



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 08:01 PM GMT

PDB ID : 4XCO
Title : Signal-sequence induced conformational changes in the signal recognition particle
Authors : Hainzl, T.; Sauer-Eriksson, A.E.
Deposited on : 2014-12-18
Resolution : 2.90 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
<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 : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
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) : rb-20026982

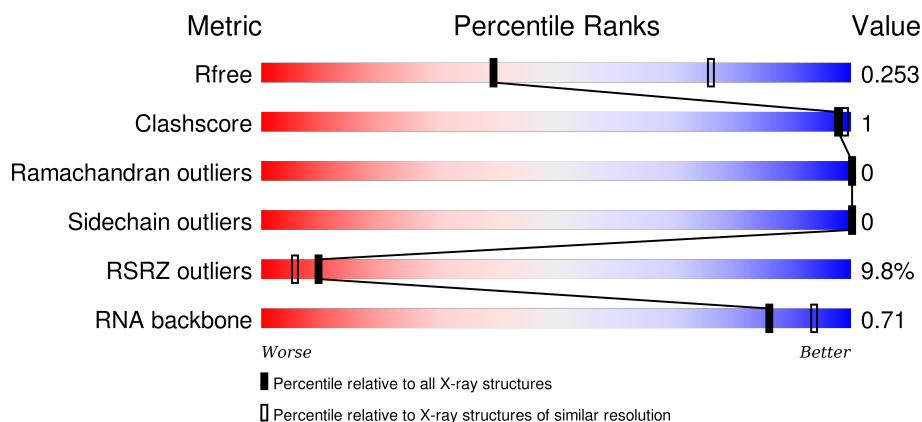
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	91344	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (2.90-2.90)
RNA backbone	2183	1093 (3.30-2.50)

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	E	96	<div> <div>2%</div> <div> <div></div> <div>86%</div> <div>13%</div> <div>.</div> </div> </div>
1	M	96	<div> <div>88%</div> <div>13%</div> </div>
2	A	87	<div> <div>%</div> <div> <div></div> <div>94%</div> <div>.</div> <div>.</div> </div> </div>
2	B	87	<div> <div>6%</div> <div> <div></div> <div>93%</div> <div>.</div> <div>.</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	C	173	
3	D	173	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	MG	E	301	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 13309 atoms, of which 5708 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 RNA chain called RNA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	M	96	Total	C	H	N	O	P	0	0	0
			3108	919	1045	385	664	95			
1	E	96	Total	C	H	N	O	P	0	0	0
			3108	919	1045	385	664	95			

- Molecule 2 is a protein called Signal recognition particle 19 kDa protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	A	85	Total	C	H	N	O	S	0	0	0
			1476	458	767	126	121	4			
2	B	84	Total	C	H	N	O	S	0	0	0
			1469	456	764	125	120	4			

- Molecule 3 is a protein called Signal recognition particle 54 kDa protein,signal sequence.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	157	Total	C	H	N	O	S	0	0	0
			2526	775	1299	217	225	10			
3	D	93	Total	C	H	N	O	S	0	0	0
			1537	465	788	138	141	5			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	303	MET	LEU	conflict	UNP Q57565
C	452	SER	-	linker	UNP Q57565
D	303	MET	LEU	conflict	UNP Q57565
D	452	SER	-	linker	UNP Q57565

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Mg 1	0	0
4	E	6	Total 6	Mg 6	0	0
4	M	7	Total 7	Mg 7	0	0

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	M	1	Total 1	Na 1	0	0


- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	M	41	Total 41	O 41	0	0
6	A	2	Total 2	O 2	0	0
6	E	26	Total 26	O 26	0	0
6	B	1	Total 1	O 1	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.

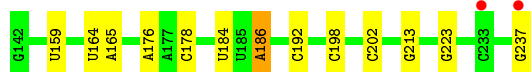
- Molecule 1: RNA

Chain M: 



- Molecule 1: RNA

Chain E: 



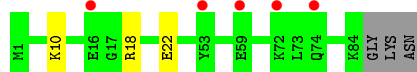
- Molecule 2: Signal recognition particle 19 kDa protein

Chain A: 




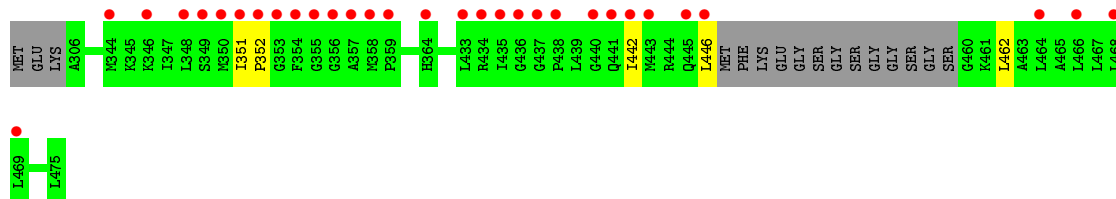
- Molecule 2: Signal recognition particle 19 kDa protein

Chain B: 

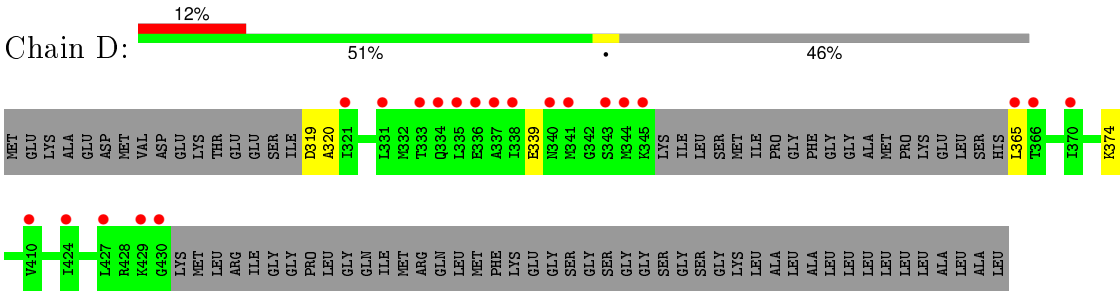


- Molecule 3: Signal recognition particle 54 kDa protein, signal sequence

Chain C: 



● Molecule 3: Signal recognition particle 54 kDa protein,signal sequence



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α , β , γ	91.23Å 112.97Å 121.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.02 – 2.90 48.02 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.6 (48.02-2.90) 99.6 (48.02-2.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 2.91Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.209 , 0.258 0.216 , 0.253	Depositor DCC
R_{free} test set	1434 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	90.0	Xtriage
Anisotropy	0.378	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 60.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	2 of 28330 reflections (0.007%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13309	wwPDB-VP
Average B, all atoms (Å ²)	106.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.48% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: NA, MG

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	E	0.20	0/2309	0.69	0/3603
1	M	0.20	0/2309	0.69	0/3603
2	A	0.23	0/722	0.41	0/962
2	B	0.22	0/718	0.39	0/957
3	C	0.23	0/1235	0.41	0/1644
3	D	0.22	0/752	0.41	0/997
All	All	0.21	0/8045	0.59	0/11766

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 [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	E	2063	1045	1045	3	0
1	M	2063	1045	1045	2	0
2	A	709	767	767	2	0
2	B	705	764	764	2	0
3	C	1227	1299	1327	4	0
3	D	749	788	798	3	0
4	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	6	0	0	0	0
4	M	7	0	0	0	0
5	M	1	0	0	0	0
6	A	2	0	0	0	0
6	B	1	0	0	0	0
6	E	26	0	0	0	0
6	M	41	0	0	0	0
All	All	7601	5708	5746	14	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 1.

All (14) 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:M:159:U:OP2	2:A:18:ARG:NH2	2.26	0.68
1:E:159:U:OP2	2:B:18:ARG:NH2	2.34	0.59
2:B:10:LYS:NZ	2:B:22:GLU:O	2.36	0.59
2:A:10:LYS:NZ	2:A:22:GLU:O	2.37	0.58
3:C:442:ILE:O	3:C:446:LEU:HG	2.08	0.52
1:E:178:C:OP1	1:E:223:G:O2'	2.27	0.52
3:D:339:GLU:OE1	3:D:374:LYS:NZ	2.44	0.51
3:D:365:LEU:O	3:D:365:LEU:HD12	2.12	0.49
1:E:184:U:HO2'	1:E:186:A:H2	1.62	0.46
3:D:319:ASP:OD1	3:D:320:ALA:N	2.48	0.45
3:C:351:ILE:HG23	3:C:352:PRO:HD3	2.02	0.42
3:C:351:ILE:N	3:C:352:PRO:HD2	2.34	0.41
1:M:178:C:OP1	1:M:223:G:O2'	2.36	0.40
3:C:446:LEU:HD13	3:C:462:LEU:HD13	2.03	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	
2	A	83/87 (95%)	77 (93%)	6 (7%)	0	100	100
2	B	82/87 (94%)	78 (95%)	4 (5%)	0	100	100
3	C	153/173 (88%)	146 (95%)	7 (5%)	0	100	100
3	D	89/173 (51%)	86 (97%)	3 (3%)	0	100	100
All	All	407/520 (78%)	387 (95%)	20 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	
2	A	78/80 (98%)	78 (100%)	0	100	100
2	B	78/80 (98%)	78 (100%)	0	100	100
3	C	133/144 (92%)	133 (100%)	0	100	100
3	D	82/144 (57%)	82 (100%)	0	100	100
All	All	371/448 (83%)	371 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	E	95/96 (98%)	9 (9%)	0
1	M	95/96 (98%)	9 (9%)	0
All	All	190/192 (98%)	18 (9%)	0

All (18) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	M	164	U
1	M	165	A
1	M	176	A
1	M	186	A
1	M	193	G
1	M	198	C
1	M	202	C
1	M	230	G
1	M	237	G
1	E	164	U
1	E	165	A
1	E	176	A
1	E	186	A
1	E	192	C
1	E	198	C
1	E	202	C
1	E	213	G
1	E	237	G

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 15 ligands modelled in this entry, 15 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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, 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	E	96/96 (100%)	0.21	2 (2%) 67 62	64, 104, 124, 144	0
1	M	96/96 (100%)	-0.03	0 100 100	63, 84, 97, 122	0
2	A	85/87 (97%)	0.42	1 (1%) 81 78	63, 79, 106, 115	0
2	B	84/87 (96%)	0.61	5 (5%) 25 18	70, 95, 114, 126	0
3	C	157/173 (90%)	1.11	31 (19%) 1 1	70, 112, 165, 182	0
3	D	93/173 (53%)	1.01	21 (22%) 1 0	71, 123, 159, 161	0
All	All	611/712 (85%)	0.61	60 (9%) 10 6	63, 95, 155, 182	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	351	ILE	8.8
3	C	358	MET	6.2
3	C	442	ILE	6.1
3	C	446	LEU	5.9
3	C	355	GLY	5.8
3	C	441	GLN	5.6
3	C	354	PHE	5.5
3	D	321	ILE	5.5
3	D	365	LEU	5.3
3	C	437	GLY	5.1
3	C	443	MET	5.1
3	C	445	GLN	5.0
3	C	357	ALA	4.7
2	B	16	GLU	4.6
3	C	348	LEU	4.4
3	C	438	PRO	4.3
3	C	352	PRO	4.3
3	C	349	SER	4.2
3	C	344	MET	4.2

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Mol	Chain	Res	Type	RSRZ
3	C	435	ILE	4.1
3	D	370	ILE	4.1
1	E	237	G	4.1
3	C	356	GLY	3.7
3	D	335	LEU	3.6
3	C	346	LYS	3.5
3	D	366	THR	3.5
3	C	468	LEU	3.4
3	C	359	PRO	3.4
3	D	341	MET	3.3
3	C	466	LEU	3.3
3	C	440	GLY	3.2
3	C	353	GLY	3.2
3	D	430	GLY	3.1
3	D	334	GLN	2.9
3	C	469	LEU	2.9
3	D	333	THR	2.7
3	D	338	ILE	2.7
3	D	424	ILE	2.7
3	D	340	ASN	2.7
3	C	433	LEU	2.6
2	B	72	LYS	2.6
3	D	429	LYS	2.6
3	C	436	GLY	2.5
3	D	344	MET	2.5
3	D	427	LEU	2.5
3	D	345	LYS	2.4
2	B	59	GLU	2.4
3	C	464	LEU	2.4
2	B	74	GLN	2.3
3	C	364	HIS	2.3
3	D	336	GLU	2.2
2	B	53	TYR	2.2
3	C	434	ARG	2.2
3	D	331	LEU	2.2
3	D	343	SER	2.1
2	A	15	ARG	2.1
1	E	233	C	2.1
3	D	410	VAL	2.1
3	D	337	ALA	2.1
3	C	350	MET	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. 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(Å ²)	Q<0.9
4	MG	E	301	1/1	0.90	0.64	23.05	78,78,78,78	0
5	NA	M	308	1/1	0.81	0.14	-0.73	94,94,94,94	0
4	MG	M	301	1/1	0.94	0.13	-1.18	83,83,83,83	0
4	MG	A	101	1/1	0.86	0.09	-1.59	89,89,89,89	0
4	MG	E	305	1/1	0.87	0.07	-1.70	84,84,84,84	0
4	MG	E	302	1/1	0.93	0.09	-5.03	75,75,75,75	0
4	MG	M	302	1/1	0.92	0.09	-5.03	83,83,83,83	0
4	MG	M	306	1/1	0.90	0.16	-	80,80,80,80	0
4	MG	M	305	1/1	0.52	0.19	-	98,98,98,98	0
4	MG	E	303	1/1	0.90	0.13	-	103,103,103,103	0
4	MG	M	304	1/1	0.94	0.07	-	87,87,87,87	0
4	MG	M	303	1/1	0.88	0.05	-	88,88,88,88	0
4	MG	E	306	1/1	0.96	0.16	-	109,109,109,109	0
4	MG	E	304	1/1	0.83	0.33	-	91,91,91,91	0
4	MG	M	307	1/1	0.93	0.10	-	99,99,99,99	0

6.5 Other polymers [i](#)

There are no such residues in this entry.