wwPDB X-ray Structure Validation Summary Report (i)

Jan 31, 2016 – 07:56 PM GMT

PDB ID	:	1HY5
Title	:	CRYSTAL STRUCTURE OF THE CATALYTIC DOMAIN OF YOPE-YERSINIA PESTIS GAP EFFECTOR PROTEIN.
Authors	:	Evdokimov, A.G.; Tropea, J.E.; Routzahn, K.M.; Waugh, D.S.
Deposited on	:	2001-01-18
Resolution	:	2.25 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
http://wwpdb.org/validation/2016/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:

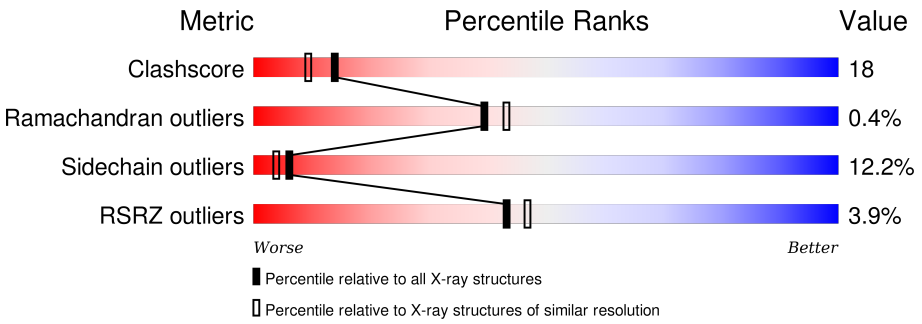
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.25 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	102246	1095 (2.26-2.26)
Ramachandran outliers	100387	1063 (2.26-2.26)
Sidechain outliers	100360	1063 (2.26-2.26)
RSRZ outliers	91569	1647 (2.28-2.24)

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 <=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	136	4% 56% 29% • 12%
1	B	136	3% 57% 28% • 11%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1843 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 YERSINIA PESTIS VIRULENCE PROTEIN YOPE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	120	883	550	149	176	3	5	0	0	0
1	B	121	893	556	152	177	3	5	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1096	MSE	MET	modified residue	UNP P31493
A	1118	MSE	MET	modified residue	UNP P31493
A	1128	MSE	MET	modified residue	UNP P31493
A	1154	MSE	MET	modified residue	UNP P31493
A	1212	MSE	MET	modified residue	UNP P31493
A	1219	MSE	MET	modified residue	UNP P31493
A	1220	HIS	-	EXPRESSION TAG	UNP P31493
A	1221	HIS	-	EXPRESSION TAG	UNP P31493
A	1222	HIS	-	EXPRESSION TAG	UNP P31493
A	1223	HIS	-	EXPRESSION TAG	UNP P31493
A	1224	HIS	-	EXPRESSION TAG	UNP P31493
A	1225	HIS	-	EXPRESSION TAG	UNP P31493
B	2096	MSE	MET	modified residue	UNP P31493
B	2118	MSE	MET	modified residue	UNP P31493
B	2128	MSE	MET	modified residue	UNP P31493
B	2154	MSE	MET	modified residue	UNP P31493
B	2212	MSE	MET	modified residue	UNP P31493
B	2219	MSE	MET	modified residue	UNP P31493
B	2220	HIS	-	EXPRESSION TAG	UNP P31493
B	2221	HIS	-	EXPRESSION TAG	UNP P31493
B	2222	HIS	-	EXPRESSION TAG	UNP P31493
B	2223	HIS	-	EXPRESSION TAG	UNP P31493
B	2224	HIS	-	EXPRESSION TAG	UNP P31493
B	2225	HIS	-	EXPRESSION TAG	UNP P31493

- Molecule 2 is water.

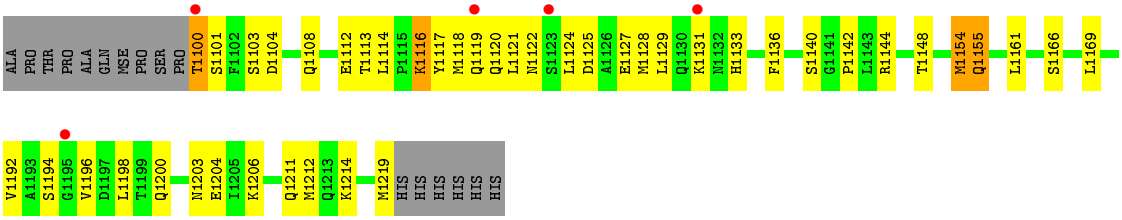
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	29	29	29	0	0
			Total	O		
2	B	38	38	38	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

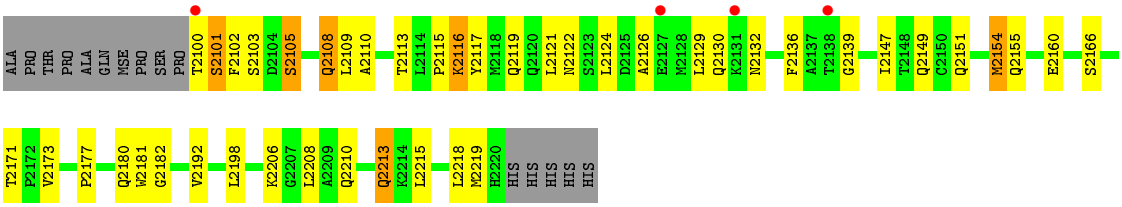
- Molecule 1: YERSINIA PESTIS VIRULENCE PROTEIN YOPE

Chain A:



- Molecule 1: YERSINIA PESTIS VIRULENCE PROTEIN YOPE

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	62.69Å 71.98Å 62.68Å 90.00° 113.06° 90.00°	Depositor
Resolution (Å)	100.00 – 2.25 19.71 – 2.25	Depositor EDS
% Data completeness (in resolution range)	96.0 (100.00-2.25) 97.6 (19.71-2.25)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) >$ [1]	4.13 (at 2.26Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.197 , 0.238 0.178 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å^2)	27.7	Xtriage
Anisotropy	0.551	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 103.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 22062 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	1843	wwPDB-VP
Average B, all atoms (Å^2)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.28% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.46	0/890	1.16	2/1193 (0.2%)
1	B	0.44	0/901	1.09	1/1208 (0.1%)
All	All	0.45	0/1791	1.13	3/2401 (0.1%)

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	B	2215	LEU	CA-CB-CG	6.35	129.91	115.30
1	A	1133	HIS	CA-CB-CG	-5.80	103.74	113.60
1	A	1100	THR	C-N-CA	5.54	135.55	121.70

There are no chirality outliers.

There are no planarity outliers.

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	883	0	875	37	0
1	B	893	0	882	28	0
2	A	29	0	0	1	0
2	B	38	0	0	1	0
All	All	1843	0	1757	65	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 18.

The worst 5 of 65 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:1114:LEU:HB3	1:A:1118:MSE:HE3	1.40	1.00
1:A:1118:MSE:HE2	1:A:1212:MSE:HB3	1.48	0.95
1:B:2122:ASN:HD21	1:B:2210:GLN:HE22	1.02	0.91
1:B:2129:LEU:HD21	1:B:2198:LEU:HB3	1.63	0.78
1:A:1192:VAL:HG13	1:A:1198:LEU:HD11	1.65	0.78

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	118/136 (87%)	116 (98%)	2 (2%)	0	100	100
1	B	119/136 (88%)	115 (97%)	3 (2%)	1 (1%)	24	21
All	All	237/272 (87%)	231 (98%)	5 (2%)	1 (0%)	39	43

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	2101	SER

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	94/102 (92%)	82 (87%)	12 (13%)	5 3
1	B	95/102 (93%)	84 (88%)	11 (12%)	7 4
All	All	189/204 (93%)	166 (88%)	23 (12%)	6 4

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1154	MSE
1	B	2101	SER
1	B	2213	GLN
1	A	1155	GLN
1	B	2103	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1155	GLN
1	B	2220	HIS
1	B	2210	GLN
1	A	1122	ASN
1	B	2213	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 carbohydrates 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	115/136 (84%)	0.08	5 (4%)	39	43	15, 28, 57, 84	0
1	B	116/136 (85%)	0.17	4 (3%)	49	53	15, 28, 60, 80	0
All	All	231/272 (84%)	0.12	9 (3%)	43	47	15, 28, 60, 84	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1100	THR	3.9
1	A	1131	LYS	2.8
1	B	2138	THR	2.3
1	A	1123	SER	2.3
1	B	2100	THR	2.3

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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.