



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 1, 2026 – 12:04 PM UTC

PDB ID : 2HPG / pdb_00002hpg
Title : The crystal structure of a thermophilic TRAP periplasmic binding protein
Authors : Cuneo, M.J.; Hellinga, H.W.
Deposited on : 2006-07-17
Resolution : 1.90 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 ⓘ 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

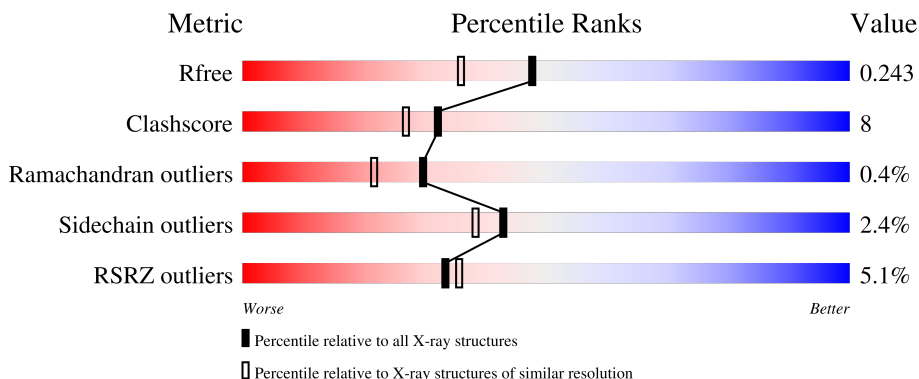
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	327	 5% 85% 11% ..
1	B	327	 % 88% 8% ..
1	C	327	 6% 79% 15% ..
1	D	327	 8% 86% 9% ..

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 10882 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 ABC transporter, periplasmic substrate-binding protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	318	2616	1693	427	480	1	15	0	11	0
1	B	316	2560	1654	420	474	1	11	0	5	0
1	C	313	2600	1684	421	481	1	13	0	15	0
1	D	316	2577	1672	423	471	1	10	0	8	0

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	MSE	-	initiating methionine	UNP Q9WYF8
A	79	MSE	MET	modified residue	UNP Q9WYF8
A	94	MSE	MET	modified residue	UNP Q9WYF8
A	102	MSE	MET	modified residue	UNP Q9WYF8
A	111	MSE	MET	modified residue	UNP Q9WYF8
A	132	MSE	MET	modified residue	UNP Q9WYF8
A	234	MSE	MET	modified residue	UNP Q9WYF8
A	268	MSE	MET	modified residue	UNP Q9WYF8
A	280	MSE	MET	modified residue	UNP Q9WYF8
A	296	MSE	MET	modified residue	UNP Q9WYF8
A	310	MSE	MET	modified residue	UNP Q9WYF8
A	337	HIS	-	expression tag	UNP Q9WYF8
A	338	HIS	-	expression tag	UNP Q9WYF8
A	339	HIS	-	expression tag	UNP Q9WYF8
A	340	HIS	-	expression tag	UNP Q9WYF8
A	341	HIS	-	expression tag	UNP Q9WYF8
A	342	HIS	-	expression tag	UNP Q9WYF8
B	16	MSE	-	initiating methionine	UNP Q9WYF8
B	79	MSE	MET	modified residue	UNP Q9WYF8
B	94	MSE	MET	modified residue	UNP Q9WYF8
B	102	MSE	MET	modified residue	UNP Q9WYF8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	111	MSE	MET	modified residue	UNP Q9WYF8
B	132	MSE	MET	modified residue	UNP Q9WYF8
B	234	MSE	MET	modified residue	UNP Q9WYF8
B	268	MSE	MET	modified residue	UNP Q9WYF8
B	280	MSE	MET	modified residue	UNP Q9WYF8
B	296	MSE	MET	modified residue	UNP Q9WYF8
B	310	MSE	MET	modified residue	UNP Q9WYF8
B	337	HIS	-	expression tag	UNP Q9WYF8
B	338	HIS	-	expression tag	UNP Q9WYF8
B	339	HIS	-	expression tag	UNP Q9WYF8
B	340	HIS	-	expression tag	UNP Q9WYF8
B	341	HIS	-	expression tag	UNP Q9WYF8
B	342	HIS	-	expression tag	UNP Q9WYF8
C	16	MSE	-	initiating methionine	UNP Q9WYF8
C	79	MSE	MET	modified residue	UNP Q9WYF8
C	94	MSE	MET	modified residue	UNP Q9WYF8
C	102	MSE	MET	modified residue	UNP Q9WYF8
C	111	MSE	MET	modified residue	UNP Q9WYF8
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C	340	HIS	-	expression tag	UNP Q9WYF8
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D	16	MSE	-	initiating methionine	UNP Q9WYF8
D	79	MSE	MET	modified residue	UNP Q9WYF8
D	94	MSE	MET	modified residue	UNP Q9WYF8
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D	132	MSE	MET	modified residue	UNP Q9WYF8
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D	280	MSE	MET	modified residue	UNP Q9WYF8
D	296	MSE	MET	modified residue	UNP Q9WYF8
D	310	MSE	MET	modified residue	UNP Q9WYF8
D	337	HIS	-	expression tag	UNP Q9WYF8

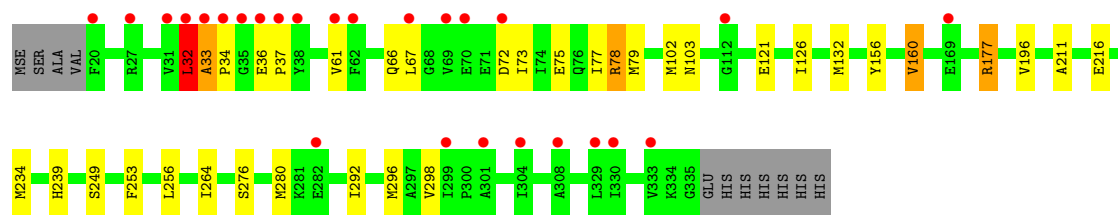
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Chain	Residue	Modelled	Actual	Comment	Reference
D	338	HIS	-	expression tag	UNP Q9WYF8
D	339	HIS	-	expression tag	UNP Q9WYF8
D	340	HIS	-	expression tag	UNP Q9WYF8
D	341	HIS	-	expression tag	UNP Q9WYF8
D	342	HIS	-	expression tag	UNP Q9WYF8

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	180	Total 180	O 180	0	0
2	B	120	Total 120	O 120	0	0
2	C	150	Total 150	O 150	0	0
2	D	79	Total 79	O 79	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	119.26Å 119.26Å 429.10Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 1.90 30.00 – 1.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (30.00-1.90) 100.0 (30.00-1.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.23 (at 1.91Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.213 , 0.239 0.218 , 0.243	Depositor DCC
R_{free} test set	7152 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	23.6	Xtrriage
Anisotropy	0.424	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 41.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10882	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.30% 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

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	0.67	0/2685	0.81	0/3600
1	B	0.67	0/2618	0.81	1/3514 (0.0%)
1	C	0.66	0/2681	0.80	2/3600 (0.1%)
1	D	0.61	1/2644 (0.0%)	0.80	1/3549 (0.0%)
All	All	0.65	1/10628 (0.0%)	0.80	4/14263 (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
1	C	0	1
1	D	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	32	LEU	CA-C	6.04	1.57	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	32	LEU	N-CA-C	8.52	123.81	112.13
1	B	216	GLU	N-CA-CB	-6.57	100.75	110.86
1	C	75	GLU	N-CA-C	-6.00	104.56	112.72
1	C	29	GLY	N-CA-C	5.04	118.58	111.42

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	74	ILE	Peptide
1	D	32	LEU	Peptide

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	2616	0	2651	46	0
1	B	2560	0	2576	41	0
1	C	2600	0	2620	63	0
1	D	2577	0	2623	40	0
2	A	180	0	0	1	0
2	B	120	0	0	0	0
2	C	150	0	0	2	0
2	D	79	0	0	2	0
All	All	10882	0	10470	167	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 8.

The worst 5 of 167 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:228:TYR:HB3	1:B:296:MSE:CE	1.68	1.23
1:B:228:TYR:HB3	1:B:296:MSE:HE2	1.24	1.11
1:C:73:ILE:HG22	1:C:73:ILE:O	1.56	1.03
1:B:94[B]:MSE:CE	1:B:181:ALA:HB1	1.90	1.02
1:B:228:TYR:CB	1:B:296:MSE:HE2	1.90	1.00

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	327/327 (100%)	318 (97%)	8 (2%)	1 (0%)	36	29
1	B	319/327 (98%)	311 (98%)	8 (2%)	0	100	100
1	C	324/327 (99%)	312 (96%)	9 (3%)	3 (1%)	14	6
1	D	322/327 (98%)	316 (98%)	5 (2%)	1 (0%)	36	29
All	All	1292/1308 (99%)	1257 (97%)	30 (2%)	5 (0%)	30	22

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	33	ALA
1	A	334	LYS
1	C	74	ILE
1	C	67	LEU
1	C	73	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	279/265 (105%)	270 (97%)	9 (3%)	34	27
1	B	271/265 (102%)	265 (98%)	6 (2%)	45	42
1	C	278/265 (105%)	271 (98%)	7 (2%)	42	37
1	D	274/265 (103%)	267 (97%)	7 (3%)	40	35
All	All	1102/1060 (104%)	1073 (97%)	29 (3%)	43	35

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	232	LYS
1	D	160	VAL

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Mol	Chain	Res	Type
1	C	103	ASN
1	D	78	ARG
1	C	74	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	76	GLN
1	D	327	ASN
1	D	221	ASN
1	B	86	ASN
1	C	208	GLN

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 [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	308/327 (94%)	0.17	15 (4%) 35 37	12, 23, 43, 54	6 (1%)
1	B	306/327 (93%)	0.08	4 (1%) 75 78	14, 26, 37, 45	4 (1%)
1	C	304/327 (92%)	0.21	18 (5%) 28 30	9, 24, 48, 68	11 (3%)
1	D	306/327 (93%)	0.70	26 (8%) 16 17	16, 35, 45, 56	8 (2%)
All	All	1224/1308 (93%)	0.29	63 (5%) 33 36	9, 27, 44, 68	29 (2%)

The worst 5 of 63 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	74	ILE	6.5
1	C	73	ILE	6.5
1	C	72[A]	ASP	6.5
1	A	335	GLY	6.5
1	C	69	VAL	6.2

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.