



## wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 01:47 PM BST

PDB ID : 2WWB  
EMDB ID: : EMD-1651  
Title : CRYO-EM STRUCTURE OF THE MAMMALIAN SEC61 COMPLEX  
BOUND TO THE ACTIVELY TRANSLATING WHEAT GERM 80S RI-  
BOSOME  
Authors : Becker, T.; Mandon, E.; Bhushan, S.; Jarasch, A.; Armache, J.P.; Funes,  
S.; Jossinet, F.; Gumbart, J.; Mielke, T.; Berninghausen, O.; Schulten, K.;  
Westhof, E.; Gilmore, R.; Beckmann, R.  
Deposited on : 2009-10-22  
Resolution : 6.48 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.  
For rigid body fitted models, validation errors reported here could  
stem from errors in the original structure(s) used in the fitting.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>

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MolProbity : 4.02b-467  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk27241

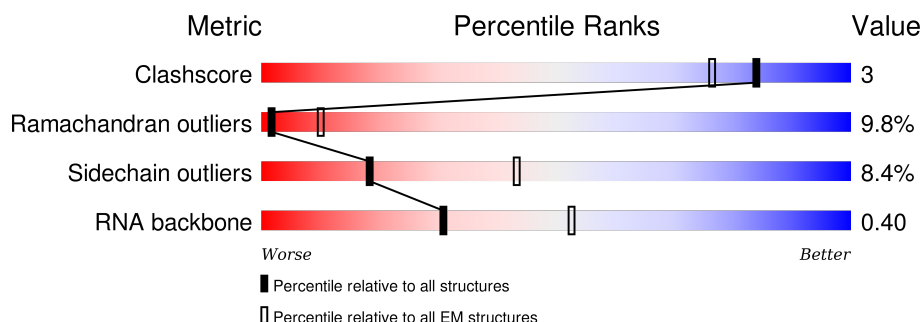
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 6.48 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)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	476	88% 9% ..
2	B	68	90% 9% .
3	C	96	34% .. 63%
4	D	63	. 38% 51% 10%
5	E	34	53% 44% .
6	F	25	72% 28%
7	G	14	36% 64%
8	H	362	48% 16% 9% . 26%

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Mol	Chain	Length	Quality of chain
9	I	184	<div><div></div><div>57%19%6%17%</div></div>
10	J	189	<div><div></div><div>26%72%</div></div>
11	K	142	<div><div></div><div>47%9%42%</div></div>
12	L	127	<div><div></div><div>74%19%6%</div></div>
13	M	113	<div><div></div><div>58%12%26%</div></div>
14	N	120	<div><div></div><div>44%9%43%</div></div>
15	O	51	<div><div></div><div>33%31%27%</div></div>

## 2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 14313 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 PROTEIN TRANSPORT PROTEIN SEC61 SUBUNIT ALPHA ISOFORM 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	476	Total	C	N	O	S	0	0
			3675	2409	591	650	25		

- Molecule 2 is a protein called PROTEIN TRANSPORT PROTEIN SEC61 SUBUNIT GAMMA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	68	Total	C	N	O	S	0	0
			543	355	94	89	5		

- Molecule 3 is a protein called PROTEIN TRANSPORT PROTEIN SEC61 SUBUNIT BETA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	36	Total	C	N	O	S	0	0
			281	188	44	47	2		

- Molecule 4 is a RNA chain called 5.8S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	63	Total	C	N	O	P	0	0
			1347	603	245	436	63		

- Molecule 5 is a RNA chain called 25S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	34	Total	C	N	O	P	0	0
			740	332	148	226	34		

- Molecule 6 is a RNA chain called 25S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	25	Total	C	N	O	P	0	0
			536	239	99	173	25		

- Molecule 7 is a RNA chain called 25S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	14	Total	C	N	O	P	0	0
			296	133	54	96	13		

- Molecule 8 is a protein called 60S RIBOSOMAL PROTEIN L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	269	Total	C	N	O	S	0	0
			2039	1281	391	363	4		

- Molecule 9 is a protein called 60S RIBOSOMAL PROTEIN L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	153	Total	C	N	O	S	0	0
			1212	756	236	219	1		

- Molecule 10 is a protein called 60S RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	53	Total	C	N	O	S	0	0
			410	254	83	72	1		

- Molecule 11 is a protein called 60S RIBOSOMAL PROTEIN L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	83	Total	C	N	O	S	0	0
			663	424	111	126	2		

- Molecule 12 is a protein called 60S RIBOSOMAL PROTEIN L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	127	Total	C	N	O	S	0	0
			1002	630	193	178	1		

- Molecule 13 is a protein called 60S RIBOSOMAL PROTEIN L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	84	Total	C	N	O	S	0	0
			706	447	140	118	1		

- Molecule 14 is a protein called 60S RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	69	Total	C	N	O	S	0	0
			547	345	101	99	2		

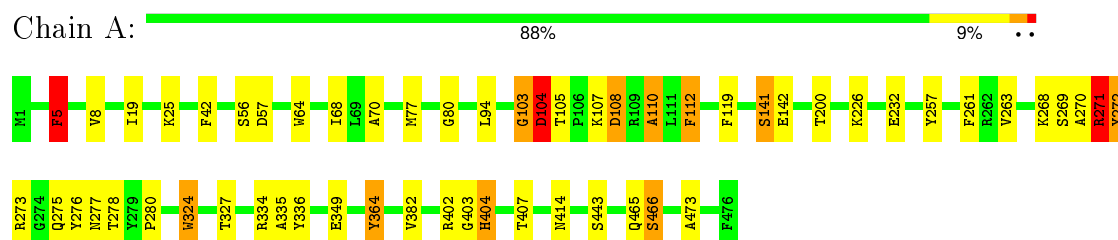
- Molecule 15 is a protein called 60S RIBOSOMAL PROTEIN L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	37	Total	C	N	O	S	0	0
			316	200	66	48	2		

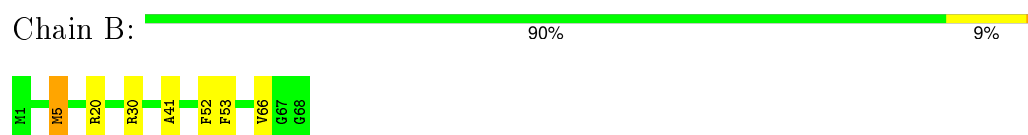
### 3 Residue-property plots

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. 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.

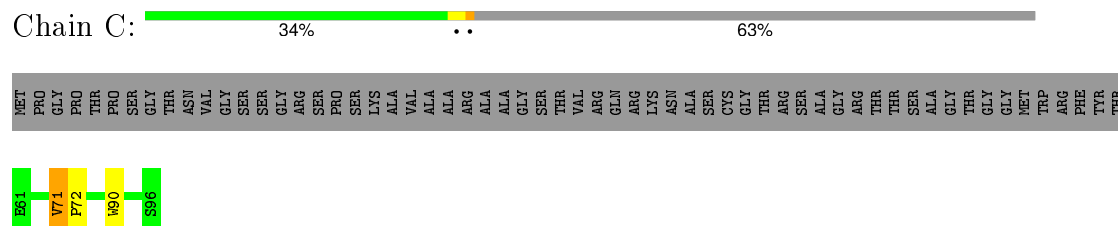
#### • Molecule 1: PROTEIN TRANSPORT PROTEIN SEC61 SUBUNIT ALPHA ISOFORM 1



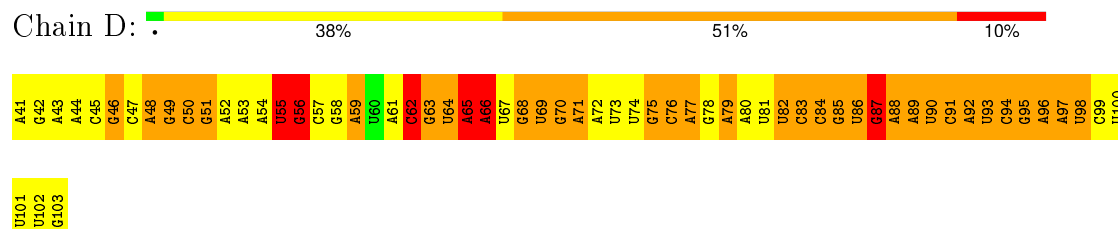
#### • Molecule 2: PROTEIN TRANSPORT PROTEIN SEC61 SUBUNIT GAMMA



#### • Molecule 3: PROTEIN TRANSPORT PROTEIN SEC61 SUBUNIT BETA



#### • Molecule 4: 5.8S RRNA



#### • Molecule 5: 25S RRNA

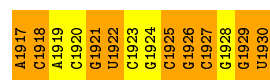




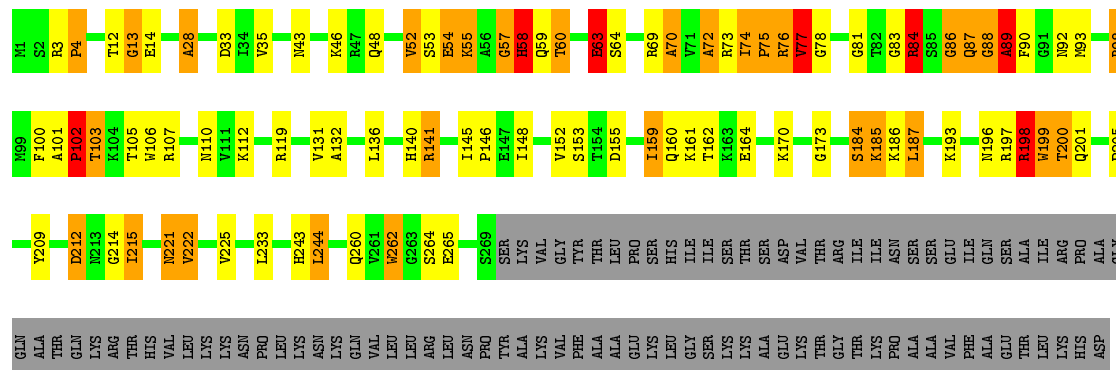
• Molecule 6: 25S rRNA



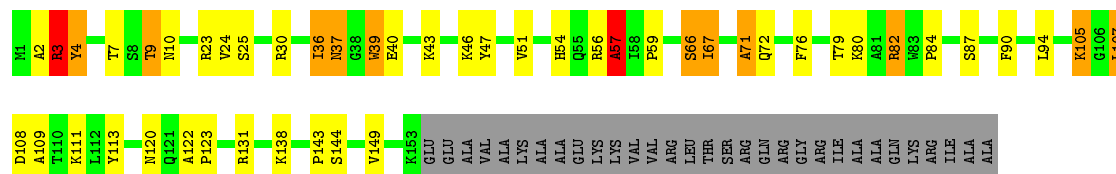
• Molecule 7: 25S rRNA



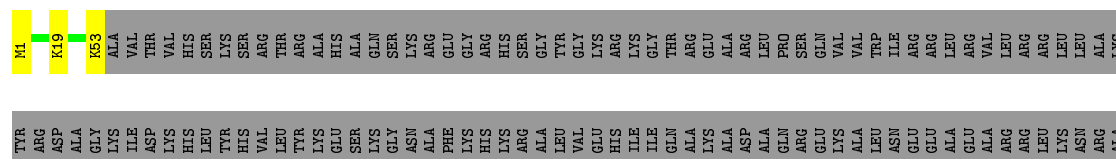
• Molecule 8: 60S RIBOSOMAL PROTEIN L4-B



• Molecule 9: 60S RIBOSOMAL PROTEIN L17-A



• Molecule 10: 60S RIBOSOMAL PROTEIN L19



ALA ARG  
ARG ASP  
ARG ARG  
ARG ALA  
GLN ARG  
VAL VAL  
ALA ALA  
GLU GLU  
LYS LYS  
ASP ASP  
ALA LEU  
LEU LEU  
LYS LYS  
GLU ASP  
ALA

• Molecule 11: 60S RIBOSOMAL PROTEIN L25

Chain K:  47% 9% 42%

MET ALA  
ALA PRO  
SER SER  
LYS ALA  
ALA ALA  
THR THR  
ALA ALA  
LYS LYS  
LYS LYS  
VAL VAL  
VAL VAL  
LYS LYS  
GLY THR  
ASN ASN  
GLY GLY  
LYS LYS  
LYS LYS  
LEU LEU  
LYS LYS  
VAL VAL  
ARG ARG  
THR THR  
SER SER  
GLY GLY  
ALA ALA  
PHE PHE  
ARG ARG  
LEU LEU  
PRO PRO  
LYS LYS  
THR THR  
LEU LEU  
LYS LYS  
ALA ALA  
ARG ARG  
ALA ALA  
PRO PRO  
LYS LYS  
TYR TYR  
ALA ALA  
SER SER  
LYS LYS  
ALA ALA  
VAL VAL  
PRO PRO  
HIS HIS  
TYR TYR  
ASN ASN  
ARG ARG  
L57 L57  
V60 V60  
P61 P61

V62 V62  
Q65 Q65  
E70 E70  
K74 K74  
K100 K100  
V105 V105  
D106 D106  
K109 K109  
V110 V110  
N111 N111  
R115 R115  
P116 P116  
N117 N117  
Y123 Y123  
D131 D131  
M137 M137  
R138 R138  
I139 I139  
GLY GLY  
TYR TYR  
ILE ILE

• Molecule 12: 60S RIBOSOMAL PROTEIN L26-A

Chain L:  74% 19% 6%

M1 M1  
L6 L6  
S10 S10  
D11 D11  
P23 P23  
R28 R28  
S36 S36  
K37 K37  
R40 R40  
I45 I45  
K46 K46  
R52 R52  
V56 V56  
L57 L57  
K64 K64  
K77 K77  
F78 F78  
D83 D83  
K84 K84  
V85 V85  
T86 T86  
K87 K87  
P96 P96  
I97 I97  
N98 N98  
I106 I106  
T107 T107  
K108 K108  
L111 L111  
D112 D112  
K113 K113  
K116 K116  
R121 R121  
K122 K122  
G123 G123  
G124 G124  
K125 K125  
L126 L126  
E127 E127

• Molecule 13: 60S RIBOSOMAL PROTEIN L31-A

Chain M:  58% 12% 26%

MET MET  
ALA ALA  
GLY GLY  
LEU LEU  
LYS LYS  
ASP ASP  
VAL VAL  
VAL VAL  
T9 T9  
R10 R10  
S24 S24  
F25 F25  
K26 K26  
K38 K38  
D47 D47  
L51 L51  
R62 R62  
G63 G63  
V64 V64  
V67 V67  
E68 E68  
V69 V69  
R74 R74  
R77 R77  
K78 K78  
R79 R79  
E82 E82  
K86 K86  
F90 F90  
S91 S91  
Y92 Y92  
VAL VAL  
GLU GLU  
PRO PRO  
VAL VAL  
LEU LEU  
VAL VAL  
ALA ALA  
SER SER  
ALA ALA  
LYS LYS  
PHE PHE  
GLY GLY  
LEU LEU  
GLN GLN  
THR THR  
VAL VAL  
VAL VAL  
GLU GLU

GLU  
ASP  
ALA

• Molecule 14: 60S RIBOSOMAL PROTEIN L35

Chain N:  44% 9% 43%

M1 M1  
A2 A2  
G3 G3  
V4 V4  
K5 K5  
L9 L9  
S13 S13  
K14 K14  
K32 K32  
V33 V33  
Q34 Q34  
S37 S37  
R38 R38  
P39 P39  
S40 S40  
L41 L41  
I44 I44  
R67 R67  
Q68 Q68  
L69 L69  
TYR TYR  
LYS LYS  
GLY GLY  
LYS LYS  
LYS LYS  
TYR TYR  
GLN GLN  
PRO PRO  
LYS LYS  
ASP ASP  
LEU LEU  
ARG ARG  
ALA ALA  
LYS LYS  
LYS LYS  
THR THR  
ARG ARG  
ALA ALA  
LEU LEU  
ARG ARG  
VAL VAL  
ALA ALA  
SER SER  
LYS LYS  
PHE PHE  
GLY GLY  
LEU LEU  
SER SER  
GLN GLN  
VAL VAL  
THR THR  
LYS LYS

GLN  
ARG  
LYS  
LYS  
GLN  
GLN  
ILE  
PHE  
PRO  
GLN  
ARG  
LYS  
LYS  
TYR  
ALA  
ILE  
LYS  
LYS  
ALA

• Molecule 15: 60S RIBOSOMAL PROTEIN L39

Chain O:  33% 31% 27%

M1 M1  
Q4 Q4  
K5 K5  
S6 S6  
F7 F7  
K17 K17  
K18 K18  
Q19 Q19  
N20 N20  
R21 R21  
P22 P22  
L23 L23  
P24 P24  
Q25 Q25  
V26 V26  
I27 I27  
R30 R30  
T31 T31  
N32 N32  
H33 H33  
T34 T34  
I35 I35  
R36 R36  
Y37 Y37  
ASN ASN  
ALA ALA  
LYS LYS  
ARG ARG  
ARG ARG  
ASN ASN  
TRP TRP  
ARG ARG  
ARG ARG  
THR THR  
LYS LYS  
MET MET  
ASN ASN  
ILE ILE

## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	DEFOCUS GROUP VOLUMES	Depositor
Microscope	OTHER	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	25	Depositor
Minimum defocus (nm)	1250	Depositor
Maximum defocus (nm)	4700	Depositor
Magnification	39000	Depositor
Image detector	KODAK SO163	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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	$\# Z  > 2$	RMSZ	$\# Z  > 2$
1	A	1.89	8/3755 (0.2%)	1.10	22/5089 (0.4%)
10	J	1.01	0/412	0.97	0/551
11	K	0.90	0/670	1.17	3/903 (0.3%)
12	L	1.02	0/1013	1.30	6/1351 (0.4%)
13	M	1.10	0/719	1.35	6/959 (0.6%)
14	N	1.05	1/549 (0.2%)	1.42	8/733 (1.1%)
15	O	1.10	0/321	1.45	4/426 (0.9%)
2	B	0.94	0/553	1.12	2/738 (0.3%)
3	C	0.86	0/289	1.10	0/391
4	D	1.62	5/1508 (0.3%)	2.64	188/2348 (8.0%)
5	E	1.67	2/833 (0.2%)	2.72	115/1298 (8.9%)
6	F	1.64	0/599	2.49	73/932 (7.8%)
7	G	1.70	2/330 (0.6%)	2.56	42/513 (8.2%)
8	H	1.00	0/2079	1.46	33/2817 (1.2%)
9	I	1.03	0/1235	1.43	17/1662 (1.0%)
All	All	1.43	18/14865 (0.1%)	1.71	519/20711 (2.5%)

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	5
11	K	0	3
12	L	0	5
13	M	0	2
14	N	0	2
15	O	0	7
3	C	0	1
4	D	0	10
5	E	0	6
6	F	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
7	G	0	1
8	H	0	12
9	I	0	6
All	All	0	63

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	104	ASP	N-CA	81.65	3.09	1.46
1	A	5	PHE	CG-CD2	29.16	1.82	1.38
1	A	5	PHE	CG-CD1	28.74	1.81	1.38
1	A	5	PHE	CE1-CZ	22.75	1.80	1.37
1	A	5	PHE	CE2-CZ	22.22	1.79	1.37

The worst 5 of 519 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	532	A	P-O3'-C3'	17.86	141.14	119.70
4	D	90	U	P-O3'-C3'	14.96	137.65	119.70
4	D	93	U	P-O3'-C3'	14.57	137.18	119.70
4	D	69	U	P-O3'-C3'	14.40	136.98	119.70
4	D	53	A	N1-C6-N6	14.32	127.19	118.60

There are no chirality outliers.

5 of 63 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	112	PHE	Sidechain
1	A	270	ALA	Peptide
1	A	271	ARG	Sidechain
1	A	336	TYR	Peptide
1	A	404	HIS	Sidechain

## 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	3675	0	3798	44	0
2	B	543	0	577	1	0
3	C	281	0	294	0	0
4	D	1347	0	678	2	0
5	E	740	0	369	1	0
6	F	536	0	272	1	0
7	G	296	0	154	0	0
8	H	2039	0	2106	16	0
9	I	1212	0	1231	8	0
10	J	410	0	452	0	0
11	K	663	0	699	4	0
12	L	1002	0	1093	2	0
13	M	706	0	741	1	0
14	N	547	0	613	8	0
15	O	316	0	349	2	0
All	All	14313	0	13426	81	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 3.

The worst 5 of 81 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:5:PHE:CE2	1:A:5:PHE:CD2	1.81	1.68
1:A:5:PHE:CE1	1:A:5:PHE:CD1	1.80	1.66
1:A:5:PHE:CE2	1:A:5:PHE:CZ	1.79	1.64
1:A:5:PHE:CG	1:A:5:PHE:CD1	1.81	1.61
1:A:5:PHE:CE1	1:A:5:PHE:CZ	1.80	1.61

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 PDB entries followed by that with respect to all EM entries.

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	474/476 (100%)	402 (85%)	46 (10%)	26 (6%)	2	28
2	B	66/68 (97%)	60 (91%)	2 (3%)	4 (6%)	2	26
3	C	34/96 (35%)	27 (79%)	4 (12%)	3 (9%)	1	17
8	H	267/362 (74%)	181 (68%)	38 (14%)	48 (18%)	0	4
9	I	151/184 (82%)	119 (79%)	15 (10%)	17 (11%)	0	10
10	J	51/189 (27%)	46 (90%)	4 (8%)	1 (2%)	9	51
11	K	81/142 (57%)	73 (90%)	5 (6%)	3 (4%)	4	37
12	L	125/127 (98%)	101 (81%)	9 (7%)	15 (12%)	0	8
13	M	82/113 (73%)	65 (79%)	8 (10%)	9 (11%)	0	11
14	N	67/120 (56%)	59 (88%)	3 (4%)	5 (8%)	1	21
15	O	35/51 (69%)	26 (74%)	0	9 (26%)	0	1
All	All	1433/1928 (74%)	1159 (81%)	134 (9%)	140 (10%)	2	14

5 of 140 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	56	SER
1	A	104	ASP
1	A	108	ASP
1	A	110	ALA
1	A	142	GLU

### 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 PDB entries followed by that with respect to all EM entries.

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	398/398 (100%)	388 (98%)	10 (2%)	55	81
2	B	59/59 (100%)	57 (97%)	2 (3%)	44	75
3	C	32/74 (43%)	32 (100%)	0	100	100
8	H	209/288 (73%)	179 (86%)	30 (14%)	4	25
9	I	124/146 (85%)	107 (86%)	17 (14%)	4	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
10	J	44/154 (29%)	42 (96%)	2 (4%)	34 69
11	K	74/118 (63%)	67 (90%)	7 (10%)	11 41
12	L	110/110 (100%)	95 (86%)	15 (14%)	5 27
13	M	74/97 (76%)	64 (86%)	10 (14%)	5 27
14	N	62/105 (59%)	57 (92%)	5 (8%)	15 50
15	O	33/46 (72%)	28 (85%)	5 (15%)	3 23
All	All	1219/1595 (76%)	1116 (92%)	103 (8%)	18 48

5 of 103 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	I	46	LYS
9	I	144	SER
14	N	34	GLN
9	I	59	PRO
9	I	79	THR

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

Mol	Chain	Res	Type
8	H	43	ASN
12	L	42	GLN
8	H	213	ASN
2	B	58	HIS
11	K	111	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	D	62/63 (98%)	27 (43%)	10 (16%)
5	E	33/34 (97%)	9 (27%)	3 (9%)
6	F	24/25 (96%)	3 (12%)	0
7	G	14/14 (100%)	6 (42%)	2 (14%)
All	All	133/136 (97%)	45 (33%)	15 (11%)

5 of 45 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	D	48	A
4	D	49	G
4	D	51	G
4	D	56	G
4	D	59	A

5 of 15 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	D	89	A
4	D	90	U
5	E	560	A
4	D	69	U
5	E	558	G

#### 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.