



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 27, 2018 – 11:57 AM EST

PDB ID : 5H7L
Title : Complex of Elongation factor 2-50S ribosomal protein L12
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Deposited on : 2016-11-18
Resolution : 3.10 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030736
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20030736

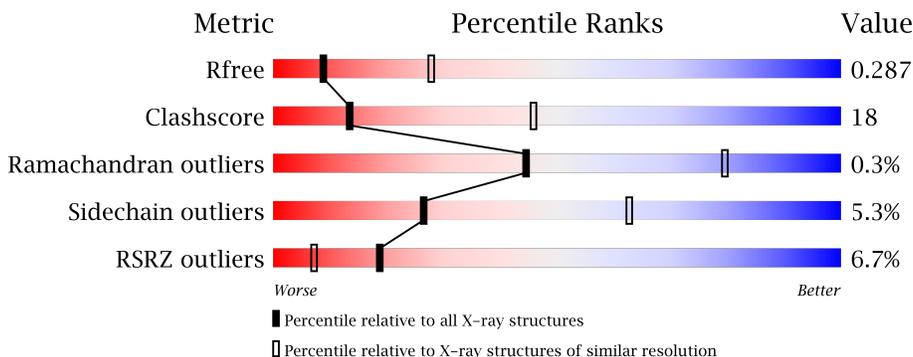
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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}	100719	1001 (3.12-3.08)
Clashscore	112137	1099 (3.12-3.08)
Ramachandran outliers	110173	1057 (3.12-3.08)
Sidechain outliers	110143	1057 (3.12-3.08)
RSRZ outliers	101464	1006 (3.12-3.08)

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	743	
1	B	743	
2	E	11	
2	G	11	

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 11115 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 Elongation factor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	694	5476	3477	959	1006	34	0	0	0
1	B	691	5452	3463	955	1000	34	0	0	0

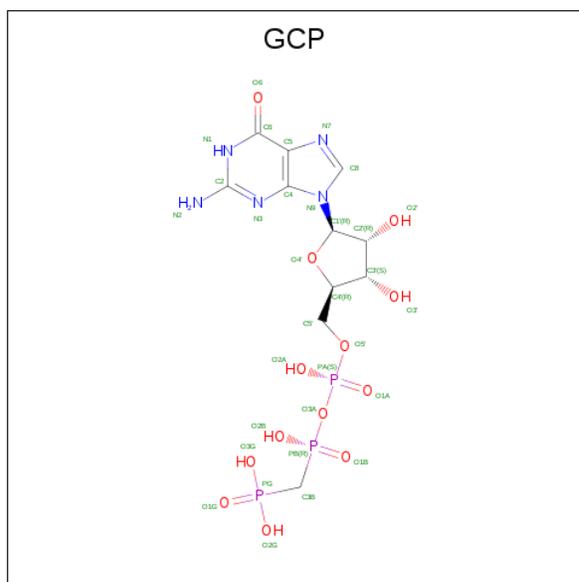
There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP O59521
A	2	VAL	-	expression tag	UNP O59521
A	3	GLU	-	expression tag	UNP O59521
A	736	LEU	-	expression tag	UNP O59521
A	737	GLU	-	expression tag	UNP O59521
A	738	HIS	-	expression tag	UNP O59521
A	739	HIS	-	expression tag	UNP O59521
A	740	HIS	-	expression tag	UNP O59521
A	741	HIS	-	expression tag	UNP O59521
A	742	HIS	-	expression tag	UNP O59521
A	743	HIS	-	expression tag	UNP O59521
B	1	MET	-	expression tag	UNP O59521
B	2	VAL	-	expression tag	UNP O59521
B	3	GLU	-	expression tag	UNP O59521
B	736	LEU	-	expression tag	UNP O59521
B	737	GLU	-	expression tag	UNP O59521
B	738	HIS	-	expression tag	UNP O59521
B	739	HIS	-	expression tag	UNP O59521
B	740	HIS	-	expression tag	UNP O59521
B	741	HIS	-	expression tag	UNP O59521
B	742	HIS	-	expression tag	UNP O59521
B	743	HIS	-	expression tag	UNP O59521

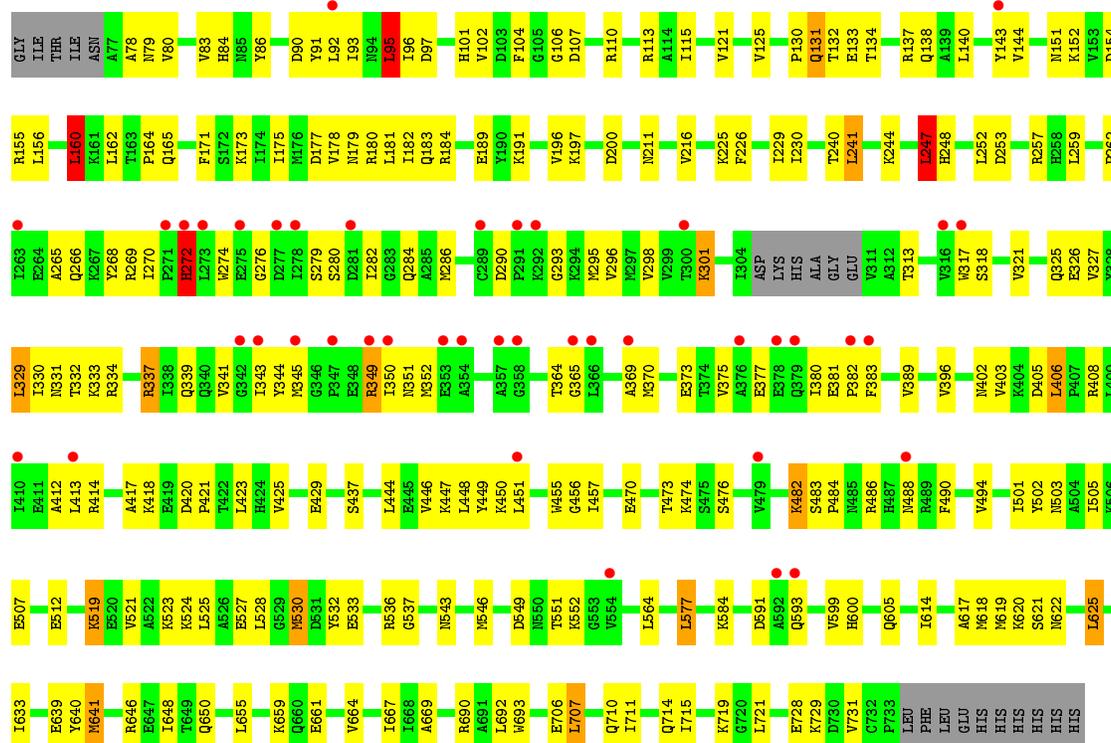
- Molecule 2 is a protein called 50S ribosomal protein L12.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	G	10	64	43	10	11	0	0	0
2	E	9	59	40	9	10	0	0	0

- Molecule 3 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃).



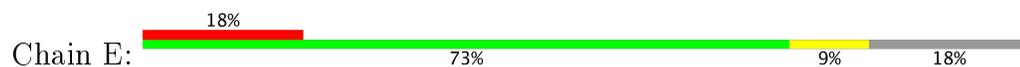
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	32	11	5	13	3	0	0
3	B	1	32	11	5	13	3	0	0



- Molecule 2: 50S ribosomal protein L12



- Molecule 2: 50S ribosomal protein L12



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	79.77Å 121.90Å 199.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.43 – 3.10 48.43 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.4 (48.43-3.10) 99.4 (48.43-3.10)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.60 (at 3.12Å)	Xtrriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.230 , 0.285 0.233 , 0.287	Depositor DCC
R_{free} test set	1794 reflections (5.01%)	DCC
Wilson B-factor (Å ²)	93.1	Xtrriage
Anisotropy	0.565	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 73.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	11115	wwPDB-VP
Average B, all atoms (Å ²)	108.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.57% 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](#)

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

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	0.54	0/5577	0.80	6/7541 (0.1%)
1	B	0.54	0/5552	0.77	4/7508 (0.1%)
2	E	0.38	0/59	0.68	0/78
2	G	0.35	0/64	0.71	0/85
All	All	0.54	0/11252	0.78	10/15212 (0.1%)

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	A	0	2
1	B	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	95	LEU	CA-CB-CG	8.16	134.07	115.30
1	B	247	LEU	CA-CB-CG	7.26	132.01	115.30
1	A	406	LEU	CA-CB-CG	5.97	129.03	115.30
1	A	19	LEU	CA-CB-CG	5.82	128.68	115.30
1	A	162	LEU	CA-CB-CG	5.65	128.30	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	377	GLU	Peptide
1	A	452	LYS	Peptide
1	B	272	HIS	Sidechain

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	5476	0	5594	223	0
1	B	5452	0	5581	181	0
2	E	59	0	62	2	0
2	G	64	0	67	3	0
3	A	32	0	14	3	0
3	B	32	0	14	2	0
All	All	11115	0	11332	404	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 404 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:104:PHE:HB3	1:B:106:GLY:H	1.25	0.98
1:A:184:ARG:NH1	1:A:639:GLU:OE2	2.01	0.94
1:B:216:VAL:HG22	2:G:106:LEU:HD11	1.46	0.94
1:A:401:LYS:HE2	1:A:402:ASN:ND2	1.84	0.93
1:B:143:TYR:HE2	1:B:272:HIS:CD2	1.87	0.92

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	688/743 (93%)	643 (94%)	41 (6%)	4 (1%)	28	67
1	B	685/743 (92%)	641 (94%)	44 (6%)	0	100	100
2	E	7/11 (64%)	7 (100%)	0	0	100	100
2	G	8/11 (73%)	8 (100%)	0	0	100	100
All	All	1388/1508 (92%)	1299 (94%)	85 (6%)	4 (0%)	44	79

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	429	GLU
1	A	529	GLY
1	A	367	ARG
1	A	428	ASP

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	595/638 (93%)	566 (95%)	29 (5%)	29	66
1	B	593/638 (93%)	560 (94%)	33 (6%)	25	61
2	E	5/6 (83%)	5 (100%)	0	100	100
2	G	5/6 (83%)	4 (80%)	1 (20%)	1	6
All	All	1198/1288 (93%)	1135 (95%)	63 (5%)	26	63

5 of 63 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	721	LEU
1	B	165	GLN
1	B	625	LEU
1	B	15	LYS

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Mol	Chain	Res	Type
1	B	95	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	340	GLN
1	B	131	GLN
1	A	402	ASN
1	A	339	GLN
1	A	434	HIS

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](#)

2 ligands are 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	GCP	A	801	-	25,34,34	2.82	6 (24%)	28,54,54	1.51	5 (17%)
3	GCP	B	801	-	25,34,34	3.07	9 (36%)	28,54,54	1.43	4 (14%)

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	GCP	A	801	-	-	0/18/38/38	0/3/3/3
3	GCP	B	801	-	-	0/18/38/38	0/3/3/3

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	801	GCP	C4-N9	-11.43	1.32	1.47
3	A	801	GCP	C4-N9	-10.87	1.33	1.47
3	B	801	GCP	C8-N9	-3.98	1.34	1.46
3	A	801	GCP	C8-N9	-3.80	1.35	1.46
3	B	801	GCP	PB-O2B	-3.47	1.47	1.56

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	801	GCP	PA-O3A-PB	-4.19	118.89	132.39
3	B	801	GCP	PA-O3A-PB	-2.63	123.91	132.39
3	B	801	GCP	C5'-C4'-C3'	-2.63	105.26	115.29
3	B	801	GCP	O6-C6-N1	-2.55	119.30	122.70
3	A	801	GCP	O3G-PG-O1G	-2.28	106.20	112.32

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	801	GCP	3	0
3	B	801	GCP	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	694/743 (93%)	0.39	46 (6%) 19 7	66, 104, 158, 170	0
1	B	691/743 (93%)	0.35	44 (6%) 20 7	55, 106, 152, 160	0
2	E	9/11 (81%)	1.10	2 (22%) 1 0	105, 114, 128, 140	0
2	G	10/11 (90%)	0.84	2 (20%) 1 0	123, 133, 145, 151	0
All	All	1404/1508 (93%)	0.38	94 (6%) 19 7	55, 105, 155, 170	0

The worst 5 of 94 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	331	ASN	9.5
1	A	376	ALA	8.9
1	A	386	LEU	6.5
1	A	275	GLU	5.5
1	A	382	PRO	5.0

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
3	GCP	A	801	32/32	0.89	0.28	0.81	82,106,123,135	0
3	GCP	B	801	32/32	0.93	0.17	-1.22	95,107,134,137	0

6.5 Other polymers [i](#)

There are no such residues in this entry.