH:O	2.44	0.51
1:A:1862:VAL:HG22	1:A:1872:THR:HG22	1.92	0.50
1:A:2060:LEU:O	1:A:2063:TYR:HB3	2.14	0.48
2:B:77:LEU:HD21	2:B:79:LYS:HE3	1.97	0.46
1:A:1962:ARG:HD3	1:A:1962:ARG:H	1.82	0.45
2:B:69:ILE:HD13	2:B:80:MET:HA	1.99	0.44
2:B:54[B]:MET:HE1	2:B:143:SER:HB3	2.00	0.44
1:A:2063:TYR:CD1	1:A:2063:TYR:C	2.96	0.44
2:B:37:PRO:HD3	2:B:105:TYR:CD1	2.53	0.44
2:B:60:PHE:CD1	2:B:80:MET:HE1	2.53	0.43
2:B:96:PHE:CD2	2:B:102:MET:HE3	2.53	0.43
2:B:277:GLU:H	2:B:277:GLU:CD	2.25	0.43
1:A:1910:LYS:O	1:A:1940:MET:HE1	2.18	0.43
2:B:96:PHE:HB2	2:B:102:MET:HE3	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:4:VAL:HG11	2:B:44[B]:ILE:HD13	1.99	0.43
1:A:2058:LEU:C	1:A:2058:LEU:HD23	2.44	0.42
1:A:1857:VAL:HG21	1:A:1913:THR:OG1	2.19	0.42
2:B:41[A]:VAL:HG12	4:B:529:HOH:O	2.20	0.41
2:B:12:GLU:HG3	2:B:25:LYS:HA	2.03	0.41
2:B:315:GLU:CD	2:B:315:GLU:H	2.27	0.41
2:B:256:VAL:O	2:B:257:PRO:C	2.62	0.40
2:B:51:ASN:OD1	2:B:53:SER:HB2	2.21	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	258/258 (100%)	250 (97%)	8 (3%)	0	100	100
2	B	315/308 (102%)	302 (96%)	13 (4%)	0	100	100
All	All	573/566 (101%)	552 (96%)	21 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	237/233 (102%)	235 (99%)	2 (1%)	73	61

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	294/284 (104%)	290 (99%)	4 (1%)	59	40
All	All	531/517 (103%)	525 (99%)	6 (1%)	68	50

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

Mol	Chain	Res	Type
1	A	1962	ARG
1	A	2060	LEU
2	B	45[A]	HIS
2	B	45[B]	HIS
2	B	281	ASP
2	B	315	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1863	HIS
2	B	2	ASN
2	B	40	HIS
2	B	259	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	VSQ	B	401	-	11,11,11	2.54	7 (63%)	13,13,13	3.07	4 (30%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	VSQ	B	401	-	-	3/5/5/5	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	401	VSQ	C6-N	-3.76	1.39	1.45
3	B	401	VSQ	C4-C3	3.61	1.45	1.39
3	B	401	VSQ	C3-N	-3.21	1.29	1.38
3	B	401	VSQ	C2-C3	-3.00	1.34	1.39
3	B	401	VSQ	C1-C2	2.97	1.44	1.38
3	B	401	VSQ	O-C7	-2.94	1.14	1.23
3	B	401	VSQ	C-C5	-2.12	1.33	1.38

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	401	VSQ	C7-C6-N	-6.04	99.21	114.44
3	B	401	VSQ	C-C1-C2	5.97	127.61	120.24
3	B	401	VSQ	C1-C2-C3	-5.75	113.10	119.73
3	B	401	VSQ	C6-N-C3	-2.82	116.96	122.42

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	401	VSQ	N-C6-C7-N1
3	B	401	VSQ	N-C6-C7-O
3	B	401	VSQ	C7-C6-N-C3

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	237/258 (91%)	2.10	109 (45%) 0 1	25, 63, 123, 184	12 (5%)
2	B	300/308 (97%)	2.00	133 (44%) 0 1	20, 63, 119, 187	9 (3%)
All	All	537/566 (94%)	2.04	242 (45%) 0 1	20, 63, 120, 187	21 (3%)

All (242) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1979[A]	MET	8.5
1	A	2069	VAL	7.8
1	A	2060	LEU	7.6
1	A	1878	CYS	7.0
2	B	282	ILE	6.9
1	A	1988	LEU	6.9
1	A	2061	THR	6.6
2	B	152	LEU	6.5
1	A	2063	TYR	6.4
1	A	1860	VAL	6.3
2	B	29	PRO	6.2
2	B	275	LEU	6.2
2	B	132	LYS	5.7
2	B	316	LEU	5.4
1	A	1927	GLU	5.4
2	B	54[A]	MET	5.4
1	A	1870	VAL	5.1
2	B	101	MET	5.1
2	B	170	SER	5.0
2	B	1	MET	4.8
2	B	308	ILE	4.8
1	A	2064	GLY	4.7
1	A	1873	LYS	4.7
1	A	1998	ARG	4.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	2017[A]	THR	4.7
1	A	2067	TYR	4.5
2	B	10	PRO	4.5
1	A	2065	ARG	4.4
1	A	2026	LEU	4.3
2	B	106	PRO	4.3
1	A	2068	ASN	4.3
2	B	93	VAL	4.3
1	A	1840	TYR	4.2
2	B	172	PRO	4.2
2	B	276	PRO	4.2
2	B	313	TYR	4.1
2	B	49	ALA	4.1
1	A	1967	ALA	4.0
2	B	174	HIS	4.0
2	B	261	LEU	3.9
2	B	279	TYR	3.9
2	B	89	PHE	3.9
1	A	2005	PHE	3.9
2	B	289	TRP	3.9
2	B	30	PHE	3.8
2	B	221	PHE	3.8
2	B	122[A]	GLN	3.8
2	B	126	ILE	3.8
1	A	1833	GLY	3.8
2	B	117	LEU	3.8
1	A	2025	ILE	3.8
2	B	280	SER	3.8
2	B	24	VAL	3.7
2	B	147	VAL	3.7
1	A	2048	TRP	3.7
2	B	294	TYR	3.7
1	A	2035	LYS	3.7
2	B	301	SER	3.7
1	A	2024[A]	MET	3.6
1	A	1834	ALA	3.6
1	A	2027	LEU	3.6
1	A	1890	PHE	3.5
1	A	1861	THR	3.5
2	B	11	ILE	3.5
2	B	297	PHE	3.5
2	B	7	THR	3.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	B	281	ASP	3.4
2	B	107	LYS	3.4
2	B	203[A]	TYR	3.4
2	B	283	LEU	3.4
1	A	1975	SER	3.4
2	B	53	SER	3.4
1	A	1931[A]	LYS	3.4
2	B	284	LEU	3.4
2	B	317	LEU	3.4
1	A	1999	ILE	3.3
2	B	108	ILE	3.3
1	A	2058	LEU	3.3
2	B	214	PHE	3.3
1	A	2040	TRP	3.3
1	A	1971	ILE	3.3
1	A	1920	LEU	3.3
1	A	2021	SER	3.2
1	A	2056[A]	ARG	3.2
1	A	1841	ALA	3.2
1	A	1881	THR	3.2
2	B	3	THR	3.2
1	A	1867	GLU	3.2
1	A	2015	LEU	3.2
1	A	1995	TRP	3.2
1	A	2032	ILE	3.1
2	B	22	PHE	3.1
2	B	198	PHE	3.1
1	A	1886	THR	3.1
1	A	2039	LEU	3.1
1	A	1866	PHE	3.1
2	B	111	ASP	3.1
1	A	2012	LEU	3.1
2	B	256	VAL	3.0
2	B	173	ALA	3.0
1	A	1989	PHE	3.0
2	B	220	TYR	3.0
1	A	2054[A]	GLN	3.0
2	B	103	VAL	3.0
2	B	31	HIS	3.0
1	A	1969	MET	2.9
1	A	2037	TYR	2.9
2	B	293	LEU	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	B	96	PHE	2.9
2	B	226	PHE	2.9
1	A	1986	MET	2.9
1	A	2055	MET	2.9
2	B	94	HIS	2.9
2	B	272	ILE	2.9
1	A	1965	PHE	2.9
2	B	288	VAL	2.9
2	B	84	ARG	2.9
1	A	1893	ILE	2.9
2	B	291	ILE	2.9
2	B	38	ILE	2.8
2	B	181	ILE	2.8
2	B	23	ASN	2.8
2	B	258	LYS	2.8
2	B	87	ALA	2.8
1	A	1863	HIS	2.8
2	B	302	LEU	2.8
1	A	1933	ILE	2.8
2	B	287	ARG	2.8
2	B	136	GLN	2.8
1	A	1835	MET	2.8
2	B	146	THR	2.8
2	B	109	ASP	2.8
2	B	199	LEU	2.8
1	A	1959	THR	2.8
1	A	1901	GLY	2.8
2	B	91	ASN	2.7
1	A	1997	ASP	2.7
1	A	1874	ALA	2.7
2	B	245	ALA	2.7
2	B	120	PHE	2.7
1	A	2033	THR	2.7
2	B	177[A]	ASN	2.7
1	A	1880	PHE	2.7
2	B	110	GLU	2.7
1	A	1837	SER	2.7
1	A	2028	SER	2.7
1	A	1924	LEU	2.7
2	B	145	THR	2.7
2	B	312	LYS	2.7
2	B	48	HIS	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	1851	PHE	2.6
1	A	1926	LYS	2.6
2	B	130	VAL	2.6
2	B	269	TYR	2.6
2	B	295	SER	2.6
1	A	1996	LEU	2.6
1	A	2010	LEU	2.6
2	B	262	ASP	2.6
2	B	277	GLU	2.6
1	A	1955	ALA	2.6
2	B	52	SER	2.6
2	B	39	GLY	2.6
1	A	1843	LEU	2.6
1	A	1917	VAL	2.6
2	B	4	VAL	2.6
1	A	2066	LYS	2.5
2	B	80	MET	2.5
2	B	58	TYR	2.5
1	A	1862	VAL	2.5
1	A	2049	ILE	2.5
1	A	2044	THR	2.5
2	B	299	LYS	2.5
1	A	2046	GLU	2.5
1	A	1961[A]	LEU	2.5
2	B	56	TYR	2.5
2	B	140	VAL	2.5
1	A	1875	ILE	2.5
2	B	270	TYR	2.5
2	B	92	ILE	2.5
1	A	1897	SER	2.5
1	A	1970	SER	2.5
1	A	1934	ILE	2.4
1	A	1987	VAL	2.4
2	B	290	ASN	2.4
2	B	300	ASN	2.4
2	B	50	ASP	2.4
2	B	133	ASP	2.4
2	B	127	ARG	2.4
2	B	131	ARG	2.3
1	A	1877	GLY	2.3
2	B	55[A]	ARG	2.3
1	A	2014	ALA	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	B	6	PHE	2.3
2	B	129	ILE	2.3
2	B	246	MET	2.3
2	B	193	HIS	2.3
2	B	104	SER	2.3
2	B	64[A]	MET	2.3
1	A	1964	PRO	2.2
1	A	1905	LEU	2.2
1	A	1977	VAL	2.2
2	B	304	ASN	2.2
2	B	268	LEU	2.2
2	B	46	PHE	2.2
1	A	2034	ILE	2.2
1	A	2051	ILE	2.2
1	A	2050	THR	2.2
2	B	257	PRO	2.2
2	B	88	LYS	2.2
1	A	2053[A]	SER	2.2
2	B	151	GLU	2.2
2	B	95	ASN	2.2
1	A	1865	THR	2.2
1	A	2030	PRO	2.2
2	B	102	MET	2.1
2	B	100	GLN	2.1
1	A	2022	ALA	2.1
1	A	2008	LEU	2.1
1	A	1838	SER	2.1
2	B	142	SER	2.1
1	A	2041	PRO	2.1
2	B	73	PRO	2.1
2	B	189	ILE	2.1
1	A	1968	ALA	2.1
2	B	307	LYS	2.1
2	B	51	ASN	2.1
2	B	77	LEU	2.1
2	B	243	TRP	2.1
2	B	267	ILE	2.1
1	A	1921	VAL	2.1
2	B	27	ASN	2.1
1	A	2062	GLU	2.1
1	A	1923	SER	2.1
1	A	2043	PHE	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	B	71	TYR	2.1
2	B	237	TYR	2.1
2	B	309	MET	2.0
1	A	1957	ARG	2.0
1	A	2042	SER	2.0
2	B	180	VAL	2.0
2	B	274	THR	2.0
2	B	171	ASP	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](#)

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
3	VSQ	B	401	11/11	0.71	0.15	20,20,20,20	11

6.5 Other polymers [i](#)

There are no such residues in this entry.