



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2018 – 01:55 am GMT

PDB ID : 4TSR
Title : The Complex Structure of Mutant Phytase with IHS
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Deposited on : 2014-06-19
Resolution : 2.07 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : trunk31020
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk31020

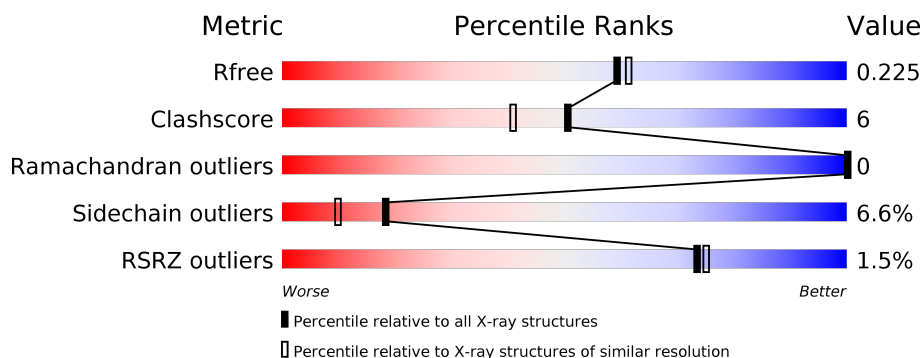
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.07 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}	111664	2250 (2.08-2.04)
Clashscore	122126	2358 (2.08-2.04)
Ramachandran outliers	120053	2339 (2.08-2.04)
Sidechain outliers	120020	2339 (2.08-2.04)
RSRZ outliers	108989	2211 (2.08-2.04)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	410	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; width: 100%;">%</div> <div style="position: absolute; top: 10px; left: 0; width: 100%;"> 82% 12% • • </div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3393 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 Periplasmic AppA protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	399	Total	C	N	O	S	0	0	0
			3054	1922	545	574	13			

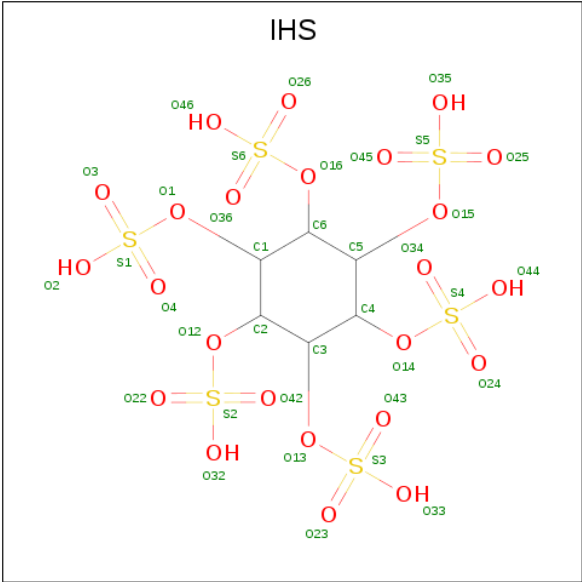
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	89	THR	VAL	engineered mutation	UNP P07102
A	116	VAL	ALA	engineered mutation	UNP P07102
A	206	ALA	SER	engineered mutation	UNP P07102

- Molecule 2 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	Ni	0	0
			4	4		

- Molecule 3 is D-MYO-INOSITOL-HEXASULPHATE (three-letter code: IHS) (formula: $C_6H_{12}O_{24}S_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	S	0	0
			36	6	24	6		

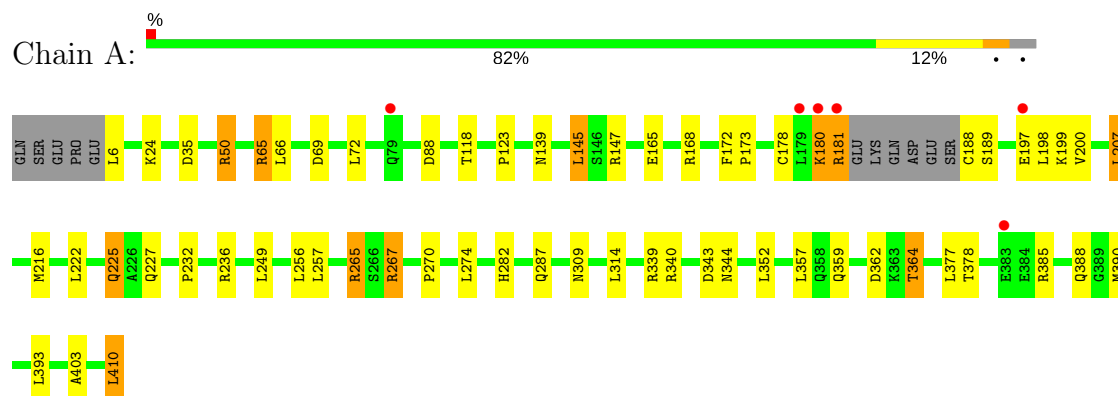
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	299	Total	O	0	0
			299	299		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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: Periplasmic AppA protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	63.80Å 47.50Å 65.63Å 90.00° 100.51° 90.00°	Depositor
Resolution (Å)	25.00 – 2.07 23.75 – 2.07	Depositor EDS
% Data completeness (in resolution range)	99.6 (25.00-2.07) 99.7 (23.75-2.07)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.54 (at 2.08Å)	Xtriage
Refinement program	REFMAC 5.8.0071	Depositor
R, R_{free}	0.172 , 0.218 0.181 , 0.225	Depositor DCC
R_{free} test set	1182 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	16.1	Xtriage
Anisotropy	0.569	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 51.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.026 for l,-k,h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3393	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.60% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NI, IHS

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	0.79	0/3119	0.96	13/4254 (0.3%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	50	ARG	NE-CZ-NH2	-12.25	114.17	120.30
1	A	265	ARG	NE-CZ-NH2	-11.71	114.45	120.30
1	A	50	ARG	NE-CZ-NH1	10.34	125.47	120.30
1	A	265	ARG	NE-CZ-NH1	10.26	125.43	120.30
1	A	236	ARG	NE-CZ-NH1	7.63	124.11	120.30
1	A	147	ARG	NE-CZ-NH1	-6.97	116.81	120.30
1	A	35	ASP	CB-CG-OD2	6.76	124.38	118.30
1	A	343	ASP	CB-CG-OD2	5.88	123.59	118.30
1	A	267	ARG	NE-CZ-NH2	-5.69	117.46	120.30
1	A	147	ARG	NE-CZ-NH2	5.49	123.04	120.30
1	A	88	ASP	CB-CG-OD1	5.46	123.21	118.30
1	A	50	ARG	CD-NE-CZ	5.32	131.05	123.60
1	A	267	ARG	NE-CZ-NH1	5.07	122.83	120.30

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	3054	0	3063	37	0
2	A	4	0	0	0	0
3	A	36	0	12	2	0
4	A	299	0	0	7	0
All	All	3393	0	3075	38	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 6.

All (38) 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:265:ARG:HD2	1:A:403:ALA:O	1.77	0.85
1:A:6:LEU:N	4:A:814:HOH:O	2.15	0.79
1:A:69:ASP:OD1	4:A:703:HOH:O	2.13	0.65
1:A:282:HIS:NE2	4:A:849:HOH:O	2.30	0.65
1:A:225:GLN:HE21	1:A:232:PRO:HG2	1.64	0.63
1:A:270:PRO:HB3	1:A:410:LEU:HD22	1.82	0.62
1:A:207:LEU:HD22	1:A:257:LEU:HD21	1.83	0.61
1:A:180:LYS:O	1:A:181:ARG:HB2	2.02	0.59
1:A:378:THR:HB	4:A:613:HOH:O	2.01	0.59
1:A:339:ARG:HH11	1:A:344:ASN:ND2	2.01	0.59
1:A:265:ARG:CD	1:A:403:ALA:O	2.49	0.59
1:A:359:GLN:HA	1:A:364:THR:HG23	1.87	0.57
1:A:165:GLU:OE2	1:A:168:ARG:NH2	2.37	0.56
1:A:172:PHE:N	1:A:173:PRO:CD	2.69	0.56
1:A:139:ASN:ND2	4:A:601:HOH:O	2.36	0.55
1:A:180:LYS:HA	1:A:180:LYS:HE2	1.89	0.55
1:A:362:ASP:HB2	1:A:364:THR:HG22	1.88	0.54
1:A:282:HIS:CE1	4:A:849:HOH:O	2.61	0.53
1:A:378:THR:CB	4:A:613:HOH:O	2.55	0.53
1:A:178:CYS:HG	1:A:188:CYS:N	2.09	0.51
1:A:225:GLN:HG2	1:A:357:LEU:HD21	1.94	0.50
1:A:6:LEU:HD13	1:A:340:ARG:HA	1.95	0.49
3:A:505:IHS:H2	3:A:505:IHS:O4	2.11	0.49
1:A:267:ARG:NH1	1:A:309:ASN:OD1	2.43	0.48
1:A:180:LYS:HD2	1:A:180:LYS:N	2.28	0.48
1:A:216:MET:CE	3:A:505:IHS:O24	2.63	0.46
1:A:50:ARG:HD2	1:A:227:GLN:HA	1.98	0.46
1:A:225:GLN:NE2	1:A:232:PRO:HG2	2.30	0.46
1:A:198:LEU:HA	1:A:207:LEU:HD13	1.98	0.45
1:A:385:ARG:HA	1:A:390:MET:O	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:123:PRO:HB2	1:A:410:LEU:HD11	2.00	0.44
1:A:198:LEU:HG	1:A:200:VAL:HG23	2.00	0.44
1:A:6:LEU:HD21	1:A:388:GLN:HE22	1.82	0.44
1:A:6:LEU:CD2	1:A:388:GLN:HE22	2.31	0.43
1:A:65:ARG:HD2	1:A:65:ARG:C	2.38	0.43
1:A:145:LEU:HD13	1:A:198:LEU:HD22	2.02	0.41
1:A:180:LYS:O	1:A:181:ARG:CB	2.69	0.41
1:A:197:GLU:OE1	1:A:199:LYS:NZ	2.54	0.41

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	395/410 (96%)	389 (98%)	6 (2%)	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	333/344 (97%)	311 (93%)	22 (7%)	18	10

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	LYS
1	A	65	ARG
1	A	66	LEU
1	A	72	LEU
1	A	118	THR
1	A	145	LEU
1	A	180	LYS
1	A	181	ARG
1	A	189	SER
1	A	207	LEU
1	A	222	LEU
1	A	225	GLN
1	A	249	LEU
1	A	256	LEU
1	A	274	LEU
1	A	287	GLN
1	A	314	LEU
1	A	352	LEU
1	A	364	THR
1	A	377	LEU
1	A	393	LEU
1	A	410	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	134	GLN
1	A	225	GLN
1	A	227	GLN
1	A	287	GLN
1	A	344	ASN
1	A	369	ASN
1	A	388	GLN

5.3.3 RNA ⓘ

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	IHS	A	505	-	36,36,36	2.14	19 (52%)	42,60,60	1.30	3 (7%)

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	IHS	A	505	-	-	0/30/54/54	0/1/1/1

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	505	IHS	O1-C1	-4.54	1.36	1.46
3	A	505	IHS	C1-C6	-3.18	1.45	1.52
3	A	505	IHS	O14-C4	-3.16	1.39	1.46
3	A	505	IHS	C2-C3	-3.01	1.45	1.52
3	A	505	IHS	O1-S1	-2.52	1.50	1.56
3	A	505	IHS	C3-C4	-2.42	1.47	1.52
3	A	505	IHS	O15-C5	-2.37	1.41	1.46
3	A	505	IHS	C6-C5	-2.35	1.47	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	505	IHS	O15-S5	-2.26	1.50	1.56
3	A	505	IHS	O4-S1	2.00	1.52	1.45
3	A	505	IHS	O3-S1	2.33	1.54	1.45
3	A	505	IHS	O23-S3	2.35	1.54	1.45
3	A	505	IHS	O24-S4	2.42	1.54	1.45
3	A	505	IHS	O22-S2	2.46	1.54	1.45
3	A	505	IHS	O43-S3	2.55	1.54	1.45
3	A	505	IHS	O42-S2	2.55	1.54	1.45
3	A	505	IHS	O34-S4	2.67	1.55	1.45
3	A	505	IHS	O45-S5	2.82	1.56	1.45
3	A	505	IHS	O36-S6	3.35	1.58	1.45

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	505	IHS	C5-O15-S5	-4.60	110.11	118.97
3	A	505	IHS	C1-O1-S1	-3.87	111.52	118.97
3	A	505	IHS	C3-O13-S3	-2.89	113.40	118.97

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	505	IHS	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, 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	399/410 (97%)	-0.28	6 (1%) 73 75	10, 17, 32, 51	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	179	LEU	2.7
1	A	181	ARG	2.6
1	A	79	GLN	2.4
1	A	180	LYS	2.2
1	A	383	GLU	2.2
1	A	197	GLU	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 carbohydrates 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, 95th 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	IHS	A	505	36/36	0.84	0.18	20,47,61,63	36

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NI	A	502	1/1	0.97	0.07	48,48,48,48	0
2	NI	A	501	1/1	0.97	0.06	40,40,40,40	0
2	NI	A	504	1/1	0.98	0.05	42,42,42,42	0
2	NI	A	503	1/1	0.99	0.06	21,21,21,21	0

6.5 Other polymers [i](#)

There are no such residues in this entry.