

wwPDB X-ray Structure Validation Summary Report (i)

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This is a wwPDB X-ray Structure Validation Summary 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	:	2.35
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)	:	2.35

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 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	527	% • 67%	28%	
1		021	% •		
1	В	527	67%	28%	••
2	\mathbf{C}	389	76%	23%	
2	D	389	65%	33%	•
			% •		
3	E	170	81%	15%	••



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Mol	Chain	Length	Quality o	f chain
2	F	170	5%	
3	Г	170	55%	41% •••



2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 17840 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 Methane monooxygenase component A alpha chain.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	А	510	Total 4138	C 2649	N 709	O 762	S 18	0	0	0
1	В	510	Total 4137	C 2646	N 711	O 762	S 18	0	0	0

• Molecule 2 is a protein called Methane monooxygenase component A beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	C	388	Total	С	Ν	Ο	S	0	0	0
	U		3163	2036	545	574	8	0		
9	Л	200	Total	С	Ν	0	S	0	0	0
2	D	388	3151	2028	543	572	8	0		0

• Molecule 3 is a protein called Methane monooxygenase component A gamma chain.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
3	Е	166	Total 1364	C 864	N 245	O 250	${S \atop 5}$	0	0	0
3	F	166	Total 1358	C 860	N 243	O 250	${ m S}{ m 5}$	0	0	0

• Molecule 4 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	2	Total Fe 2 2	0	0
4	В	2	Total Fe 2 2	0	0

• Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	1	Total Ca 1 1	0	0
5	С	1	Total Ca 1 1	0	0

• Molecule 6 is 3-BROMOBUT-3-EN-1-OL (three-letter code: 3BB) (formula: C_4H_7BrO).



Mol	Chain	Residues	A	Aton	ıs		ZeroOcc	AltConf
6	Δ	1	Total	Br	С	0	0	0
0	Π	1	6	1	4	1	0	0
6	Δ	1	Total	Br	С	Ο	0	0
0	11	1	6	1	4	1	0	0
6	Δ	1	Total	Br	С	Ο	0	0
0	11	1	6	1	4	1	0	0
6	Δ	1	Total	Br	С	Ο	0	0
0	11	1	6	1	4	1	0	0
6	В	1	Total	Br	С	0	0	0
0	D		6	1	4	1	0	0
6	В	1	Total	Br	С	Ο	0	0
0	D	1	6	1	4	1	0	0
6	В	1	Total	Br	С	Ο	0	0
0	D	1	6	1	4	1	0	0
6	C	1	Total	Br	С	Ο	0	0
0	U	1	6	1	4	1	0	0
6	C	1	Total	Br	С	Ο	0	0
		1	6	1	4	1	0	0
6		1	Total	Br	С	0	0	0
		1	6	1	4	1	0	



• Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	А	112	Total O 112 112	0	0
7	В	100	Total O 100 100	0	0
7	С	123	Total O 123 123	0	0
7	D	46	Total O 46 46	0	0
7	Е	65	$\begin{array}{cc} \text{Total} & \text{O} \\ 65 & 65 \end{array}$	0	0
7	F	17	Total O 17 17	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: Methane monooxygenase component A alpha chain













4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	70.47Å 171.94Å 220.50Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Bosolution (Å)	29.80 - 2.40	Depositor
Resolution (A)	29.80 - 2.40	EDS
% Data completeness	89.9 (29.80-2.40)	Depositor
(in resolution range)	90.0 (29.80-2.40)	EDS
R_{merge}	0.08	Depositor
R _{sym}	0.08	Depositor
$< I/\sigma(I) > 1$	$3.68 (at 2.39 \text{\AA})$	Xtriage
Refinement program	CNS 1.0	Depositor
B B.	0.202 , 0.260	Depositor
II, II, <i>free</i>	0.199 , 0.258	DCC
R_{free} test set	9570 reflections (9.37%)	wwPDB-VP
Wilson B-factor $(Å^2)$	34.8	Xtriage
Anisotropy	0.113	Xtriage
Bulk solvent $k_{sol}(e/A^3), B_{sol}(A^2)$	0.34 , 47.1	EDS
L-test for $twinning^2$	$ < L >=0.49, < L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	17840	wwPDB-VP
Average B, all atoms $(Å^2)$	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.47% 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: CA, 3BB, FE

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).

Mal	Chain	Bond	lengths	Bond angles		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.36	0/4263	0.59	0/5797	
1	В	0.35	0/4262	0.57	0/5796	
2	С	0.39	0/3259	0.59	0/4430	
2	D	0.34	0/3247	0.55	0/4417	
3	Е	0.38	0/1392	0.61	0/1876	
3	F	0.32	0/1387	0.55	0/1873	
All	All	0.36	0/17810	0.58	0/24189	

There are no bond length outliers.

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	А	4138	0	3897	129	0
1	В	4137	0	3888	137	0
2	С	3163	0	2986	83	0
2	D	3151	0	2960	113	0
3	Е	1364	0	1352	24	0
3	F	1358	0	1335	65	0
4	А	2	0	0	0	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	В	2	0	0	0	0
5	А	1	0	0	0	0
5	С	1	0	0	0	0
6	А	24	0	19	4	0
6	В	18	0	14	2	0
6	С	12	0	10	2	0
6	D	6	0	5	2	0
7	А	112	0	0	2	0
7	В	100	0	0	4	0
7	С	123	0	0	1	0
7	D	46	0	0	0	0
7	Ε	65	0	0	1	0
7	F	17	0	0	0	0
All	All	17840	0	16466	485	0

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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 14.

The worst 5 of 485 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)
3:F:80:LYS:HE2	3:F:84:GLY:HA2	1.23	1.10
2:D:352:ILE:HD13	2:D:388:LEU:HD21	1.51	0.92
1:A:44:THR:HG22	1:A:46:TYR:H	1.34	0.92
1:B:352:ALA:HA	1:B:404:PRO:HB2	1.53	0.90
1:B:44:THR:HG22	1:B:46:TYR:H	1.38	0.88

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	А	508/527~(96%)	481 (95%)	22~(4%)	5 (1%)	15 23
1	В	508/527~(96%)	463 (91%)	39~(8%)	6 (1%)	13 19
2	С	386/389~(99%)	373~(97%)	12 (3%)	1 (0%)	41 55
2	D	386/389~(99%)	357~(92%)	23 (6%)	6 (2%)	9 13
3	Ε	164/170~(96%)	158 (96%)	6 (4%)	0	100 100
3	F	164/170~(96%)	142 (87%)	18 (11%)	4 (2%)	6 6
All	All	2116/2172~(97%)	1974 (93%)	120 (6%)	22 (1%)	15 23

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	В	40	LYS
1	А	315	GLY
1	В	311	GLU
1	В	316	ILE
2	D	64	ALA

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	А	423/442~(96%)	404 (96%)	19 (4%)	27	44	
1	В	422/442~(96%)	409 (97%)	13 (3%)	40	60	
2	С	315/323~(98%)	307~(98%)	8 (2%)	47	67	
2	D	312/323~(97%)	302~(97%)	10 (3%)	39	59	
3	Ε	143/147~(97%)	140 (98%)	3(2%)	53	72	
3	F	142/147~(97%)	138~(97%)	4 (3%)	43	63	
All	All	1757/1824~(96%)	1700 (97%)	57 (3%)	39	59	

 $5~{\rm of}~57$ residues with a non-rotameric side chain are listed below:

Mol	Chain	\mathbf{Res}	Type
1	В	302	VAL



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Mol	Chain	Res	Type
3	F	44	ARG
2	С	153	LEU
3	F	23	ASN
2	D	385	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
3	Ε	144	ASN
3	F	7	HIS
3	F	167	GLN
1	В	133	GLN
1	В	108	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 16 ligands modelled in this entry, 6 are monoatomic - leaving 10 for Mogul analysis.

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).



Mal	Turne	Chain	Dec	Tiple	B	ond leng	gths	В	Sond ang	gles
	туре	Unam	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
6	3BB	А	1174	-	$4,\!5,\!5$	0.29	0	$2,\!5,\!5$	0.63	0
6	3BB	С	510	-	$4,\!5,\!5$	0.39	0	$2,\!5,\!5$	0.30	0
6	3BB	В	1176	4	$4,\!5,\!5$	0.34	0	$2,\!5,\!5$	0.68	0
6	3BB	А	1172	4	$4,\!5,\!5$	0.29	0	$2,\!5,\!5$	0.74	0
6	3BB	С	508	-	$4,\!5,\!5$	0.32	0	$2,\!5,\!5$	0.28	0
6	3BB	А	1175	-	$4,\!5,\!5$	0.40	0	$2,\!5,\!5$	0.43	0
6	3BB	В	1178	-	$4,\!5,\!5$	0.45	0	$2,\!5,\!5$	0.49	0
6	3BB	В	1177	-	$4,\!5,\!5$	0.19	0	$2,\!5,\!5$	0.35	0
6	3BB	D	509	-	$4,\!5,\!5$	0.39	0	$2,\!5,\!5$	0.30	0
6	3BB	А	1173	-	$4,\!5,\!5$	0.20	0	$2,\!5,\!5$	0.30	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
6	3BB	А	1174	-	-	0/1/3/3	-
6	3BB	С	510	-	-	0/1/3/3	-
6	3BB	В	1176	4	-	0/1/3/3	-
6	3BB	А	1172	4	-	0/1/3/3	-
6	3BB	С	508	-	-	0/1/3/3	-
6	3BB	А	1175	-	-	0/1/3/3	-
6	3BB	В	1178	-	-	0/1/3/3	-
6	3BB	В	1177	-	-	0/1/3/3	-
6	3BB	D	509	-	-	0/1/3/3	-
6	3BB	А	1173	-	-	0/1/3/3	-

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.

6 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	А	1174	3BB	1	0
6	С	510	3BB	2	0
6	В	1176	3BB	1	0
6	А	1175	3BB	3	0



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Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	В	1178	3BB	1	0
6	D	509	3BB	2	0

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	510/527~(96%)	-0.29	6 (1%) 79 77	20, 36, 64, 94	0
1	В	510/527~(96%)	-0.26	7 (1%) 75 73	22, 38, 74, 92	0
2	С	388/389~(99%)	-0.53	2 (0%) 91 89	15, 28, 53, 78	0
2	D	388/389~(99%)	0.07	15 (3%) 39 38	25, 47, 79, 104	0
3	Е	166/170~(97%)	-0.47	1 (0%) 89 88	18, 32, 55, 86	0
3	F	166/170~(97%)	0.49	9 (5%) 25 24	40, 61, 85, 107	0
All	All	2128/2172 (97%)	-0.21	40 (1%) 66 64	15, 38, 73, 107	0

The worst 5 of 40 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	389	LYS	5.2
2	D	2	SER	4.5
2	С	2	SER	3.8
1	А	316	ILE	3.4
3	F	100	ALA	3.3

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	$B-factors(A^2)$	Q<0.9
6	3BB	С	510	6/6	0.79	0.37	95,97,99,102	0
6	3BB	D	509	6/6	0.81	0.29	91,93,94,95	0
6	3BB	А	1174	6/6	0.83	0.26	84,90,92,98	0
6	3BB	В	1177	6/6	0.83	0.38	105,107,109,112	0
6	3BB	А	1175	6/6	0.88	0.31	69,72,75,81	0
6	3BB	А	1173	6/6	0.88	0.27	101,102,102,107	0
6	3BB	А	1172	6/6	0.91	0.18	78,82,84,90	0
6	3BB	С	508	6/6	0.92	0.16	91,96,97,102	0
6	3BB	В	1176	6/6	0.92	0.21	104,112,114,121	0
6	3BB	В	1178	6/6	0.92	0.30	62,65,66,71	0
5	CA	А	673	1/1	0.93	0.10	56, 56, 56, 56	0
5	CA	С	674	1/1	0.96	0.10	48,48,48,48	0
4	FE	В	1174	1/1	0.97	0.07	44,44,44,44	0
4	FE	В	1175	1/1	0.98	0.07	37,37,37,37	0
4	FE	A	1171	1/1	0.99	0.07	37,37,37,37	0
4	FE	А	1170	1/1	1.00	0.07	39,39,39,39	0

6.5 Other polymers (i)

There are no such residues in this entry.

