Full wwPDB X-ray Structure Validation Report (i)

Feb 6, 2025 – 05:30 PM JST

PDB ID	:	8ZHT
Title	:	Structure of PpiD-YfgM complex
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Deposited on	:	2024-05-11
Resolution	:	3.00 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 (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:

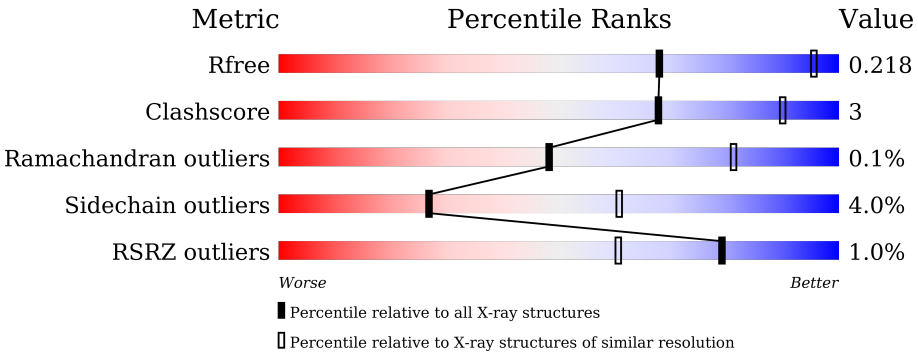
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

1 Overall quality at a glance (i)

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

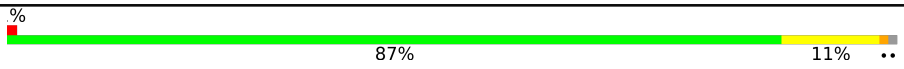
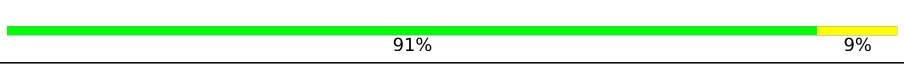
The reported resolution of this entry is 3.00 Å.

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))
R_{free}	164625	2511 (3.00-3.00)
Clashscore	180529	2866 (3.00-3.00)
Ramachandran outliers	177936	2778 (3.00-3.00)
Sidechain outliers	177891	2781 (3.00-3.00)
RSRZ outliers	164620	2523 (3.00-3.00)

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	673	
2	B	173	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6875 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.

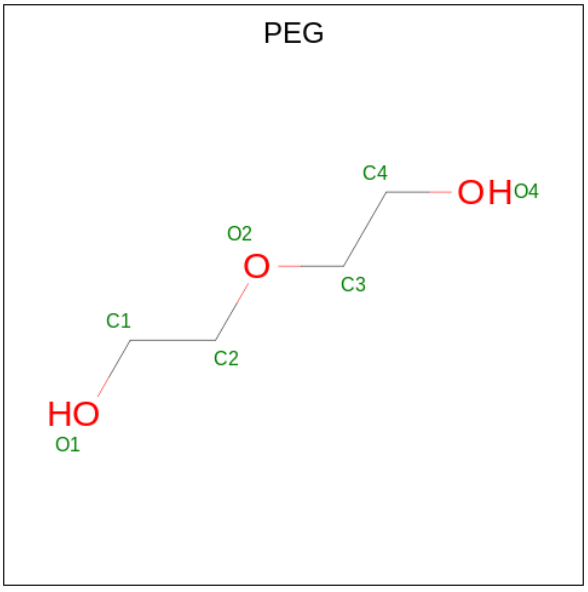
- Molecule 1 is a protein called Peptidyl-prolyl cis-trans isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	663	Total	C	N	O	S	0	0	0
			5166	3261	870	1021	14			

- Molecule 2 is a protein called Tetratricopeptide repeat protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	173	Total	C	N	O	S	0	0	0
			1325	841	214	263	7			

- Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		

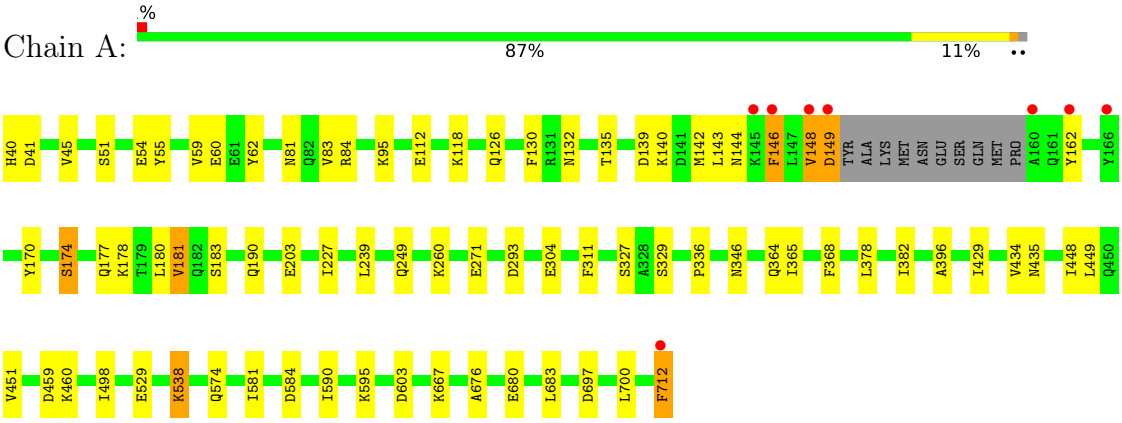
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	302	Total O 302 302	0	0
4	B	75	Total O 75 75	0	0

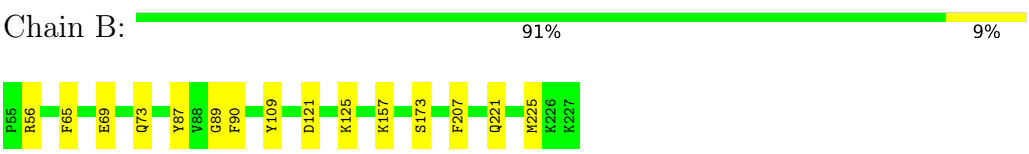
3 Residue-property plots (i)

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: Peptidyl-prolyl cis-trans isomerase



• Molecule 2: Tetratricopeptide repeat protein



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α, β, γ	76.57Å 81.35Å 212.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.19 – 3.00 34.19 – 3.00	Depositor EDS
% Data completeness (in resolution range)	98.3 (34.19-3.00) 98.2 (34.19-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.49 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.181 , 0.218 0.181 , 0.218	Depositor DCC
R_{free} test set	26594 reflections (3.05%)	wwPDB-VP
Wilson B-factor (Å^2)	37.4	Xtriage
Anisotropy	0.251	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 33.3	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	0.93	EDS
Total number of atoms	6875	wwPDB-VP
Average B, all atoms (Å^2)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.92% 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

5.1 Standard geometry

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

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	0.41	0/5252	0.57	0/7105
2	B	0.45	0/1346	0.57	0/1808
All	All	0.42	0/6598	0.57	0/8913

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

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	5166	0	5109	40	0
2	B	1325	0	1300	8	0
3	A	7	0	10	0	0
4	A	302	0	0	6	0
4	B	75	0	0	0	0
All	All	6875	0	6419	45	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 3.

All (45) 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:62:TYR:HD2	1:A:83:VAL:HG13	1.54	0.72
1:A:203:GLU:HG2	1:A:683:LEU:HD13	1.74	0.70
1:A:365:ILE:HG23	1:A:448:ILE:HB	1.75	0.68
1:A:271:GLU:HG3	4:A:1112:HOH:O	1.94	0.66
1:A:132:ASN:HD22	1:A:135:THR:HG23	1.65	0.59
1:A:146:PHE:HB2	1:A:148:VAL:HG23	1.84	0.58
1:A:260:LYS:HD2	1:A:498:ILE:HG12	1.87	0.57
1:A:118:LYS:NZ	4:A:906:HOH:O	2.39	0.56
1:A:190:GLN:HG2	4:A:1180:HOH:O	2.06	0.54
1:A:529:GLU:HB2	4:A:1066:HOH:O	2.12	0.50
1:A:62:TYR:CD2	1:A:83:VAL:HG13	2.41	0.50
1:A:130:PHE:CE1	1:A:143:LEU:HA	2.46	0.50
1:A:177:GLN:O	1:A:181:VAL:HG13	2.13	0.49
1:A:81:ASN:HA	1:A:84:ARG:HG3	1.95	0.49
1:A:112:GLU:HG3	2:B:65:PHE:CD1	2.48	0.49
1:A:676:ALA:O	1:A:680:GLU:HG3	2.13	0.49
1:A:239:LEU:HD23	1:A:581:ILE:HD12	1.96	0.47
1:A:700:LEU:HD23	1:A:700:LEU:HA	1.70	0.47
1:A:139:ASP:OD2	1:A:142:MET:HG2	2.15	0.47
1:A:697:ASP:OD1	2:B:173:SER:OG	2.34	0.46
1:A:249:GLN:HA	2:B:207:PHE:CZ	2.50	0.46
1:A:378:LEU:O	1:A:382:ILE:HG13	2.15	0.46
1:A:55:TYR:O	1:A:59:VAL:HG13	2.16	0.46
1:A:336:PRO:HA	1:A:346:ASN:O	2.16	0.45
1:A:118:LYS:HG2	1:A:140:LYS:HD3	1.99	0.45
1:A:434:VAL:O	1:A:435:ASN:HB2	2.17	0.45
1:A:170:TYR:O	1:A:174:SER:HB2	2.18	0.44
2:B:69:GLU:O	2:B:73:GLN:HG3	2.18	0.44
1:A:95:LYS:HA	1:A:95:LYS:HD3	1.72	0.44
1:A:365:ILE:HD12	1:A:396:ALA:HA	1.99	0.44
2:B:121:ASP:O	2:B:125:LYS:HG3	2.18	0.44
1:A:603:ASP:HB2	4:A:969:HOH:O	2.19	0.43
1:A:51:SER:OG	1:A:54:GLU:HG3	2.19	0.43
1:A:712:PHE:HB2	4:A:1108:HOH:O	2.18	0.43
1:A:180:LEU:HD12	1:A:180:LEU:HA	1.79	0.42
1:A:434:VAL:HA	1:A:451:VAL:HG12	2.01	0.42
1:A:178:LYS:HD2	1:A:178:LYS:HA	1.59	0.42
2:B:221:GLN:O	2:B:225:MET:HG3	2.20	0.42
1:A:148:VAL:O	1:A:149:ASP:HB2	2.19	0.42
2:B:87:TYR:CE2	2:B:89:GLY:HA2	2.55	0.42
1:A:311:PHE:HB3	1:A:460:LYS:HB3	2.03	0.41
1:A:429:ILE:HG13	1:A:449:LEU:HD11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:90:PHE:CE2	2:B:109:TYR:HB3	2.56	0.41
1:A:538:LYS:N	1:A:538:LYS:HD2	2.36	0.40
1:A:227:ILE:HD11	1:A:590:ILE:HG13	2.04	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	659/673 (98%)	636 (96%)	22 (3%)	1 (0%)	44 77
2	B	171/173 (99%)	168 (98%)	3 (2%)	0	100 100
All	All	830/846 (98%)	804 (97%)	25 (3%)	1 (0%)	48 81

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	144	ASN

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	545/554 (98%)	520 (95%)	25 (5%)	23 56
2	B	131/131 (100%)	129 (98%)	2 (2%)	60 83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	676/685 (99%)	649 (96%)	27 (4%)	27 61

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	HIS
1	A	41	ASP
1	A	45	VAL
1	A	60	GLU
1	A	126	GLN
1	A	146	PHE
1	A	148	VAL
1	A	149	ASP
1	A	162	TYR
1	A	174	SER
1	A	181	VAL
1	A	183	SER
1	A	293	ASP
1	A	304	GLU
1	A	327	SER
1	A	329	SER
1	A	364	GLN
1	A	368	PHE
1	A	459	ASP
1	A	538	LYS
1	A	574	GLN
1	A	584	ASP
1	A	595	LYS
1	A	667	LYS
1	A	712	PHE
2	B	56	ARG
2	B	157	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	ASN
1	A	132	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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

1 ligand is modelled in this entry.

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	PEG	A	801	-	6,6,6	0.13	0	5,5,5	0.12	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
3	PEG	A	801	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	801	PEG	O1-C1-C2-O2
3	A	801	PEG	C1-C2-O2-C3

There are no ring outliers.

No monomer is involved in short contacts.

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	663/673 (98%)	-0.30	8 (1%) 76 56	26, 45, 85, 133	0
2	B	173/173 (100%)	-0.58	0 100 100	26, 34, 50, 69	0
All	All	836/846 (98%)	-0.36	8 (0%) 79 60	26, 43, 81, 133	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	149	ASP	5.3
1	A	712	PHE	3.7
1	A	162	TYR	3.1
1	A	146	PHE	2.8
1	A	148	VAL	2.8
1	A	145	LYS	2.5
1	A	166	TYR	2.2
1	A	160	ALA	2.1

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

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(Å^2)	Q<0.9
3	PEG	A	801	7/7	0.83	0.17	55,60,64,65	0

6.5 Other polymers (i)

There are no such residues in this entry.