wwPDB X-ray Structure Validation Summary Report (i)

May 13, 2020 – 01:36 am BST

PDB ID	:	2BSK
Title	:	Crystal structure of the TIM9 Tim10 hexameric complex
Authors	:	Webb, C.T.; Gorman, M.A.; Lazarus, M.; Ryan, M.T.; Gulbis, J.M.
Deposited on	:	2005-05-23
Resolution	:	3.30 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 (i) symbol.

The following versions of software and data (see references (i)) were used in the production of this report:

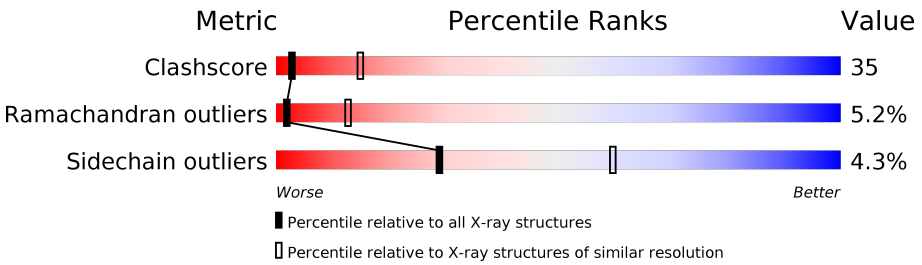
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 3.30 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	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)

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 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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	89	47% 29% 6% 18%
1	C	89	44% 38% 6% • 11%
1	E	89	37% 34% 29%
2	B	90	36% 34% • 28%
2	D	90	39% 51% 10%
2	F	90	30% 38% • 29%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3334 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 MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM9 A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	73	573	360	97	110	6	0	0	0
1	C	79	604	385	101	112	6	0	0	0
1	E	63	509	324	84	95	6	0	0	0

- Molecule 2 is a protein called MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM10.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
2	B	65	507	311	89	97	4	6	0	0	0
2	D	90	660	406	115	127	4	8	0	0	0
2	F	64	481	296	84	92	4	5	0	0	0

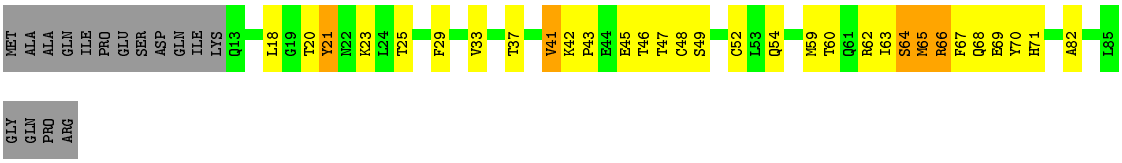
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

Note EDS was not executed.

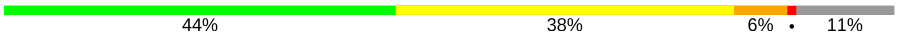
• Molecule 1: MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM9 A

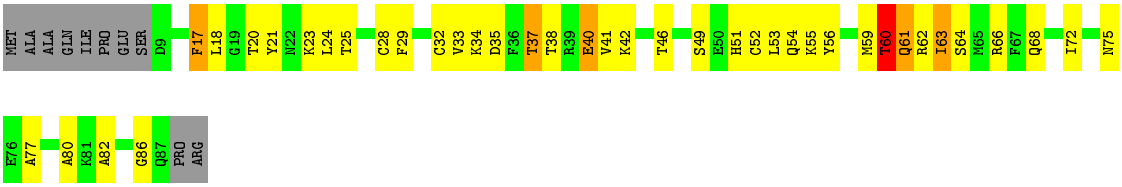
Chain A:



• Molecule 1: MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM9 A

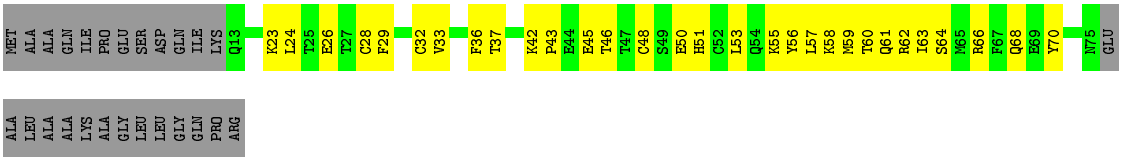
Chain C:





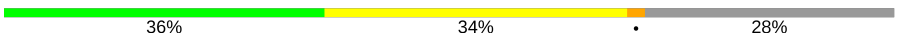
• Molecule 1: MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM9 A

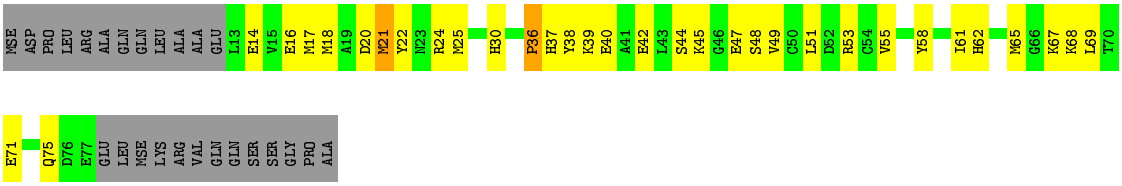
Chain E:



• Molecule 2: MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM10

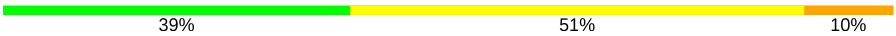
Chain B:

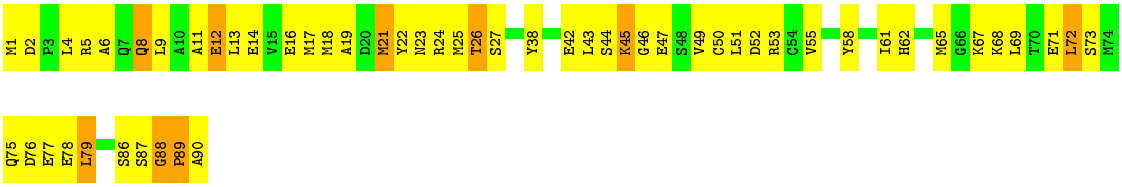




• Molecule 2: MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM10

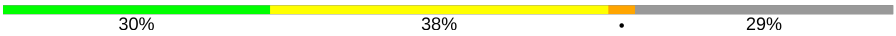
Chain D:

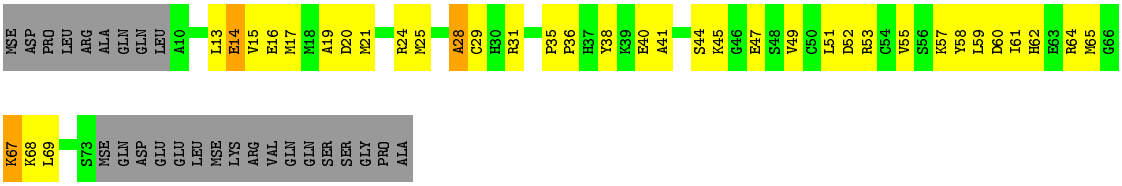




• Molecule 2: MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM10

Chain F:





4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	107.43Å 107.43Å 110.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	16.00 – 3.30	Depositor
% Data completeness (in resolution range)	92.6 (16.00-3.30)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.268 , 0.319	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3334	wwPDB-VP
Average B, all atoms (Å^2)	72.0	wwPDB-VP

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	0.41	0/583	0.64	0/785
1	C	0.47	0/613	0.72	0/825
1	E	0.38	0/519	0.60	0/698
2	B	0.36	0/508	0.65	0/670
2	D	0.50	0/662	0.75	1/882 (0.1%)
2	F	0.42	0/483	0.70	0/641
All	All	0.43	0/3368	0.68	1/4501 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	79	LEU	N-CA-C	-5.71	95.58	111.00

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	573	0	527	32	0
1	C	604	0	567	55	0
1	E	509	0	474	26	0
2	B	507	0	484	27	0
2	D	660	0	614	83	0
2	F	481	0	448	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	3334	0	3114	228	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 35.

The worst 5 of 228 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)
2:D:44:SER:HB3	2:D:47:GLU:HG3	1.17	1.10
1:E:62:ARG:HH12	1:E:66:ARG:HH21	1.04	0.98
2:D:61:ILE:O	2:D:65:MSE:HG2	1.74	0.86
2:F:44:SER:HB3	2:F:47:GLU:HG3	1.55	0.86
1:C:37:THR:HA	2:F:53:ARG:NH1	1.92	0.84

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	71/89 (80%)	51 (72%)	14 (20%)	6 (8%)	1 5
1	C	76/89 (85%)	55 (72%)	17 (22%)	4 (5%)	2 12
1	E	61/89 (68%)	51 (84%)	9 (15%)	1 (2%)	9 36
2	B	63/90 (70%)	56 (89%)	6 (10%)	1 (2%)	9 36
2	D	88/90 (98%)	65 (74%)	18 (20%)	5 (6%)	1 11
2	F	62/90 (69%)	45 (73%)	12 (19%)	5 (8%)	1 6
All	All	421/537 (78%)	323 (77%)	76 (18%)	22 (5%)	2 13

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	72	LEU
2	D	89	PRO
1	A	41	VAL
1	A	69	GLU
1	A	82	ALA

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	59/80 (74%)	57 (97%)	2 (3%)	37	65
1	C	61/80 (76%)	57 (93%)	4 (7%)	16	46
1	E	55/80 (69%)	55 (100%)	0	100	100
2	B	56/72 (78%)	54 (96%)	2 (4%)	35	63
2	D	67/72 (93%)	62 (92%)	5 (8%)	13	39
2	F	50/72 (69%)	48 (96%)	2 (4%)	31	61
All	All	348/456 (76%)	333 (96%)	15 (4%)	29	59

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	60	THR
1	C	61	GLN
2	D	45	LYS
1	C	40	GLU
2	D	26	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	30	HIS
1	E	51	HIS
2	D	8	GLN
1	A	75	ASN

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Mol	Chain	Res	Type
2	B	75	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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	9:ASP	C	10:GLN	N	2.92

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.