Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 02:57 AM UTC

PDB ID	:	7CYG / pdb_00007cyg
Title	:	Crystal structure of a cysteine-pair mutant (Y113C-P190C) of a bacterial bile acid transporter before disulfide bond formation
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Deposited on	:	2020-09-03
Resolution	:	3.20 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:

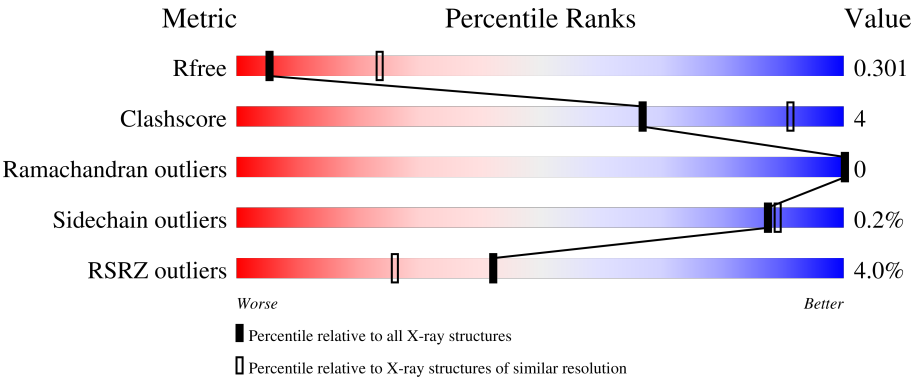
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.20 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	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	307	2% 91% 9%
1	B	307	6% 88% 10%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 4511 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 Transporter, sodium/bile acid symporter family.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	306	Total	C	N	O	S	0	0	0
			2285	1510	369	390	16			
1	B	299	Total	C	N	O	S	0	0	0
			2226	1473	359	378	16			

There are 4 discrepancies between the modelled and reference sequences:

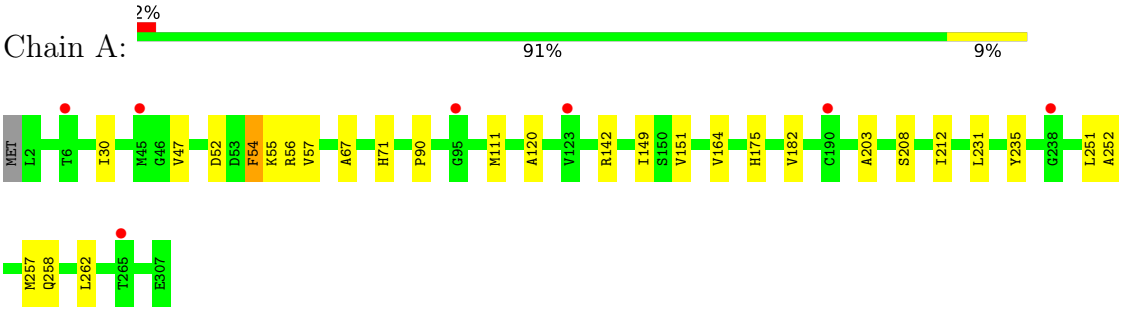
Chain	Residue	Modelled	Actual	Comment	Reference
A	113	CYS	TYR	engineered mutation	UNP A0A380PV03
A	190	CYS	PRO	engineered mutation	UNP A0A380PV03
B	113	CYS	TYR	engineered mutation	UNP A0A380PV03
B	190	CYS	PRO	engineered mutation	UNP A0A380PV03

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.

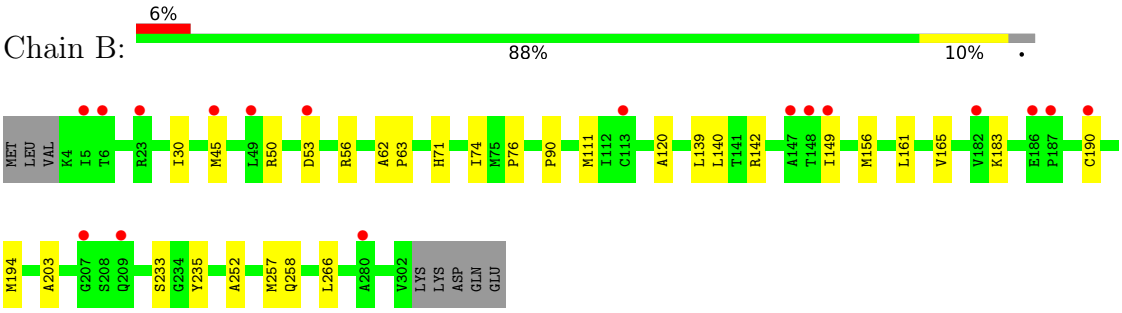
• Molecule 1: Transporter, sodium/bile acid symporter family

Chain A:



• Molecule 1: Transporter, sodium/bile acid symporter family

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	189.60Å 47.16Å 70.68Å 90.00° 100.84° 90.00°	Depositor
Resolution (Å)	35.68 – 3.20 35.68 – 3.20	Depositor EDS
% Data completeness (in resolution range)	91.6 (35.68-3.20) 91.5 (35.68-3.20)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.38 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.263 , 0.301 0.265 , 0.301	Depositor DCC
R_{free} test set	474 reflections (4.54%)	wwPDB-VP
Wilson B-factor (Å^2)	53.3	Xtriage
Anisotropy	0.265	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 37.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.86	EDS
Total number of atoms	4511	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 24.32 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.9214e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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

5.1 Standard geometry

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	0.20	0/2337	0.37	3/3189 (0.1%)
1	B	0.09	0/2278	0.24	0/3111
All	All	0.16	0/4615	0.32	3/6300 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	54	PHE	CA-C-N	6.45	130.11	120.31
1	A	54	PHE	C-N-CA	6.45	130.11	120.31
1	A	57	VAL	N-CA-C	-5.02	104.77	111.05

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2285	0	2424	16	0
1	B	2226	0	2360	18	0
All	All	4511	0	4784	34	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 (34) 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:56:ARG:NH2	1:A:120:ALA:HB1	2.02	0.73
1:A:56:ARG:CZ	1:A:120:ALA:HB1	2.23	0.68
1:B:50:ARG:HH22	1:B:183:LYS:HE2	1.59	0.68
1:B:235:TYR:HB2	1:B:252:ALA:HB2	1.85	0.59
1:A:71:HIS:NE2	1:A:258:GLN:OE1	2.31	0.59
1:B:90:PRO:HB3	1:B:149:ILE:HD11	1.87	0.57
1:A:52:ASP:HA	1:A:55:LYS:HD3	1.87	0.55
1:A:30:ILE:HB	1:A:203:ALA:HB2	1.92	0.52
1:A:90:PRO:HB3	1:A:149:ILE:HD11	1.91	0.52
1:A:47:VAL:O	1:A:175:HIS:ND1	2.41	0.52
1:B:53:ASP:HA	1:B:56:ARG:HH12	1.75	0.51
1:B:111:MET:HE1	1:B:257:MET:HE3	1.92	0.50
1:A:111:MET:HE1	1:A:257:MET:HE3	1.93	0.50
1:A:235:TYR:HB2	1:A:252:ALA:HB2	1.95	0.49
1:B:71:HIS:NE2	1:B:258:GLN:OE1	2.38	0.48
1:A:175:HIS:HA	1:A:182:VAL:HG21	1.97	0.45
1:B:139:LEU:HD23	1:B:139:LEU:HA	1.87	0.45
1:B:142:ARG:NH2	1:B:149:ILE:O	2.47	0.45
1:B:161:LEU:HA	1:B:165:VAL:HB	2.00	0.43
1:B:45:MET:HE3	1:B:45:MET:HB3	1.94	0.43
1:B:53:ASP:HA	1:B:56:ARG:NH1	2.34	0.43
1:B:76:PRO:HG2	1:B:140:LEU:HD13	2.00	0.43
1:A:231:LEU:HD21	1:A:257:MET:HE2	2.01	0.42
1:B:30:ILE:HB	1:B:203:ALA:HB2	2.01	0.42
1:B:74:ILE:HD13	1:B:233:SER:HB3	2.01	0.42
1:B:56:ARG:CZ	1:B:120:ALA:HB1	2.49	0.42
1:A:164:VAL:HG21	1:A:262:LEU:HD22	2.01	0.42
1:A:142:ARG:HD2	1:A:151:VAL:HB	2.01	0.42
1:A:208:SER:O	1:A:212:ILE:HG13	2.19	0.42
1:B:156:MET:HE3	1:B:266:LEU:HD13	2.02	0.42
1:B:190:CYS:O	1:B:194:MET:HG3	2.20	0.41
1:A:67:ALA:HB2	1:A:251:LEU:HG	2.01	0.41
1:A:142:ARG:NH2	1:A:149:ILE:O	2.51	0.41
1:B:62:ALA:HB3	1:B:63:PRO:HD3	2.02	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	304/307 (99%)	301 (99%)	3 (1%)	0	100	100
1	B	297/307 (97%)	294 (99%)	3 (1%)	0	100	100
All	All	601/614 (98%)	595 (99%)	6 (1%)	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	248/249 (100%)	247 (100%)	1 (0%)	84	86
1	B	241/249 (97%)	241 (100%)	0	100	100
All	All	489/498 (98%)	488 (100%)	1 (0%)	87	89

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54	PHE

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 oligosaccharides 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, 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	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	306/307 (99%)	0.51	7 (2%)	61	41	18, 29, 61, 77	0
1	B	299/307 (97%)	0.66	17 (5%)	29	19	18, 32, 61, 82	0
All	All	605/614 (98%)	0.58	24 (3%)	42	26	18, 30, 61, 82	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	190	CYS	3.8
1	A	95	GLY	3.7
1	B	45	MET	3.1
1	A	6	THR	3.0
1	B	113	CYS	2.9
1	A	238	GLY	2.9
1	A	123	VAL	2.8
1	B	6	THR	2.7
1	B	53	ASP	2.7
1	B	147	ALA	2.5
1	A	190	CYS	2.4
1	A	45	MET	2.4
1	A	265	THR	2.3
1	B	148	THR	2.3
1	B	182	VAL	2.3
1	B	5	ILE	2.2
1	B	280	ALA	2.2
1	B	187	PRO	2.1
1	B	23	ARG	2.1
1	B	186	GLU	2.1
1	B	207	GLY	2.1
1	B	209	GLN	2.0
1	B	49	LEU	2.0
1	B	149	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 oligosaccharides 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.