wwPDB X-ray Structure Validation Summary Report (i)

Oct 11, 2021 – 06:54 AM EDT

PDB ID	:	2RF1
Title	:	Crystal structure of ChoX in an unliganded closed conformation
Authors	:	Oswald, C.; Smits, S.H.J.; Hoeing, M.; Sohn-Boeser, L.; Le Rudulier, D.; Schmitt, L.; Bremer, E.
Deposited on	:	2007-09-27
Resolution	:	2.00 Å(reported)

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 following versions of software and data (see references (1)) were used in the production of this report:

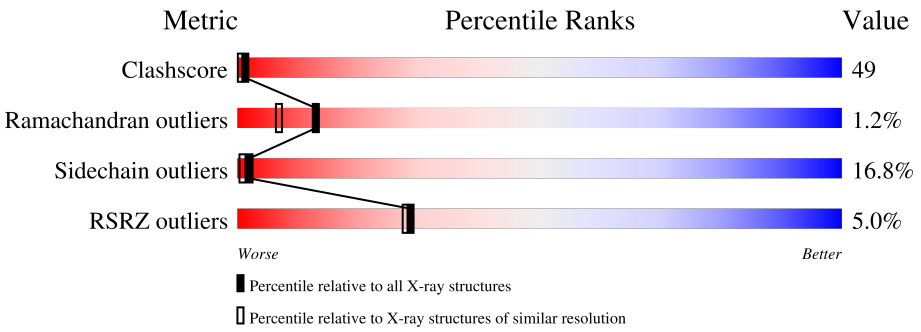
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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))
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	A	298	4%; 31%; 55%; 11%; •
1	B	298	6%; 30%; 56%; 10%; •

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4573 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 PUTATIVE GLYCINE BETAINE-BINDING ABC TRANSPORTER PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	290	2192	1381	359	443	9	0	0	0
1	B	289	2184	1375	358	442	9	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	251	ASP	GLY	engineered mutation	UNP Q92N37
A	319	GLU	-	expression tag	UNP Q92N37
A	320	HIS	-	expression tag	UNP Q92N37
A	321	HIS	-	expression tag	UNP Q92N37
A	322	HIS	-	expression tag	UNP Q92N37
A	323	HIS	-	expression tag	UNP Q92N37
A	324	HIS	-	expression tag	UNP Q92N37
A	325	HIS	-	expression tag	UNP Q92N37
B	251	ASP	GLY	engineered mutation	UNP Q92N37
B	319	GLU	-	expression tag	UNP Q92N37
B	320	HIS	-	expression tag	UNP Q92N37
B	321	HIS	-	expression tag	UNP Q92N37
B	322	HIS	-	expression tag	UNP Q92N37
B	323	HIS	-	expression tag	UNP Q92N37
B	324	HIS	-	expression tag	UNP Q92N37
B	325	HIS	-	expression tag	UNP Q92N37

- Molecule 2 is water.

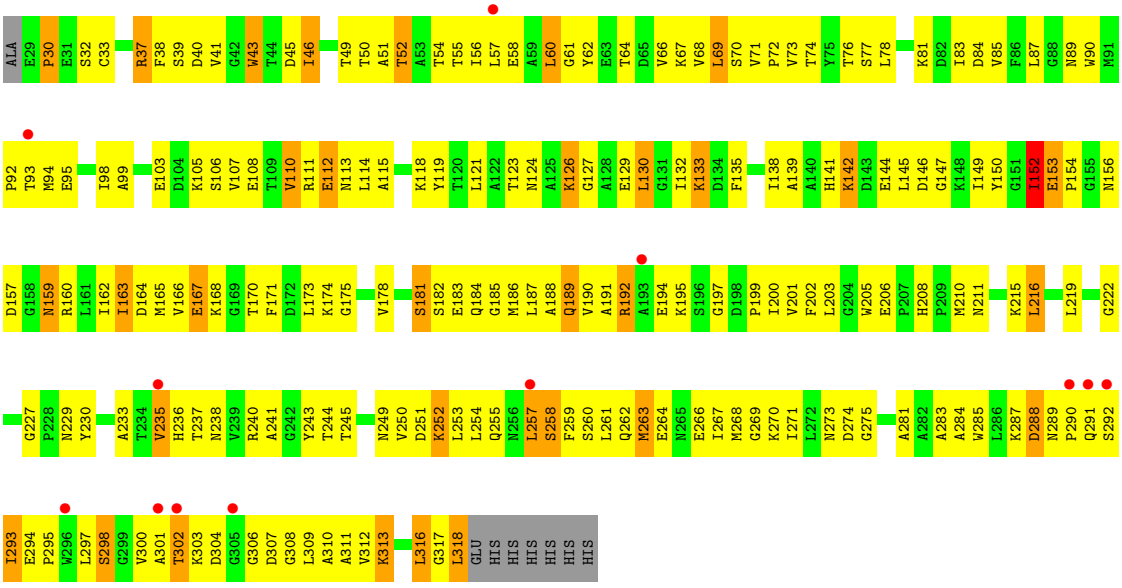
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	105	105	105	0	0
2	B	92	92	92	0	0

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.

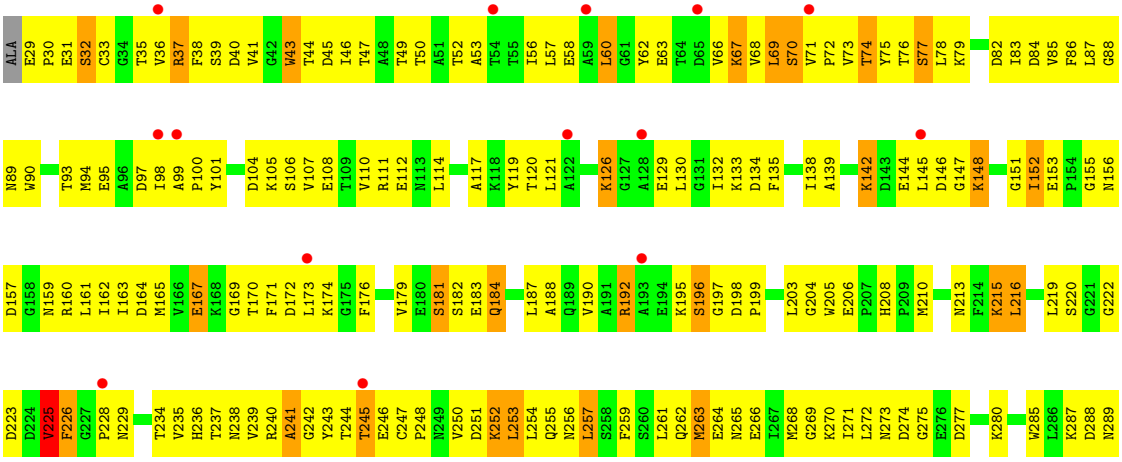
• Molecule 1: PUTATIVE GLYCINE BETAINE-BINDING ABC TRANSPORTER PROTEIN

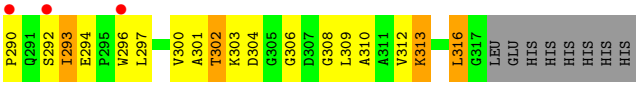
Chain A: 4% 31% 55% 11%



• Molecule 1: PUTATIVE GLYCINE BETAINE-BINDING ABC TRANSPORTER PROTEIN

Chain B: 6% 30% 56% 10%




P290
Q291
S292
I293
E294
P295
W296
L297
V300
A301
T302
K303
D304
G305
G306
D307
G308
L309
A310
A311
V312
K313
L316
G317
LEU
GLU
HIS
HIS
HIS
HIS
HIS
HIS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	30.90Å 196.20Å 42.80Å 90.00° 90.10° 90.00°	Depositor
Resolution (Å)	10.00 – 2.00 10.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	93.9 (10.00-2.00) 93.9 (10.00-2.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	8.83 (at 2.01Å)	Xtriage
Refinement program	SHELX, SHELXL-97	Depositor
R, R_{free}	0.201 , 0.235 0.237 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	16.6	Xtriage
Anisotropy	0.394	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.15 , 91.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	0.089 for h,-k,-l	Xtriage
F_o,F_c correlation	0.86	EDS
Total number of atoms	4573	wwPDB-VP
Average B, all atoms (Å^2)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.57% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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)

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	0.22	0/2234	0.37	0/3033
1	B	0.64	2/2226 (0.1%)	0.79	4/3022 (0.1%)
All	All	0.48	2/4460 (0.0%)	0.61	4/6055 (0.1%)

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
1	B	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	226	PHE	C-N	-24.68	0.88	1.33
1	B	225	VAL	C-N	-11.82	1.06	1.34

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	226	PHE	O-C-N	-27.20	76.96	123.20
1	B	226	PHE	CA-C-N	22.53	161.27	116.20
1	B	226	PHE	C-N-CA	10.74	144.85	122.30
1	B	225	VAL	O-C-N	-6.63	112.08	122.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	225	VAL	Mainchain
1	B	226	PHE	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	A	2192	0	2135	210	0
1	B	2184	0	2122	222	0
2	A	105	0	0	50	0
2	B	92	0	0	44	0
All	All	4573	0	4257	427	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 49.

The worst 5 of 427 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:B:84:ASP:HA	1:B:240:ARG:HG2	1.44	0.99
1:B:38:PHE:HB2	1:B:66:VAL:HG22	1.49	0.94
1:A:252:LYS:HB3	1:A:300:VAL:HG22	1.50	0.93
1:B:162:ILE:HD11	1:B:203:LEU:HD21	1.53	0.90
1:B:89:ASN:HB2	1:B:238:ASN:HD21	1.37	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	A	288/298 (97%)	268 (93%)	17 (6%)	3 (1%)	15 9
1	B	287/298 (96%)	266 (93%)	17 (6%)	4 (1%)	11 5

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	575/596 (96%)	534 (93%)	34 (6%)	7 (1%)	13 7

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	241	ALA
1	A	152	ILE
1	B	181	SER
1	B	70	SER
1	B	152	ILE

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	232/240 (97%)	186 (80%)	46 (20%)	1 0
1	B	231/240 (96%)	199 (86%)	32 (14%)	3 2
All	All	463/480 (96%)	385 (83%)	78 (17%)	2 1

5 of 78 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	130	LEU
1	B	257	LEU
1	B	148	LYS
1	B	215	LYS
1	B	302	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	208	HIS
1	B	262	GLN
1	B	291	GLN

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Mol	Chain	Res	Type
1	B	273	ASN
1	A	238	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)

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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	225:VAL	C	226:PHE	N	1.06
1	B	226:PHE	C	227:GLY	N	0.88

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, 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	290/298 (97%)	0.58	12 (4%)	37	36	10, 22, 33, 41	0
1	B	289/298 (96%)	0.76	17 (5%)	22	21	12, 25, 36, 46	0
All	All	579/596 (97%)	0.67	29 (5%)	28	28	10, 23, 36, 46	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	301	ALA	3.6
1	A	302	THR	3.4
1	A	305	GLY	3.1
1	B	292	SER	3.1
1	B	59	ALA	2.9

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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.