

Full wwPDB X-ray Structure Validation Report (i)

Oct 25, 2022 – 08:54 PM EDT

PDB ID	:	7FMQ
Title	:	PanDDA analysis group deposition – Aar2/RNaseH in complex with fragment
		P06E04 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	:	1.58 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 (i) 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 (1)) were used in the production of this report:

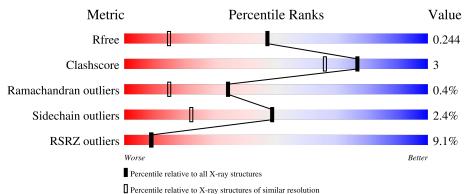
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.31.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.58 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	5534 (1.60-1.56)
Clashscore	141614	5861 (1.60-1.56)
Ramachandran outliers	138981	5708 (1.60-1.56)
Sidechain outliers	138945	5703 (1.60-1.56)
RSRZ outliers	127900	5431 (1.60-1.56)

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 <=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	А	258	83%	8%	8%
2	В	308	87%	89	% • •



7FMQ

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9280 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	
1	А	237	Total 4068	C 1287	Н 2060	N 336	O 373	S 12	0	21	0

There are 3 discrepancies between the modelled and reference sequences:

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

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

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace			
2	В	300	Total 5044	C 1654	Н 2464	N 421	O 485	S 20	11	17	0

There are 20 discrepancies between the modelled and reference sequences:

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

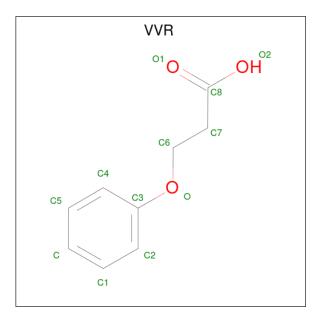
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Contentia	Continueu from previous page								
Chain	Residue	Modelled	Actual	Comment	Reference				
В	?	-	MET	deletion	UNP P32357				
В	?	-	GLU	deletion	UNP P32357				
В	?	-	ALA	deletion	UNP P32357				
В	?	-	LYS	deletion	UNP P32357				
В	?	-	ASN	deletion	UNP P32357				
В	?	-	GLU	deletion	UNP P32357				
В	170	SER	ASP	conflict	UNP P32357				

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• Molecule 3 is 3-phenoxypropanoic acid (three-letter code: VVR) (formula: $C_9H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	А	1	Total 12	С 9	O 3	0	0

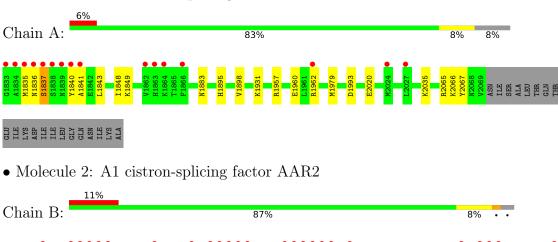
• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	97	Total O 97 97	0	0
4	В	59	Total O 59 59	0	0



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



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	87.32Å 85.69Å 93.28Å	Depositor
a, b, c, α , β , γ	90.00° 110.54° 90.00°	Depositor
Resolution (Å)	44.06 - 1.58	Depositor
Resolution (A)	44.06 - 1.58	EDS
% Data completeness	99.1 (44.06-1.58)	Depositor
(in resolution range)	99.1 (44.06-1.58)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$0.96 (at 1.58 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
D D	0.220 , 0.241	Depositor
R, R_{free}	0.225 , 0.244	DCC
R_{free} test set	2101 reflections (2.40%)	wwPDB-VP
Wilson B-factor $(Å^2)$	31.0	Xtriage
Anisotropy	0.187	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.40 , 42.6	EDS
L-test for twinning ²	$ L > = 0.51, < L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9280	wwPDB-VP
Average B, all atoms $(Å^2)$	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.70% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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: VVR

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	Bo	nd lengths	Bond angles	
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.57	1/2149~(0.0%)	0.70	1/2911~(0.0%)
2	В	0.67	4/2739~(0.1%)	0.74	2/3699~(0.1%)
All	All	0.63	5/4888~(0.1%)	0.72	3/6610~(0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	В	0	2

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	В	37	PRO	N-CA	11.41	1.66	1.47
1	А	1883	ASN	C-N	9.01	1.51	1.34
2	В	119	GLU	CD-OE2	-7.83	1.17	1.25
2	В	40	HIS	C-O	-6.50	1.11	1.23
2	В	36	ILE	C-N	5.05	1.43	1.34

All (5) bond length outliers are listed below:

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
2	В	37	PRO	N-CA-C	-8.77	89.31	112.10
1	А	1993	ASP	CB-CA-C	5.52	121.45	110.40
2	В	37	PRO	CA-N-CD	-5.45	103.87	111.50

There are no chirality outliers.

All (2) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
2	В	122[A]	GLN	Mainchain
2	В	122[B]	GLN	Mainchain

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	А	2008	2060	1974	9	1
2	В	2580	2464	2398	18	1
3	А	12	0	0	0	0
4	А	97	0	0	1	0
4	В	59	0	0	3	0
All	All	4756	4524	4372	27	1

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 3.

All (27) 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:95:ASN:O	2:B:98:GLU:N	2.15	0.80
2:B:100:GLN:HA	4:B:453:HOH:O	1.92	0.70
2:B:287:ARG:O	2:B:291:ILE:HD13	1.96	0.66
2:B:275:LEU:CD2	2:B:283:LEU:HD13	2.31	0.61
2:B:94:HIS:HB2	4:B:455:HOH:O	2.06	0.56
2:B:54[A]:MET:HE2	4:B:456:HOH:O	2.09	0.52
1:A:2066:LYS:HD2	1:A:2067:TYR:CE1	2.46	0.51
2:B:77:LEU:N	2:B:77:LEU:HD23	2.26	0.51
2:B:51:ASN:OD1	2:B:53:SER:HB2	2.12	0.50
2:B:275:LEU:HD21	2:B:283:LEU:HD13	1.93	0.49
2:B:94:HIS:CG	2:B:94:HIS:O	2.67	0.47
2:B:95:ASN:HA	2:B:98:GLU:HB2	1.96	0.47
2:B:77:LEU:HD23	2:B:77:LEU:H	1.79	0.47
1:A:1836:ASN:HB3	1:A:1960[A]:GLU:HB2	1.98	0.46
1:A:1895:HIS:O	1:A:1898[A]:VAL:HG22	2.16	0.45
1:A:1848:ILE:H	1:A:1931[A]:LYS:HZ2	1.65	0.45
2:B:203[A]:TYR:CZ	2:B:207:THR:HG21	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:99:ARG:O	2:B:100:GLN:HB2	2.17	0.44
2:B:258:LYS:HD2	2:B:258:LYS:H	1.83	0.44
1:A:1837:SER:HA	1:A:1840:TYR:HB2	2.00	0.43
2:B:96:PHE:HB3	2:B:102:MET:CE	2.49	0.43
1:A:2035:LYS:HA	1:A:2035:LYS:HD3	1.91	0.42
1:A:1843:LEU:HA	1:A:1849:LYS:HD2	2.01	0.42
1:A:2065:ARG:NE	4:A:2202:HOH:O	2.52	0.42
2:B:41[B]:VAL:HG11	2:B:121:VAL:HG12	2.03	0.41
2:B:277:GLU:H	2:B:277:GLU:CD	2.24	0.41

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All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1841:ALA:HB3	2:B:115:TYR:OH[4_555]	1.39	0.21

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	Percer	ntiles
1	А	258/258~(100%)	251 (97%)	7 (3%)	0	100	100
2	В	315/308~(102%)	298~(95%)	14 (4%)	3~(1%)	15	3
All	All	573/566~(101%)	549 (96%)	21 (4%)	3~(0%)	34	10

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	В	54[A]	MET
2	В	54[B]	MET
2	В	106	PRO



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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	237/233~(102%)	230~(97%)	7 (3%)	41 15
2	В	294/284~(104%)	287~(98%)	7(2%)	49 22
All	All	531/517~(103%)	517~(97%)	14 (3%)	49 19

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	1835	MET
1	А	1837	SER
1	А	1962	ARG
1	А	1979[A]	MET
1	А	1979[B]	MET
1	А	1979[C]	MET
1	А	2020	GLU
2	В	52	SER
2	В	96	PHE
2	В	99	ARG
2	В	115	TYR
2	В	258	LYS
2	В	260	MET
2	В	301	SER

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)

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	Mol Type Chain Res		E Link Bond lengths		hs Bond angles			les		
Moi Type (Unam	nes Li		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2	
3	VVR	А	2101	-	12,12,12	2.90	7 (58%)	13,14,14	0.89	0

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	VVR	А	2101	-	-	2/6/6/6	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	А	2101	VVR	O2-C8	-4.75	1.14	1.30
3	А	2101	VVR	C1-C2	-4.58	1.29	1.38
3	А	2101	VVR	C5-C4	-4.06	1.30	1.38
3	А	2101	VVR	C4-C3	-3.79	1.31	1.38
3	А	2101	VVR	O-C3	-3.67	1.29	1.37
3	А	2101	VVR	O-C6	-2.07	1.36	1.43
3	А	2101	VVR	C-C1	-2.04	1.32	1.38

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
3	А	2101	VVR	C6-C7-C8-O2
3	А	2101	VVR	C6-C7-C8-O1

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 (i)

6.1 Protein, DNA and RNA chains (i)

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^{th} 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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	237/258~(91%)	0.48	16 (6%) 17 17	24, 32, 74, 135	0
2	В	300/308~(97%)	0.75	33 (11%) 5 5	25, 38, 87, 149	0
All	All	537/566~(94%)	0.63	49 (9%) 9 9	24, 34, 81, 149	0

All (49) RSRZ outliers are listed below:

2 B 108 ILE 19.9 1 A 1834 ALA 10.6 2 B 109 ASP 10.1 1 A 1837 SER 9.6 1 A 1836 ASN 9.2 1 A 1836 ASN 9.2 1 A 1836 PHE 8.9 2 B 96 PHE 8.7 1 A 1838 SER 8.2 2 B 99 ARG 8.0 1 A 1835 MET 6.7 2 B 99 ARG 8.0 1 A 1835 MET 6.7 2 B 107 LYS 6.3 2 B 100 GLU 6.3 2 B 97 LYS 5.3 2 B 115 TYR 5.2 1 A 1839 ASN 4.6 2 B	Mol	Chain	Res	Type	RSRZ
2 B 109 ASP 10.1 1 A 1837 SER 9.6 1 A 1836 ASN 9.2 1 A 1836 ASN 9.2 1 A 1833 GLY 9.1 1 A 1866 PHE 8.9 2 B 96 PHE 8.7 1 A 1838 SER 8.2 2 B 99 ARG 8.0 1 A 1835 MET 6.7 2 B 316 LEU 6.4 2 B 107 LYS 6.3 2 B 98 GLU 6.3 2 B 97 LYS 5.3 2 B 97 LYS 5.3 2 B 115 TYR 5.2 1 A 1839 ASN 4.6 2 B 170 SER 4.5 2 B <	2	В	108	ILE	19.9
1 A 1837 SER 9.6 1 A 1836 ASN 9.2 1 A 1833 GLY 9.1 1 A 1866 PHE 8.9 2 B 96 PHE 8.7 1 A 1838 SER 8.2 2 B 99 ARG 8.0 1 A 1835 MET 6.7 2 B 316 LEU 6.4 2 B 107 LYS 6.3 2 B 98 GLU 6.3 2 B 100 GLN 5.8 2 B 100 GLN 5.8 2 B 115 TYR 5.2 1 A 1839 ASN 4.6 2 B 170 SER 4.5 2 B 170 SER 4.5 2 B 38 ILE 4.4 2 B <t< td=""><td>1</td><td>А</td><td>1834</td><td>ALA</td><td>10.6</td></t<>	1	А	1834	ALA	10.6
1 A 1836 ASN 9.2 1 A 1833 GLY 9.1 1 A 1866 PHE 8.9 2 B 96 PHE 8.7 1 A 1838 SER 8.2 2 B 99 ARG 8.0 1 A 1835 MET 6.7 2 B 316 LEU 6.4 2 B 107 LYS 6.3 2 B 100 GLN 5.8 2 B 100 GLN 5.8 2 B 115 TYR 5.2 1 A 1839 ASN 4.6 2 B 170 SER 4.5 2 B 38 ILE 4.4 2 B 111 ASP 4.4 2 B 1 MET 4.2	2	В	109	ASP	10.1
1 A 1833 GLY 9.1 1 A 1866 PHE 8.9 2 B 96 PHE 8.7 1 A 1838 SER 8.2 2 B 99 ARG 8.0 1 A 1835 MET 6.7 2 B 99 ARG 8.0 1 A 1835 MET 6.7 2 B 316 LEU 6.4 2 B 107 LYS 6.3 2 B 98 GLU 6.3 2 B 100 GLN 5.8 2 B 97 LYS 5.3 2 B 115 TYR 5.2 1 A 1839 ASN 4.6 2 B 170 SER 4.5 2 B 38 ILE 4.4 2 B 111 ASP 4.4 2 B 1	1	А	1837	SER	9.6
1 A 1866 PHE 8.9 2 B 96 PHE 8.7 1 A 1838 SER 8.2 2 B 99 ARG 8.0 1 A 1835 MET 6.7 2 B 316 LEU 6.4 2 B 107 LYS 6.3 2 B 107 LYS 6.3 2 B 98 GLU 6.3 2 B 100 GLN 5.8 2 B 115 TYR 5.2 1 A 1839 ASN 4.6 2 B 170 SER 4.5 2 B 170 SER 4.5 2 B 38 ILE 4.4 2 B 111 ASP 4.4 2 B 1 MET 4.2	1	А	1836	ASN	9.2
2 B 96 PHE 8.7 1 A 1838 SER 8.2 2 B 99 ARG 8.0 1 A 1835 MET 6.7 2 B 316 LEU 6.4 2 B 107 LYS 6.3 2 B 98 GLU 6.3 2 B 97 LYS 5.3 2 B 97 LYS 5.3 2 B 115 TYR 5.2 1 A 1839 ASN 4.6 2 B 170 SER 4.5 2 B 38 ILE 4.4 2 B 111 ASP 4.4 2 B 1 MET 4.2	1	А	1833	GLY	9.1
1 A 1838 SER 8.2 2 B 99 ARG 8.0 1 A 1835 MET 6.7 2 B 316 LEU 6.4 2 B 107 LYS 6.3 2 B 98 GLU 6.3 2 B 97 LYS 5.3 2 B 97 LYS 5.3 2 B 115 TYR 5.2 1 A 1839 ASN 4.6 2 B 258 LYS 4.6 2 B 170 SER 4.5 2 B 38 ILE 4.4 2 B 111 ASP 4.4 2 B 1 MET 4.2	1	А	1866	PHE	8.9
2 B 99 ARG 8.0 1 A 1835 MET 6.7 2 B 316 LEU 6.4 2 B 107 LYS 6.3 2 B 98 GLU 6.3 2 B 98 GLU 6.3 2 B 97 LYS 5.3 2 B 97 LYS 5.3 2 B 115 TYR 5.2 1 A 1839 ASN 4.6 2 B 258 LYS 4.6 2 B 170 SER 4.5 2 B 38 ILE 4.4 2 B 111 ASP 4.4 2 B 1 MET 4.2	2	В	96	PHE	8.7
1 A 1835 MET 6.7 2 B 316 LEU 6.4 2 B 107 LYS 6.3 2 B 98 GLU 6.3 2 B 98 GLU 6.3 2 B 97 LYS 5.3 2 B 97 LYS 5.3 2 B 115 TYR 5.2 1 A 1839 ASN 4.6 2 B 258 LYS 4.6 2 B 170 SER 4.5 2 B 38 ILE 4.4 2 B 111 ASP 4.4 2 B 1 MET 4.2	1	А	1838	SER	8.2
2 B 316 LEU 6.4 2 B 107 LYS 6.3 2 B 98 GLU 6.3 2 B 100 GLN 5.8 2 B 97 LYS 5.3 2 B 115 TYR 5.2 1 A 1839 ASN 4.6 2 B 258 LYS 4.6 2 B 170 SER 4.5 2 B 38 ILE 4.4 2 B 111 ASP 4.4 2 B 1 MET 4.2	2	В	99	ARG	8.0
2 B 107 LYS 6.3 2 B 98 GLU 6.3 2 B 100 GLN 5.8 2 B 97 LYS 5.3 2 B 97 LYS 5.3 2 B 115 TYR 5.2 1 A 1839 ASN 4.6 2 B 258 LYS 4.6 2 B 170 SER 4.5 2 B 38 ILE 4.4 2 B 111 ASP 4.4 2 B 1 MET 4.2	1	А	1835	MET	6.7
2 B 98 GLU 6.3 2 B 100 GLN 5.8 2 B 97 LYS 5.3 2 B 115 TYR 5.2 1 A 1839 ASN 4.6 2 B 258 LYS 4.6 2 B 170 SER 4.5 2 B 38 ILE 4.4 2 B 111 ASP 4.4 2 B 1 MET 4.2	2	В	316	LEU	6.4
2 B 100 GLN 5.8 2 B 97 LYS 5.3 2 B 115 TYR 5.2 1 A 1839 ASN 4.6 2 B 258 LYS 4.6 2 B 170 SER 4.5 2 B 38 ILE 4.4 2 B 111 ASP 4.4 2 B 1 MET 4.2	2	В	107	LYS	6.3
2 B 97 LYS 5.3 2 B 115 TYR 5.2 1 A 1839 ASN 4.6 2 B 258 LYS 4.6 2 B 170 SER 4.5 2 B 183 ILE 4.4 2 B 111 ASP 4.4 2 B 111 ASP 4.4 2 B 1 MET 4.2	2	В	98	GLU	6.3
2 B 115 TYR 5.2 1 A 1839 ASN 4.6 2 B 258 LYS 4.6 2 B 170 SER 4.5 2 B 38 ILE 4.4 2 B 111 ASP 4.4 2 B 1 MET 4.2	2	В	100	GLN	5.8
1A1839ASN4.62B258LYS4.62B170SER4.52B38ILE4.42B111ASP4.42B1MET4.2	2	В	97	LYS	5.3
2 B 258 LYS 4.6 2 B 170 SER 4.5 2 B 38 ILE 4.4 2 B 111 ASP 4.4 2 B 1 MET 4.2	2	В	115	TYR	5.2
2 B 170 SER 4.5 2 B 38 ILE 4.4 2 B 111 ASP 4.4 2 B 1 MET 4.2	1	А	1839	ASN	4.6
2 B 38 ILE 4.4 2 B 111 ASP 4.4 2 B 1 MET 4.2	2	В	258	LYS	4.6
2 B 111 ASP 4.4 2 B 1 MET 4.2	2	В	170	SER	4.5
2 B 1 MET 4.2	2	В	38	ILE	4.4
	2	В	111	ASP	4.4
2 B 110 GLU 4.0	2	В	1	MET	4.2
	2	В	110	GLU	4.0

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Mol	Chain	Res	Type	RSRZ
2	В	259	HIS	3.8
1	А	1864	LYS	3.7
2	В	54[A]	MET	3.7
2	В	173	ALA	3.6
2	В	40	HIS	3.5
1	А	1840	TYR	3.4
2	В	41[A]	VAL	3.3
2	В	39	GLY	3.2
2	В	279	TYR	3.2
2	В	283	LEU	3.0
2	В	94	HIS	3.0
2	В	317	LEU	3.0
2	В	280	SER	2.9
1	А	1862	VAL	2.9
2	В	172	PRO	2.6
1	А	2024[A]	MET	2.6
1	А	1841	ALA	2.5
2	В	174	HIS	2.5
1	А	1863	HIS	2.5
2	В	37	PRO	2.5
2	В	313	TYR	2.3
2	В	278	GLN	2.2
1	А	1962	ARG	2.1
1	А	2027	LEU	2.0
2	В	106	PRO	2.0

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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 monosaccharides 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, 95^{th} 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	VVR	А	2101	12/12	0.90	0.21	20,20,20,20	0

6.5 Other polymers (i)

There are no such residues in this entry.

