wwPDB X-ray Structure Validation Summary Report (i)

Jun 23, 2024 – 01:04 AM EDT

PDB ID	:	6JLY
Title	:	eIF2a - eIF2B complex
Authors	:	Kashiwagi, K.; Ito, T.
Deposited on	:	2019-03-07
Resolution	:	3.50 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

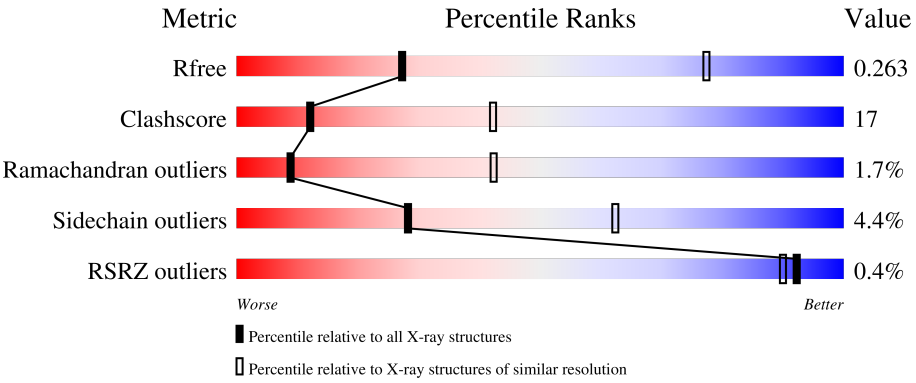
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 3.50 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}	130704	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

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	341	52% 40% • 7%
1	B	341	% 51% 40% • 7%
2	C	399	50% 33% • 15%
2	D	399	54% 29% • 16%
3	E	458	% 50% 37% • 10%

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Mol	Chain	Length	Quality of chain
3	F	458	51% 36% 10%
4	G	467	49% 26% 22%
4	H	467	% 48% 28% 22%
5	I	678	38% 24% 37%
5	J	678	39% 23% 37%
6	L	304	% 30% 24% 46%
6	M	304	31% 23% 45%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 31811 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 Translation initiation factor eIF-2B subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	316	Total	C	N	O	S	0	0	0
			2467	1568	431	455	13			
1	B	316	Total	C	N	O	S	0	0	0
			2465	1566	429	457	13			

- Molecule 2 is a protein called Probable translation initiation factor eIF-2B subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	338	Total	C	N	O	S	0	0	0
			2617	1660	443	502	12			
2	D	337	Total	C	N	O	S	0	0	0
			2609	1654	442	501	12			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	GLY	-	expression tag	UNP Q9UT76
C	-4	PRO	-	expression tag	UNP Q9UT76
C	-3	ILE	-	expression tag	UNP Q9UT76
C	-2	SER	-	expression tag	UNP Q9UT76
C	-1	GLU	-	expression tag	UNP Q9UT76
C	0	PHE	-	expression tag	UNP Q9UT76
D	-5	GLY	-	expression tag	UNP Q9UT76
D	-4	PRO	-	expression tag	UNP Q9UT76
D	-3	ILE	-	expression tag	UNP Q9UT76
D	-2	SER	-	expression tag	UNP Q9UT76
D	-1	GLU	-	expression tag	UNP Q9UT76
D	0	PHE	-	expression tag	UNP Q9UT76

- Molecule 3 is a protein called Probable translation initiation factor eIF-2B subunit gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	414	Total	C	N	O	S	0	0	0
			3216	2040	555	604	17			
3	F	412	Total	C	N	O	S	0	0	0
			3204	2034	553	600	17			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	157	TYR	ILE	conflict	UNP P56288
E	158	THR	TYR	conflict	UNP P56288
E	159	VAL	GLY	conflict	UNP P56288
F	157	TYR	ILE	conflict	UNP P56288
F	158	THR	TYR	conflict	UNP P56288
F	159	VAL	GLY	conflict	UNP P56288

- Molecule 4 is a protein called Probable translation initiation factor eIF-2B subunit delta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	G	363	Total	C	N	O	S	0	0	0
			2869	1834	486	536	13			
4	H	363	Total	C	N	O	S	0	0	0
			2869	1834	486	536	13			

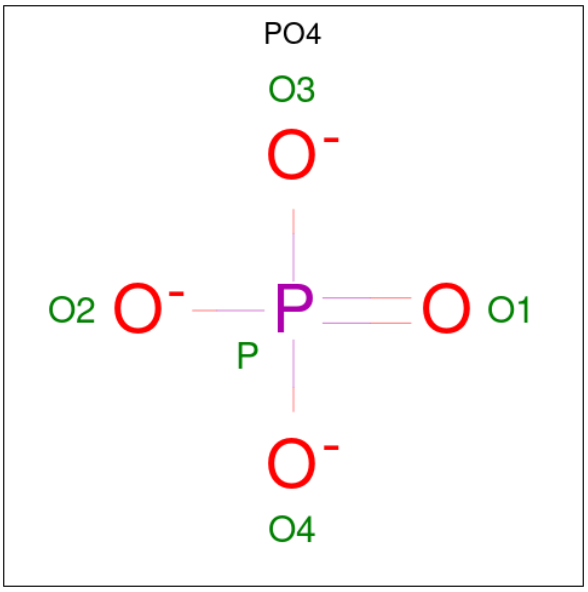
- Molecule 5 is a protein called Probable translation initiation factor eIF-2B subunit epsilon.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	I	428	Total	C	N	O	S	0	0	0
			3377	2123	592	647	15			
5	J	426	Total	C	N	O	S	0	0	0
			3362	2115	587	645	15			

- Molecule 6 is a protein called Eukaryotic translation initiation factor 2 subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	L	165	Total	C	N	O	S	0	0	0
			1353	863	226	258	6			
6	M	166	Total	C	N	O	S	0	0	0
			1363	872	227	258	6			

- Molecule 7 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



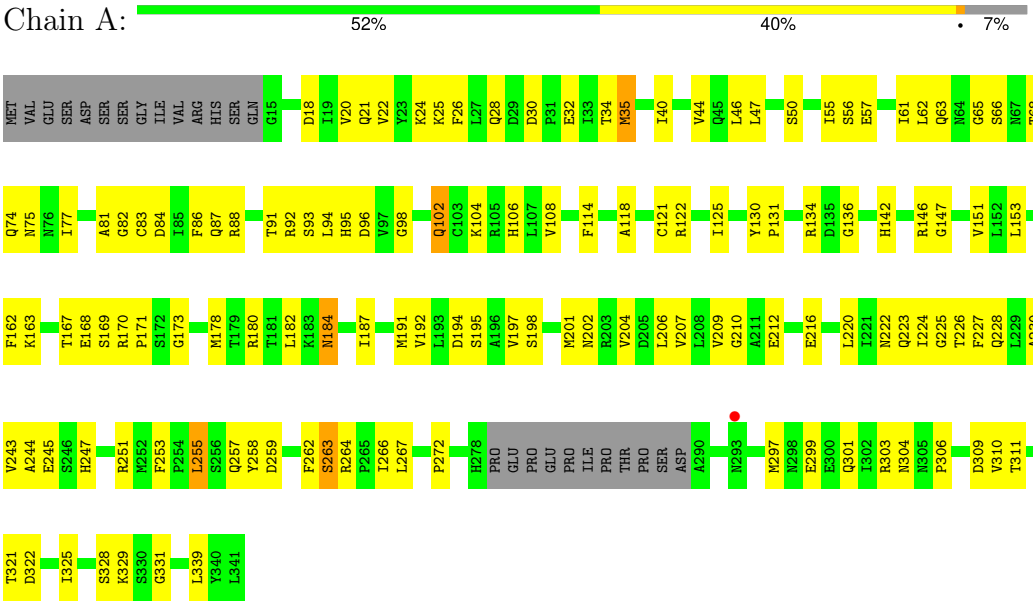
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	C	1	Total O P 5 4 1	0	0
7	D	1	Total O P 5 4 1	0	0
7	E	1	Total O P 5 4 1	0	0
7	E	1	Total O P 5 4 1	0	0
7	F	1	Total O P 5 4 1	0	0
7	F	1	Total O P 5 4 1	0	0
7	G	1	Total O P 5 4 1	0	0
7	H	1	Total O P 5 4 1	0	0

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.

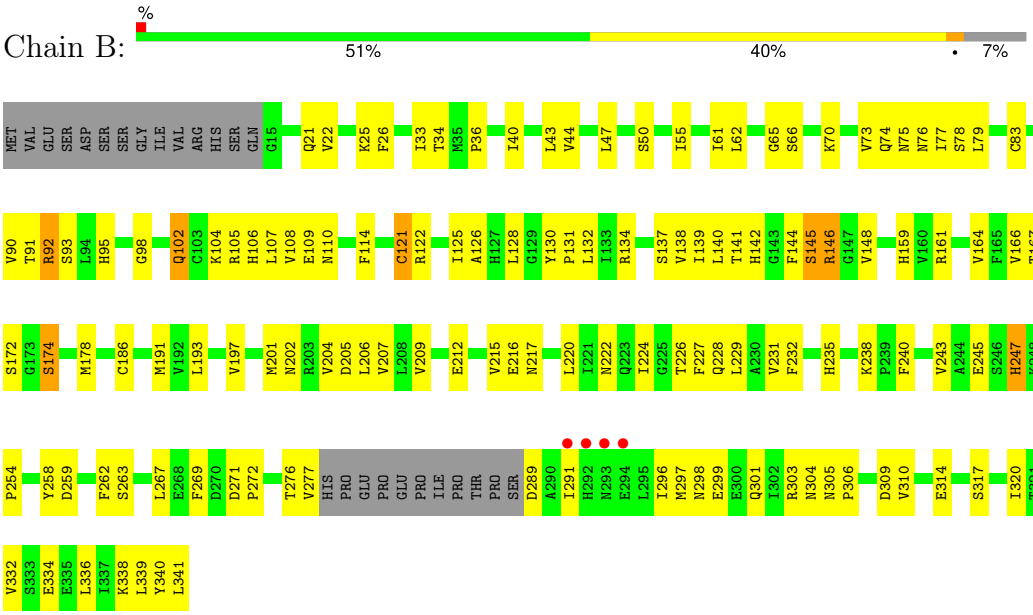
• Molecule 1: Translation initiation factor eIF-2B subunit alpha

Chain A:



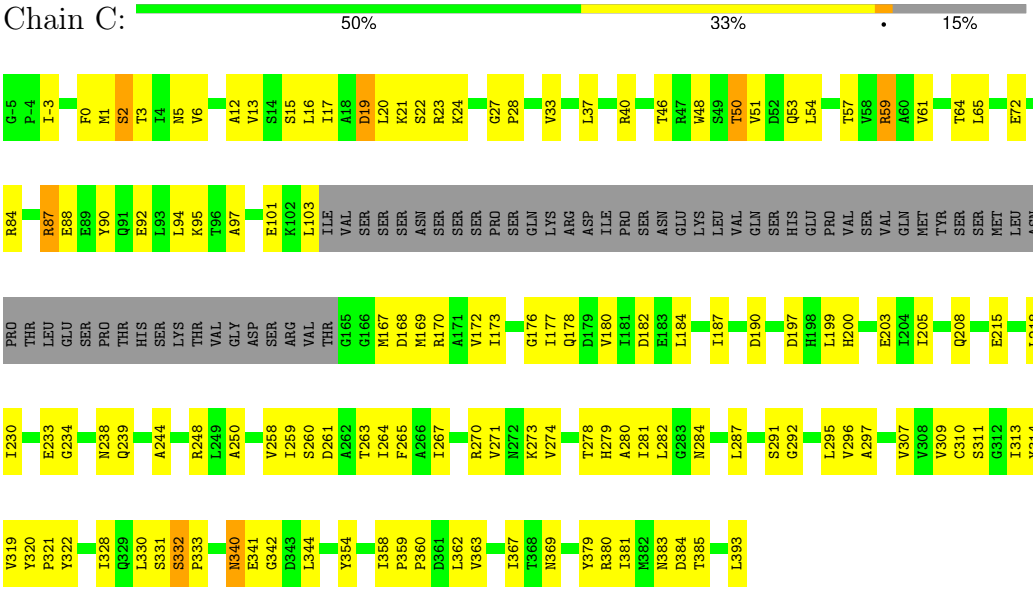
• Molecule 1: Translation initiation factor eIF-2B subunit alpha

Chain B:



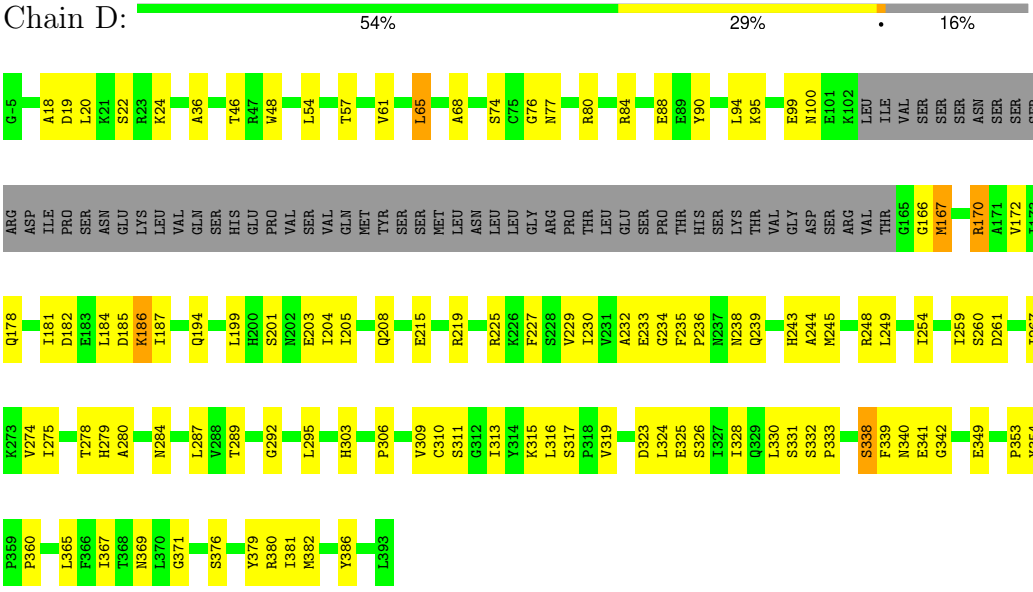
• Molecule 2: Probable translation initiation factor eIF-2B subunit beta

Chain C:



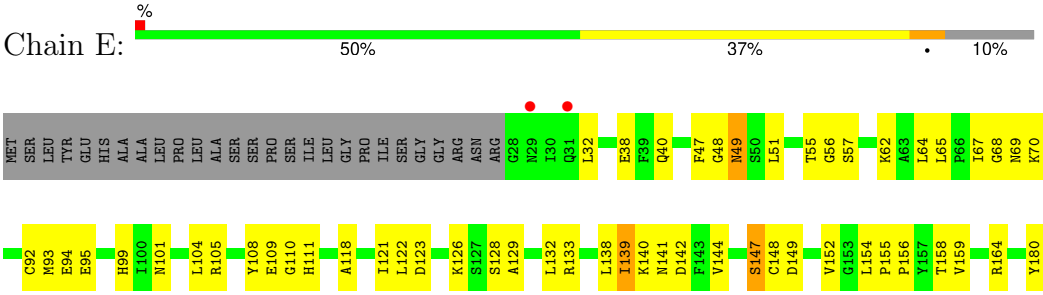
• Molecule 2: Probable translation initiation factor eIF-2B subunit beta

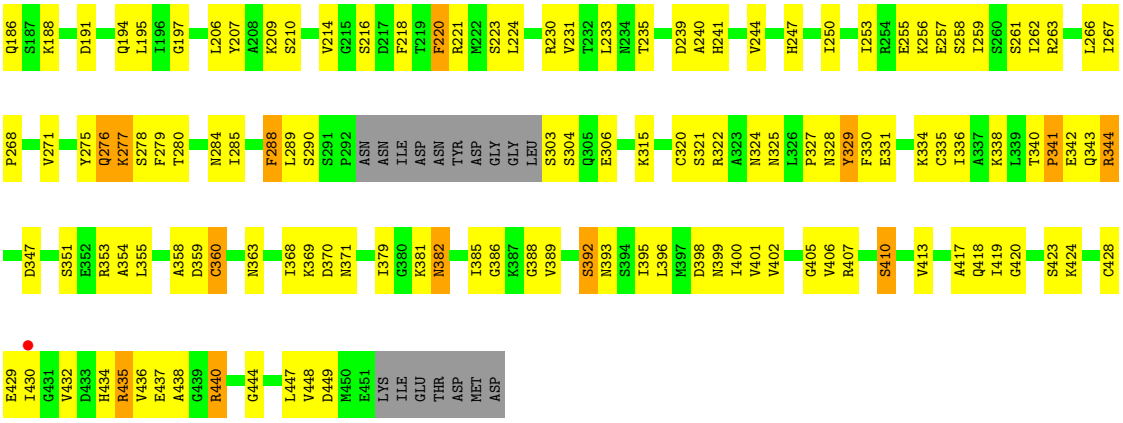
Chain D:



• Molecule 3: Probable translation initiation factor eIF-2B subunit gamma

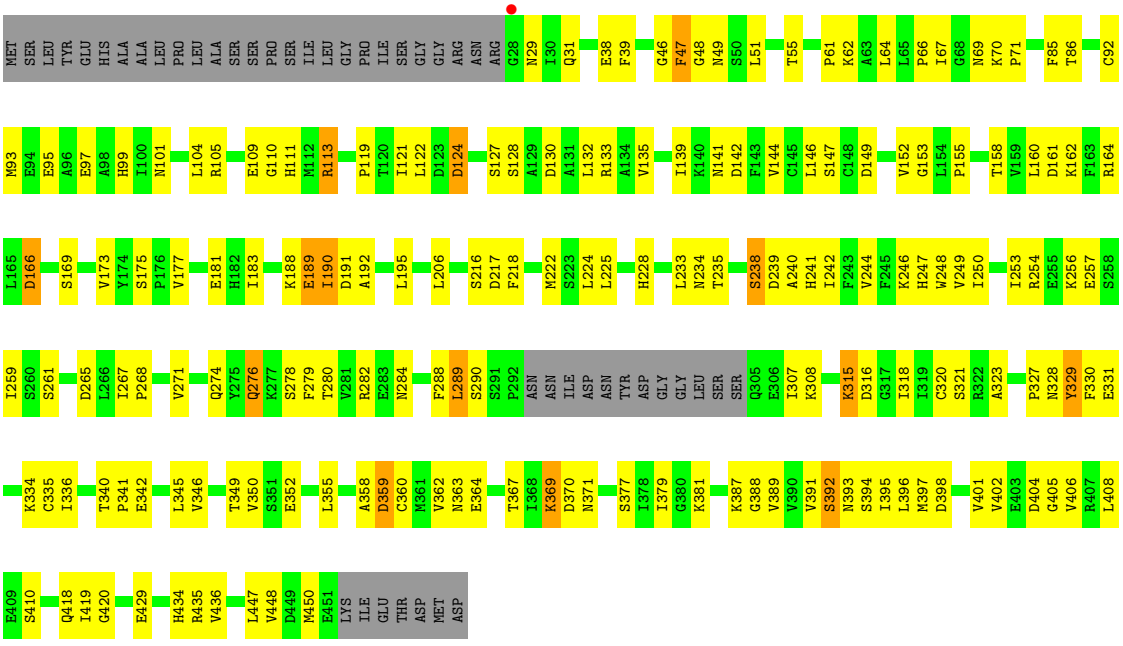
Chain E:





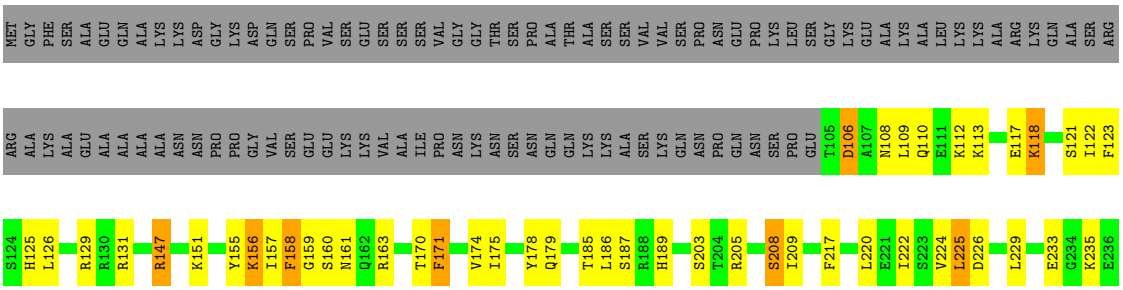
• Molecule 3: Probable translation initiation factor eIF-2B subunit gamma

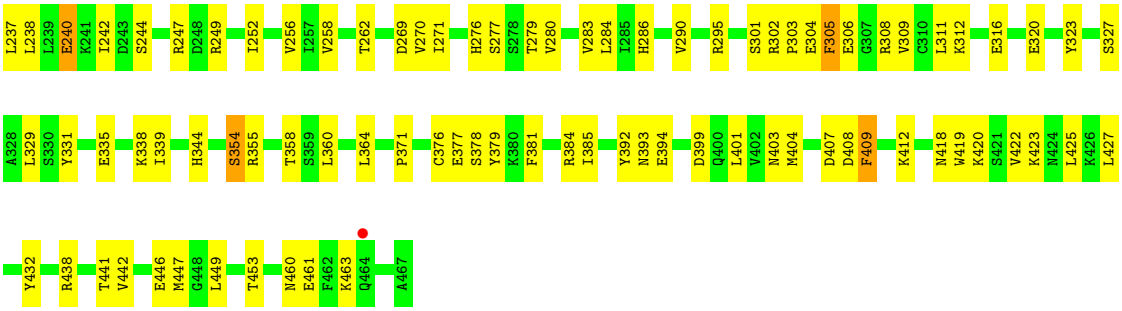
Chain F:

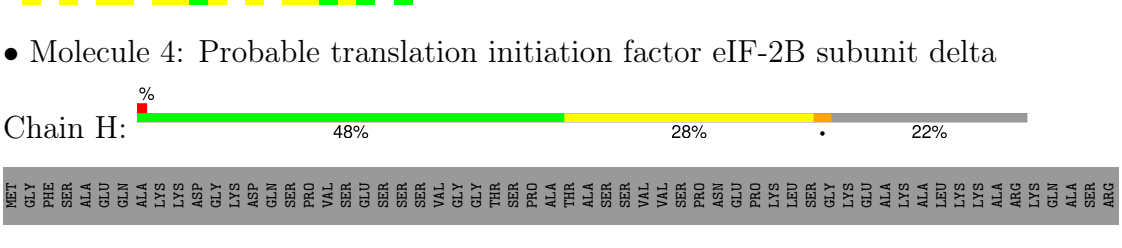


• Molecule 4: Probable translation initiation factor eIF-2B subunit delta

Chain G:

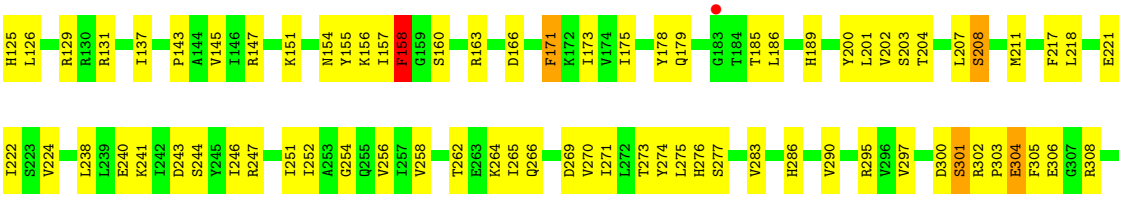


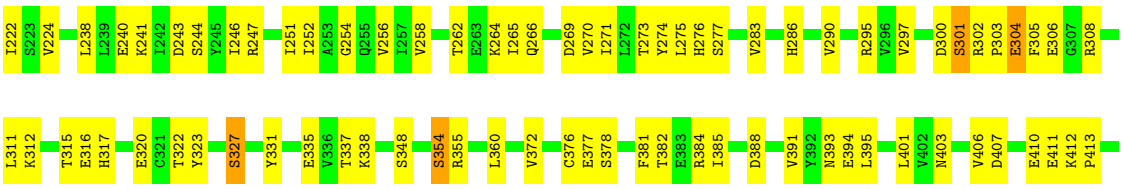


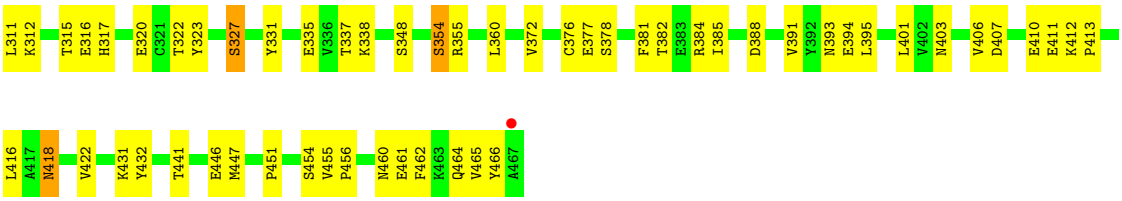


• Molecule 4: Probable translation initiation factor eIF-2B subunit delta

Chain H:

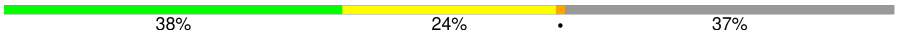


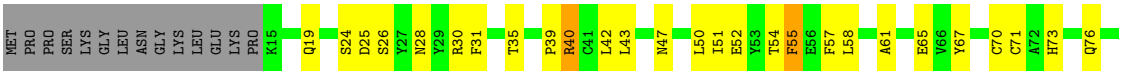


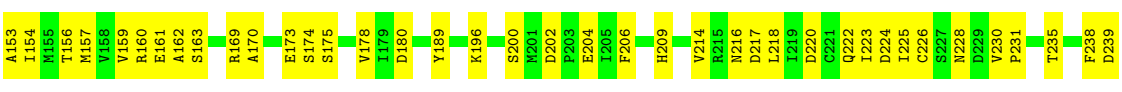


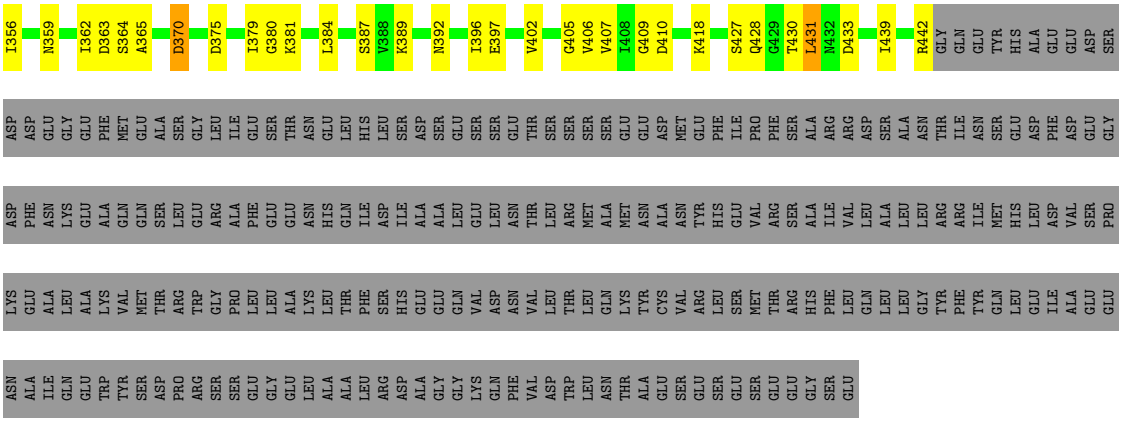
• Molecule 5: Probable translation initiation factor eIF-2B subunit epsilon

Chain I:



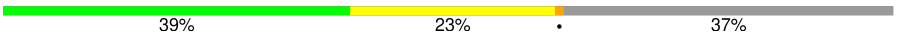


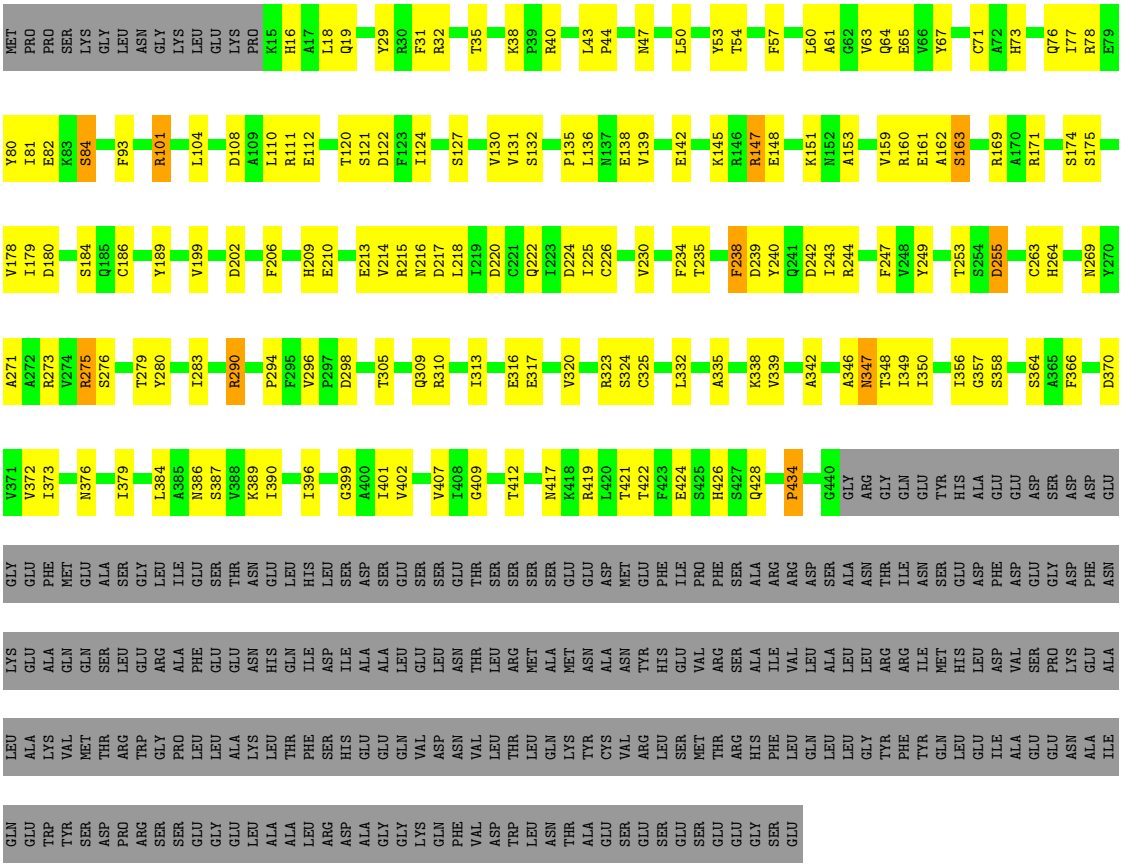




• Molecule 5: Probable translation initiation factor eIF-2B subunit epsilon

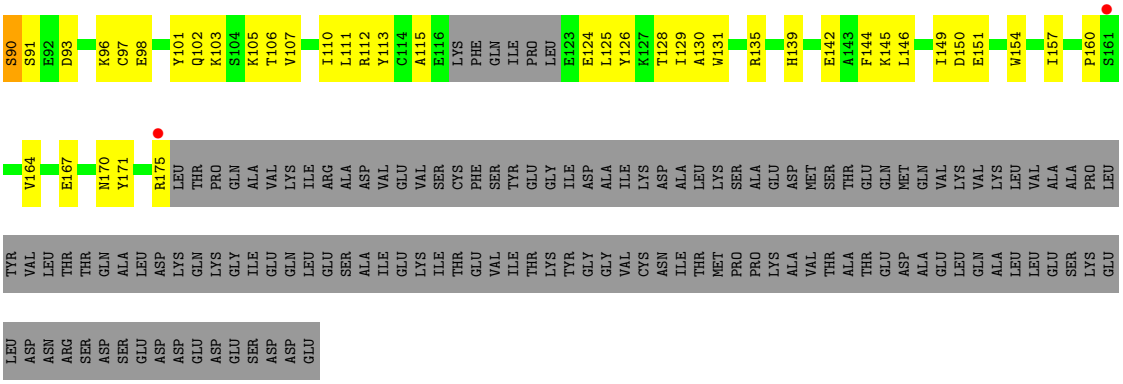
Chain J:





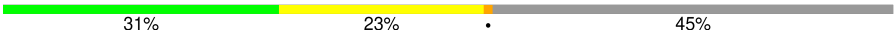
• Molecule 6: Eukaryotic translation initiation factor 2 subunit alpha

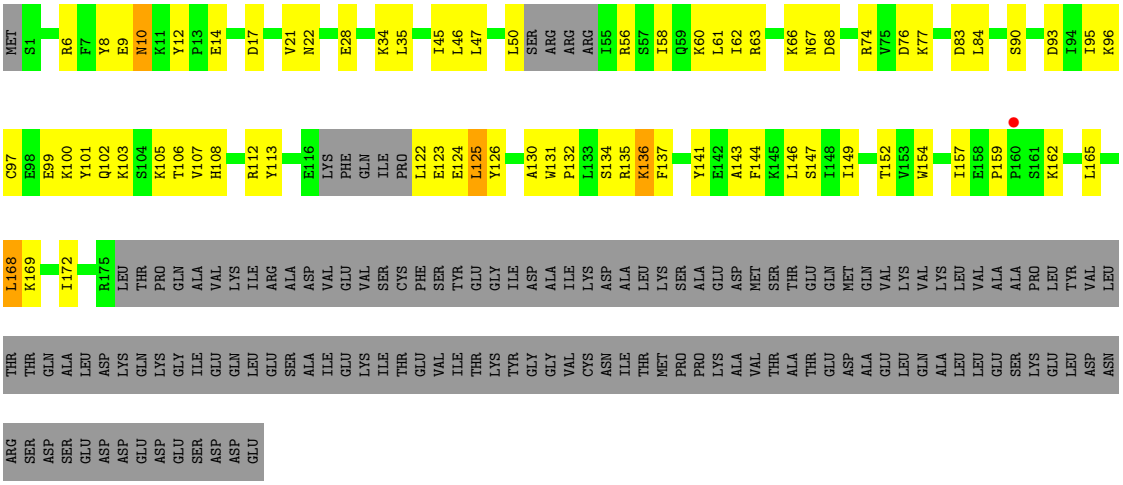
Chain L:



• Molecule 6: Eukaryotic translation initiation factor 2 subunit alpha

Chain M:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	155.56Å 207.99Å 155.59Å 90.00° 97.20° 90.00°	Depositor
Resolution (Å)	49.31 – 3.50 49.31 – 3.50	Depositor EDS
% Data completeness (in resolution range)	97.6 (49.31-3.50) 88.8 (49.31-3.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.53 (at 3.48Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.224 , 0.260 0.227 , 0.263	Depositor DCC
R_{free} test set	1979 reflections (1.62%)	wwPDB-VP
Wilson B-factor (Å^2)	122.1	Xtriage
Anisotropy	0.078	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 81.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.380 for l,-k,h	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	31811	wwPDB-VP
Average B, all atoms (Å^2)	144.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.27% 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: PO4

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	0.28	0/2513	0.44	0/3399
1	B	0.28	0/2510	0.43	0/3395
2	C	0.30	0/2661	0.43	0/3611
2	D	0.30	0/2653	0.44	0/3600
3	E	0.30	0/3272	0.48	0/4427
3	F	0.29	0/3260	0.49	0/4411
4	G	0.31	0/2917	0.45	0/3951
4	H	0.31	0/2917	0.44	0/3951
5	I	0.29	0/3437	0.45	0/4658
5	J	0.29	0/3422	0.47	0/4639
6	L	0.27	0/1374	0.42	0/1845
6	M	0.26	0/1384	0.44	0/1859
All	All	0.29	0/32320	0.45	0/43746

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	2467	0	2490	99	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2465	0	2487	111	0
2	C	2617	0	2653	102	0
2	D	2609	0	2642	83	0
3	E	3216	0	3273	131	0
3	F	3204	0	3263	116	0
4	G	2869	0	2958	90	0
4	H	2869	0	2958	85	0
5	I	3377	0	3361	134	0
5	J	3362	0	3345	121	0
6	L	1353	0	1374	51	0
6	M	1363	0	1391	48	0
7	C	5	0	0	1	0
7	D	5	0	0	0	0
7	E	10	0	0	1	0
7	F	10	0	0	0	0
7	G	5	0	0	1	0
7	H	5	0	0	1	0
All	All	31811	0	32195	1094	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 17.

The worst 5 of 1094 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)
4:H:126:LEU:HB3	4:H:395:LEU:HD11	1.55	0.89
3:E:139:ILE:HG12	3:E:250:ILE:HG12	1.56	0.87
5:I:143:HIS:HD1	5:I:156:THR:HG1	1.21	0.83
5:J:101:ARG:H	5:J:101:ARG:HD3	1.44	0.83
3:E:402:VAL:HG23	3:E:419:ILE:HD11	1.62	0.81

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	312/341 (92%)	271 (87%)	36 (12%)	5 (2%)	9 43
1	B	312/341 (92%)	268 (86%)	39 (12%)	5 (2%)	9 43
2	C	334/399 (84%)	299 (90%)	33 (10%)	2 (1%)	25 64
2	D	333/399 (84%)	300 (90%)	27 (8%)	6 (2%)	8 41
3	E	410/458 (90%)	327 (80%)	72 (18%)	11 (3%)	5 33
3	F	408/458 (89%)	344 (84%)	51 (12%)	13 (3%)	4 29
4	G	361/467 (77%)	321 (89%)	36 (10%)	4 (1%)	14 52
4	H	361/467 (77%)	330 (91%)	20 (6%)	11 (3%)	4 30
5	I	426/678 (63%)	369 (87%)	54 (13%)	3 (1%)	22 61
5	J	424/678 (62%)	378 (89%)	43 (10%)	3 (1%)	22 61
6	L	159/304 (52%)	134 (84%)	23 (14%)	2 (1%)	12 48
6	M	160/304 (53%)	133 (83%)	23 (14%)	4 (2%)	5 34
All	All	4000/5294 (76%)	3474 (87%)	457 (11%)	69 (2%)	9 42

5 of 69 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	E	289	LEU
3	E	359	ASP
4	G	303	PRO
4	H	303	PRO
6	M	61	LEU

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	274/298 (92%)	263 (96%)	11 (4%)	31 64
1	B	274/298 (92%)	264 (96%)	10 (4%)	35 66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	291/350 (83%)	280 (96%)	11 (4%)	33	65
2	D	290/350 (83%)	281 (97%)	9 (3%)	40	70
3	E	359/395 (91%)	334 (93%)	25 (7%)	15	46
3	F	357/395 (90%)	335 (94%)	22 (6%)	18	51
4	G	326/408 (80%)	307 (94%)	19 (6%)	20	53
4	H	326/408 (80%)	310 (95%)	16 (5%)	25	59
5	I	379/596 (64%)	370 (98%)	9 (2%)	49	76
5	J	378/596 (63%)	366 (97%)	12 (3%)	39	69
6	L	152/274 (56%)	145 (95%)	7 (5%)	27	61
6	M	153/274 (56%)	146 (95%)	7 (5%)	27	61
All	All	3559/4642 (77%)	3401 (96%)	158 (4%)	28	62

5 of 158 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	H	208	SER
5	J	424	GLU
4	H	317	HIS
5	I	255	ASP
6	L	154	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
3	F	393	ASN
4	G	179	GLN
6	M	102	GLN
5	I	117	GLN
6	M	59	GLN

5.3.3 RNA

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

8 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	$\#\|Z\| > 2$
7	PO4	E	502	-	4,4,4	0.99	0	6,6,6	0.48	0
7	PO4	H	501	-	4,4,4	1.03	0	6,6,6	0.47	0
7	PO4	F	502	-	4,4,4	0.99	0	6,6,6	0.48	0
7	PO4	E	501	-	4,4,4	1.03	0	6,6,6	0.48	0
7	PO4	G	501	-	4,4,4	1.02	0	6,6,6	0.53	0
7	PO4	F	501	-	4,4,4	1.05	0	6,6,6	0.42	0
7	PO4	D	401	-	4,4,4	1.02	0	6,6,6	0.42	0
7	PO4	C	401	-	4,4,4	1.01	0	6,6,6	0.46	0

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.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	E	502	PO4	1	0
7	H	501	PO4	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	G	501	PO4	1	0
7	C	401	PO4	1	0

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	316/341 (92%)	-0.40	1 (0%) 94 91	109, 145, 196, 237	0
1	B	316/341 (92%)	-0.31	4 (1%) 77 71	106, 146, 196, 238	0
2	C	338/399 (84%)	-0.31	0 100 100	79, 121, 185, 214	0
2	D	337/399 (84%)	-0.31	0 100 100	76, 120, 189, 232	0
3	E	414/458 (90%)	-0.31	3 (0%) 87 83	88, 139, 206, 234	0
3	F	412/458 (89%)	-0.35	1 (0%) 95 93	93, 138, 205, 236	0
4	G	363/467 (77%)	-0.31	1 (0%) 94 91	87, 122, 187, 235	0
4	H	363/467 (77%)	-0.26	3 (0%) 86 81	88, 119, 191, 228	0
5	I	428/678 (63%)	-0.38	0 100 100	101, 141, 187, 209	0
5	J	426/678 (62%)	-0.40	0 100 100	100, 141, 184, 222	0
6	L	165/304 (54%)	-0.36	2 (1%) 79 73	121, 203, 232, 244	0
6	M	166/304 (54%)	-0.43	1 (0%) 89 86	121, 202, 236, 253	0
All	All	4044/5294 (76%)	-0.34	16 (0%) 92 90	76, 137, 209, 253	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	H	467	ALA	5.9
3	E	31	GLN	5.5
3	E	29	ASN	4.3
1	B	292	HIS	3.6
3	F	28	GLY	3.1

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 (i)

There are no monosaccharides 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. 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
7	PO4	F	502	5/5	0.89	0.19	172,179,190,228	0
7	PO4	G	501	5/5	0.90	0.23	115,136,151,154	0
7	PO4	E	501	5/5	0.91	0.19	114,122,147,186	0
7	PO4	C	401	5/5	0.92	0.19	98,137,158,184	0
7	PO4	H	501	5/5	0.92	0.20	105,106,166,171	0
7	PO4	F	501	5/5	0.93	0.24	113,128,142,183	0
7	PO4	D	401	5/5	0.95	0.26	80,107,166,167	0
7	PO4	E	502	5/5	0.95	0.20	171,171,195,223	0

6.5 Other polymers (i)

There are no such residues in this entry.