



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 10:29 PM GMT

PDB ID : 1TNZ
Title : Rat Protein Geranylgeranyltransferase Type-I Complexed with a GGPP analog and a RRCVLL Peptide Derived from Cdc42 splice isoform-2
Authors : Reid, T.S.; Terry, K.L.; Casey, P.J.; Beese, L.S.
Deposited on : 2004-06-11
Resolution : 2.90 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
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) : trunk26865

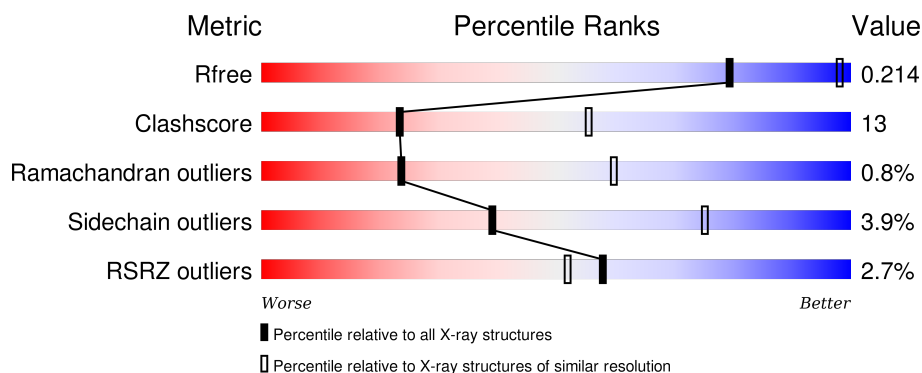
1 Overall quality at a glance ⓘ

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)

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	377	<div> <div>3%</div> <div>58%</div> <div>24%</div> <div>•</div> <div>17%</div> </div>
1	C	377	<div> <div>4%</div> <div>60%</div> <div>22%</div> <div>•</div> <div>17%</div> </div>
1	E	377	<div> <div>2%</div> <div>60%</div> <div>21%</div> <div>•</div> <div>17%</div> </div>
1	G	377	<div> <div>4%</div> <div>60%</div> <div>22%</div> <div>•</div> <div>17%</div> </div>
1	I	377	<div> <div>2%</div> <div>61%</div> <div>21%</div> <div>•</div> <div>17%</div> </div>

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Mol	Chain	Length	Quality of chain
1	K	377	
2	B	377	
2	D	377	
2	F	377	
2	H	377	
2	J	377	
2	L	377	
3	M	6	
3	N	6	
3	O	6	
3	P	6	
3	Q	6	
3	R	6	

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
7	MGM	D	380	-	-	-	X
7	MGM	H	380	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 32873 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 geranylgeranyltransferase type I alpha subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	314	Total	C	N	O	S	0	0	0
			2636	1682	463	486	5			
1	C	314	Total	C	N	O	S	0	0	0
			2655	1695	465	490	5			
1	E	314	Total	C	N	O	S	0	0	0
			2664	1698	466	495	5			
1	G	314	Total	C	N	O	S	0	0	0
			2651	1694	465	487	5			
1	I	314	Total	C	N	O	S	0	0	0
			2648	1691	461	491	5			
1	K	314	Total	C	N	O	S	0	0	0
			2675	1705	468	497	5			

- Molecule 2 is a protein called Geranylgeranyl transferase type I beta subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	346	Total	C	N	O	S	0	0	0
			2703	1709	468	502	24			
2	D	346	Total	C	N	O	S	0	0	0
			2706	1713	467	502	24			
2	F	346	Total	C	N	O	S	0	0	0
			2717	1716	473	504	24			
2	H	346	Total	C	N	O	S	0	0	0
			2694	1705	464	501	24			
2	J	346	Total	C	N	O	S	0	0	0
			2708	1711	471	502	24			
2	L	346	Total	C	N	O	S	0	0	0
			2719	1718	473	504	24			

- Molecule 3 is a protein called Cell division control protein 42 homolog (Cdc42).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	M	5	Total	C	N	O	S	2	0	0
			41	26	8	6	1			
3	N	5	Total	C	N	O	S	2	0	0
			41	26	8	6	1			
3	O	5	Total	C	N	O	S	2	0	0
			41	26	8	6	1			
3	P	5	Total	C	N	O	S	2	0	0
			41	26	8	6	1			
3	Q	5	Total	C	N	O	S	2	0	0
			41	26	8	6	1			
3	R	5	Total	C	N	O	S	2	0	0
			41	26	8	6	1			

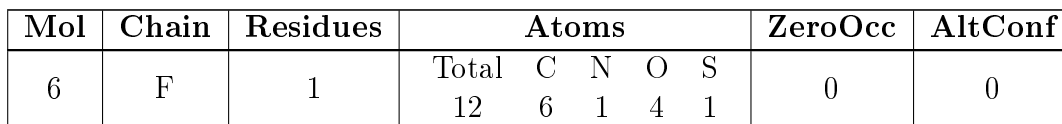
- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	J	1	Total	Zn	0	0
			1	1		
4	D	1	Total	Zn	0	0
			1	1		
4	H	1	Total	Zn	0	0
			1	1		
4	B	1	Total	Zn	0	0
			1	1		
4	L	1	Total	Zn	0	0
			1	1		
4	F	1	Total	Zn	0	0
			1	1		

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	1	Total	Cl	0	0
			1	1		
5	D	1	Total	Cl	0	0
			1	1		
5	F	1	Total	Cl	0	0
			1	1		

- Molecule 6 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C₆H₁₃NO₄S).



- MGM
-
- The chemical structure of MGM (methylgeranyl pyrophosphate) is shown. It consists of a methylgeranyl chain (C1-C15) attached to a pyrophosphate group (C16-C18). The chain is a branched alkyl chain with a methyl group at C15, a double bond between C12 and C13, and a double bond between C14 and C15. The pyrophosphate group is attached to the chain at C16. The pyrophosphate group consists of two phosphate groups linked by an oxygen atom (C17). The first phosphate group is linked to the chain at C16 and has a negative charge (C18). The second phosphate group is linked to the first phosphate group at C17 and has a negative charge (C19). The structure is labeled with atom numbers 1 through 19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	B	1	Total 29	C 19	N 1	O 7	P 2	0	0
7	D	1	Total 29	C 19	N 1	O 7	P 2	0	0



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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	F	1	Total	C	N	O	P	0	0
			29	19	1	7	2		
7	H	1	Total	C	N	O	P	0	0
			29	19	1	7	2		
7	J	1	Total	C	N	O	P	0	0
			29	19	1	7	2		
7	L	1	Total	C	N	O	P	0	0
			29	19	1	7	2		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	19	Total	O	0	0
			19	19		
8	B	11	Total	O	0	0
			11	11		
8	C	16	Total	O	0	0
			16	16		
8	D	12	Total	O	0	0
			12	12		
8	E	14	Total	O	0	0
			14	14		
8	F	26	Total	O	0	0
			26	26		
8	G	18	Total	O	0	0
			18	18		
8	H	10	Total	O	0	0
			10	10		
8	I	14	Total	O	0	0
			14	14		
8	J	18	Total	O	0	0
			18	18		
8	K	55	Total	O	0	0
			55	55		
8	L	37	Total	O	0	0
			37	37		
8	M	2	Total	O	0	0
			2	2		
8	N	2	Total	O	0	0
			2	2		
8	Q	1	Total	O	0	0
			1	1		

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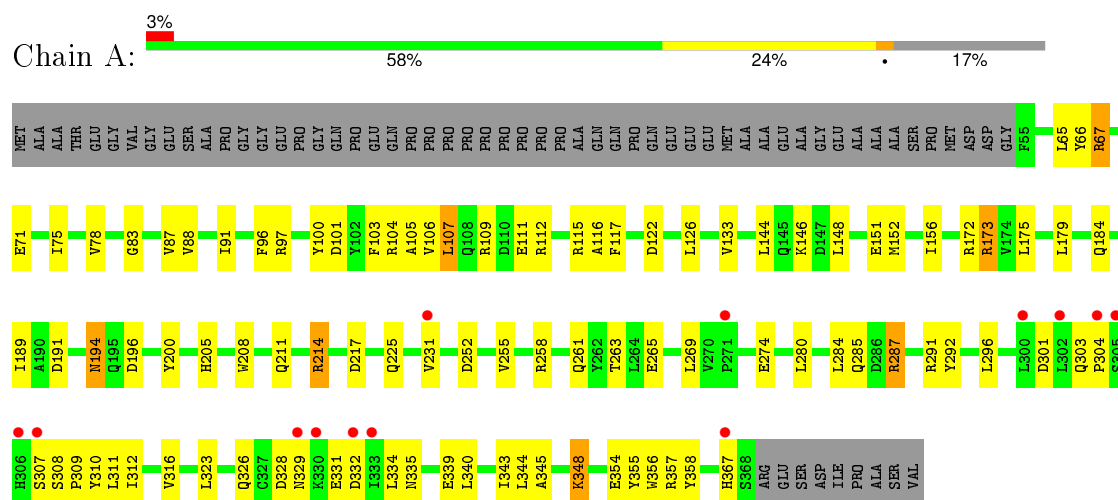
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	R	1	Total	O	0	0
			1	1		

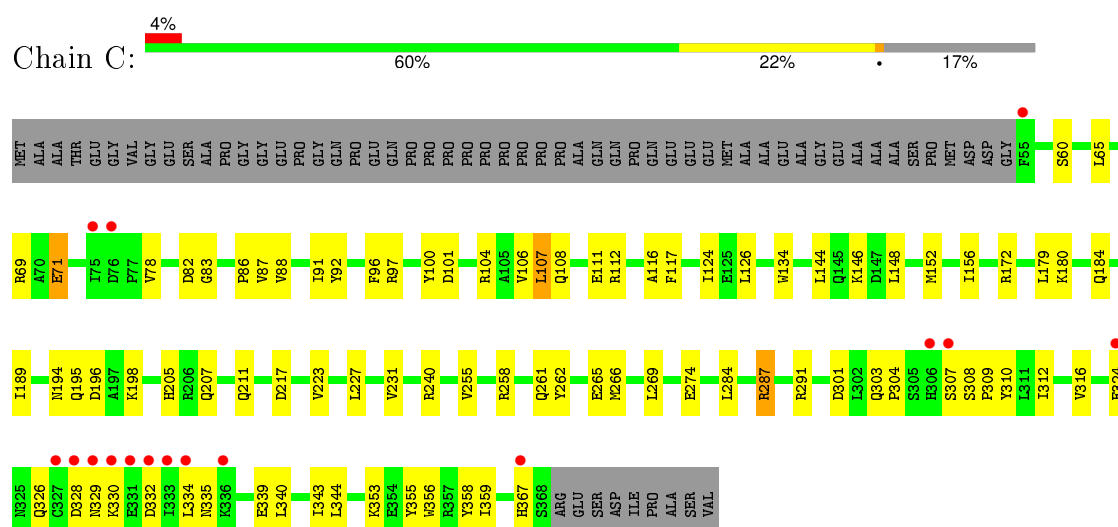
3 Residue-property plots

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 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: geranylgeranyltransferase type I alpha subunit

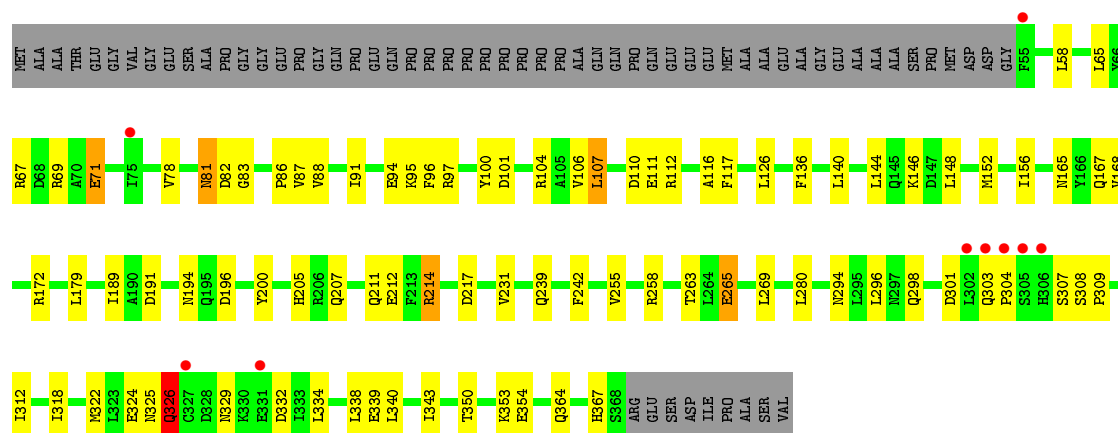


- Molecule 1: geranylgeranyltransferase type I alpha subunit

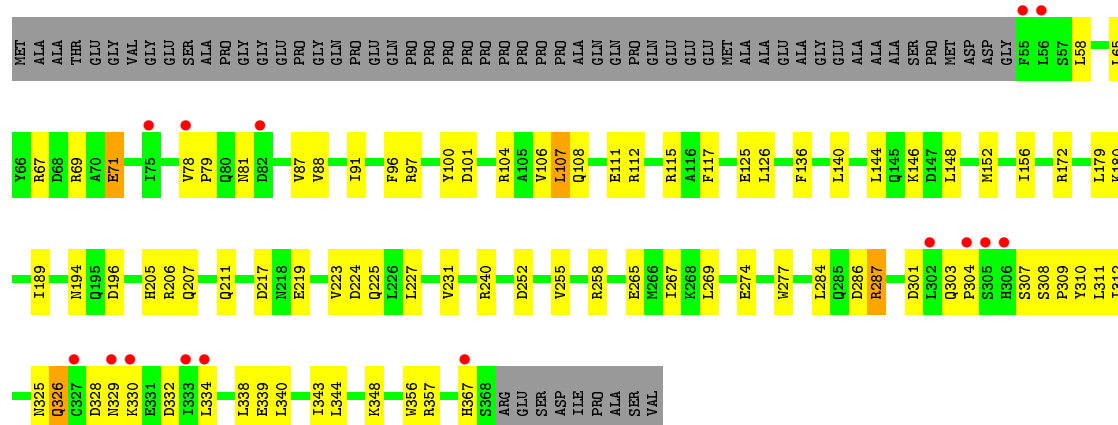


- Molecule 1: geranylgeranyltransferase type I alpha subunit

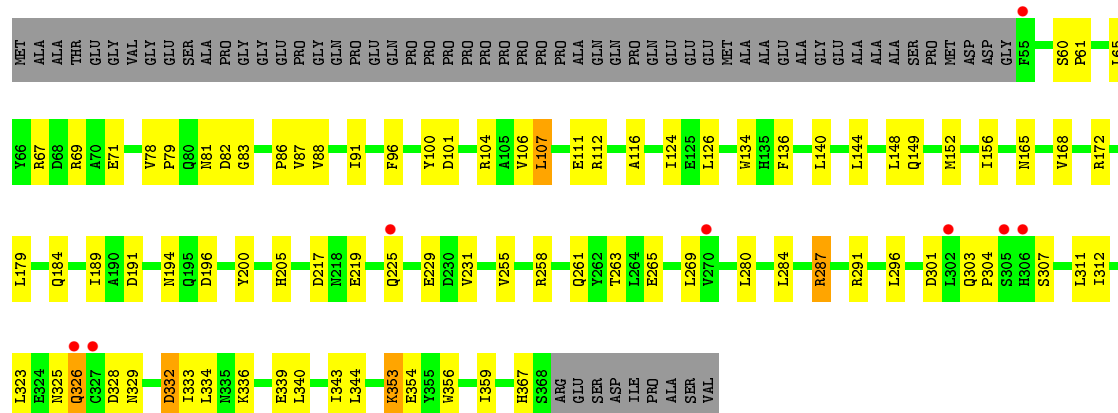




- Molecule 1: geranylgeranyltransferase type I alpha subunit

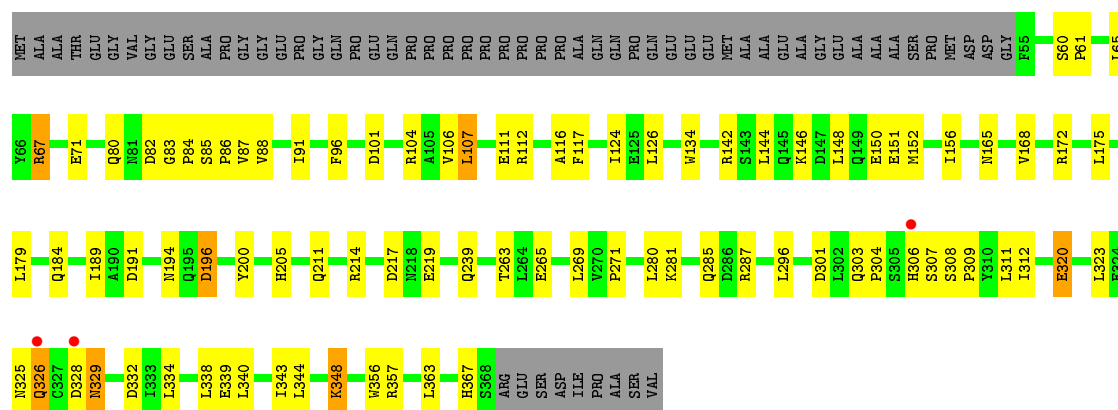


- Molecule 1: geranylgeranyltransferase type I alpha subunit

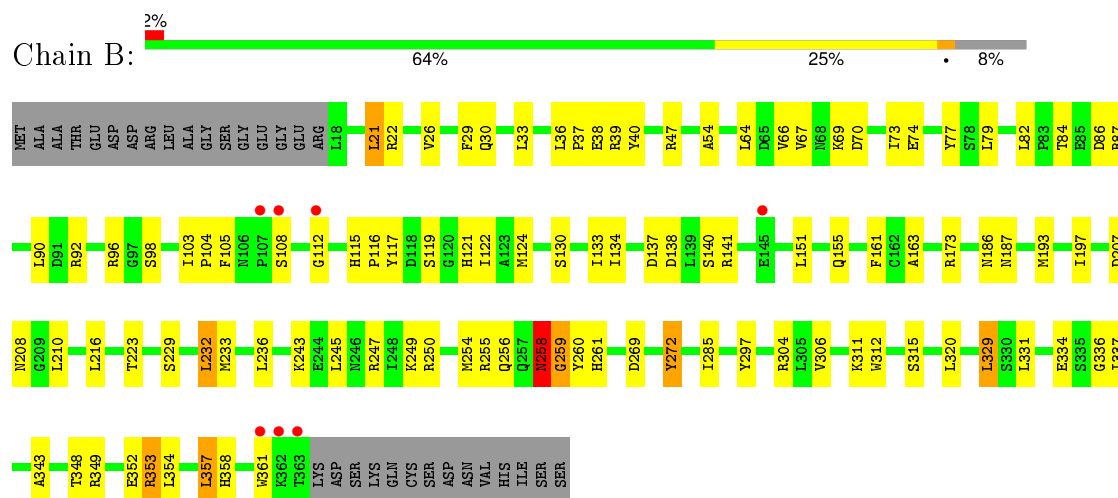


- Molecule 1: geranylgeranyltransferase type I alpha subunit

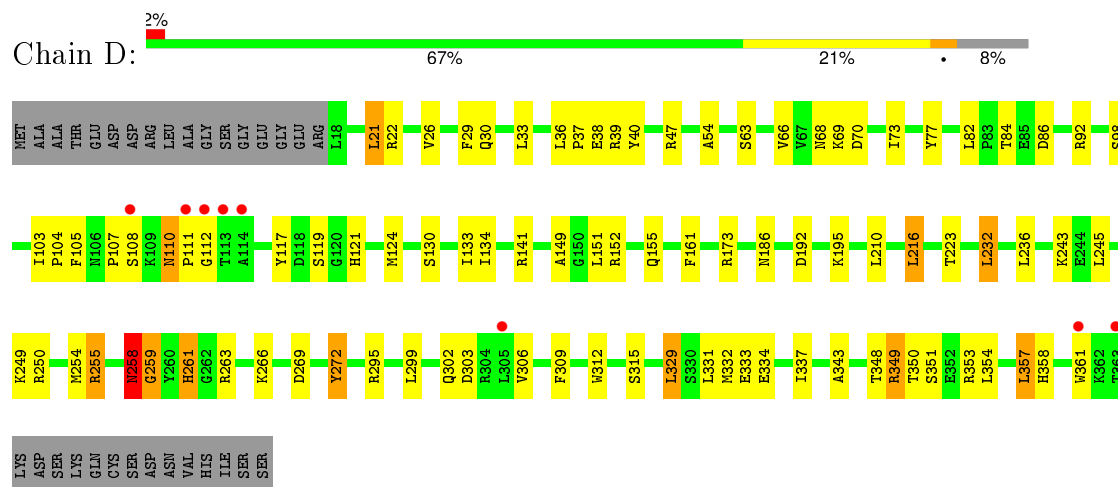




• Molecule 2: Geranylgeranyl transferase type I beta subunit

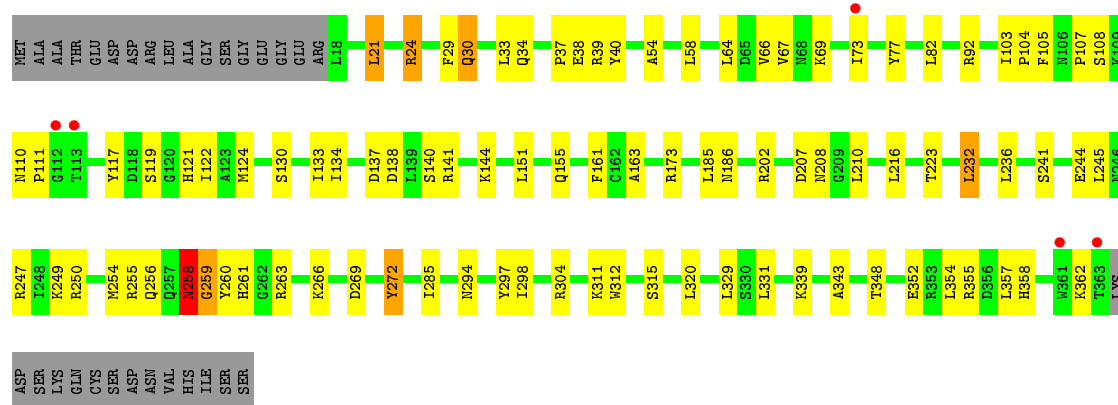


• Molecule 2: Geranylgeranyl transferase type I beta subunit

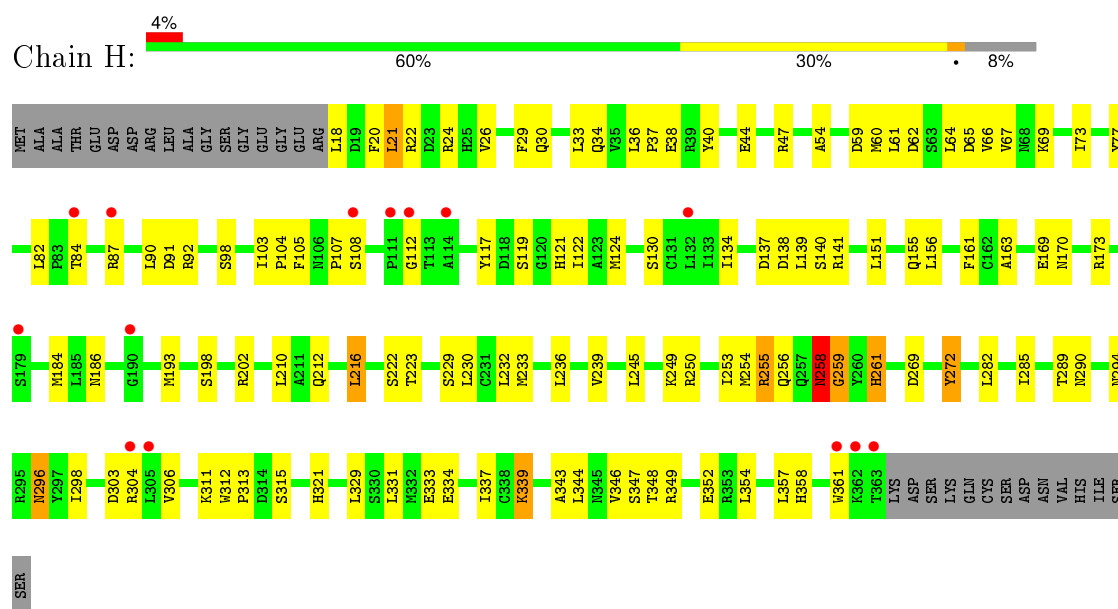


• Molecule 2: Geranylgeranyl transferase type I beta subunit

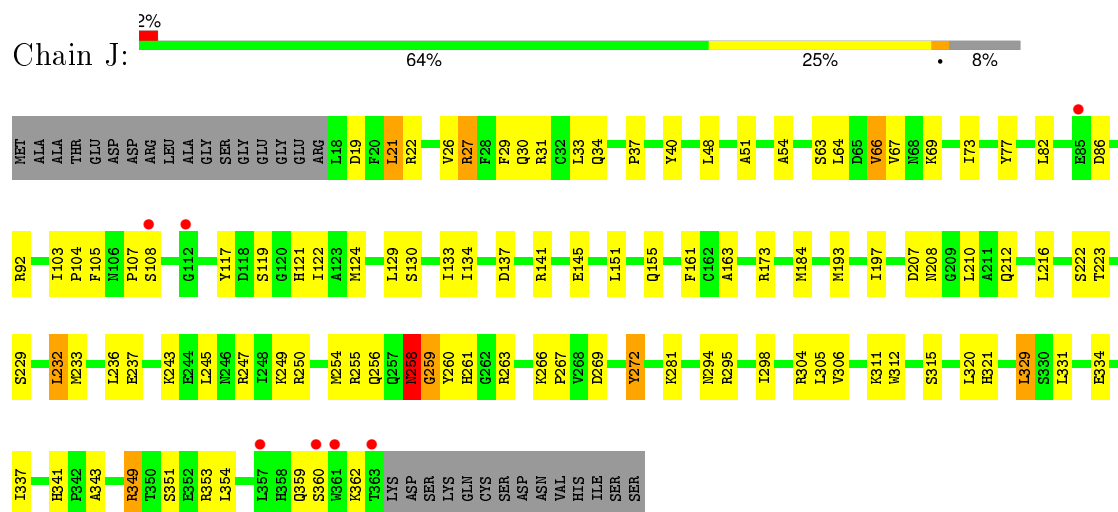




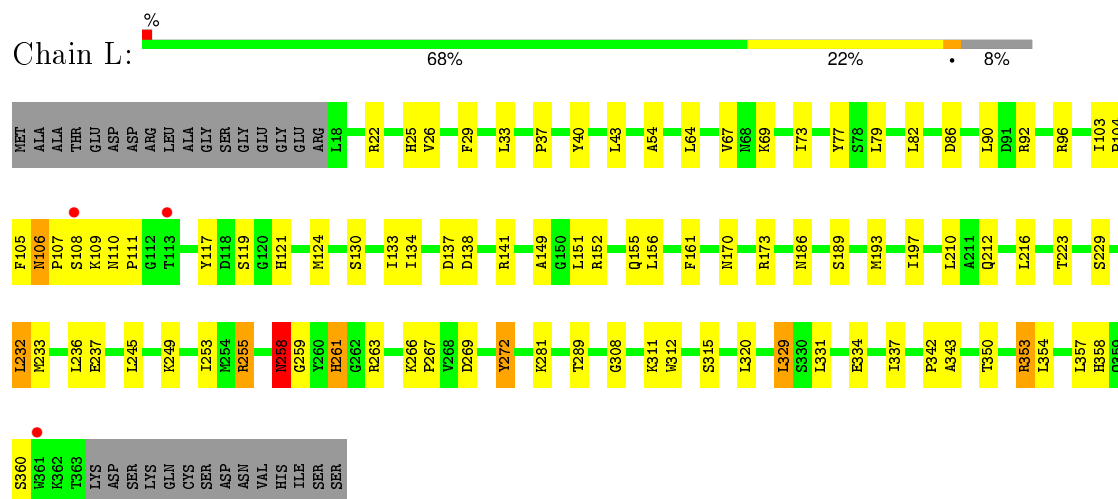
• Molecule 2: Geranylgeranyl transferase type I beta subunit



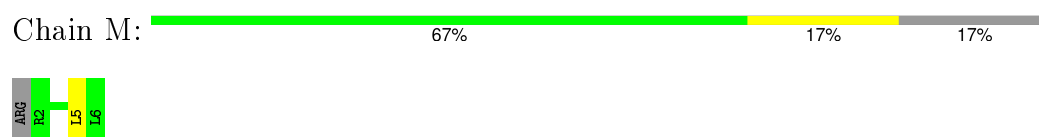
• Molecule 2: Geranylgeranyl transferase type I beta subunit



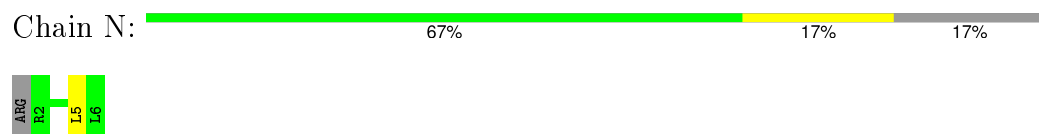
• Molecule 2: Geranylgeranyl transferase type I beta subunit



- Molecule 3: Cell division control protein 42 homolog (Cdc42)



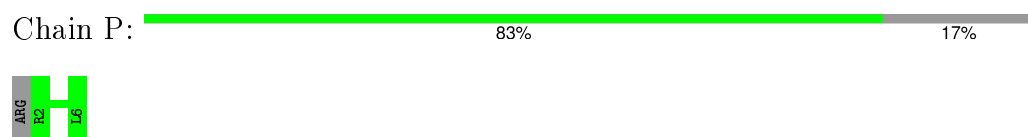
- Molecule 3: Cell division control protein 42 homolog (Cdc42)



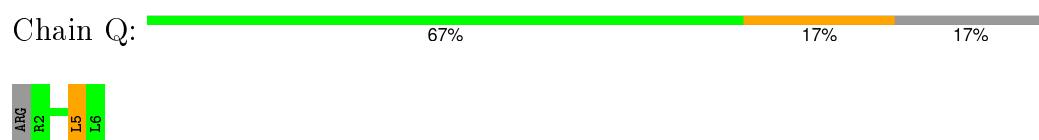
- Molecule 3: Cell division control protein 42 homolog (Cdc42)



- Molecule 3: Cell division control protein 42 homolog (Cdc42)



- Molecule 3: Cell division control protein 42 homolog (Cdc42)



- Molecule 3: Cell division control protein 42 homolog (Cdc42)

Chain R:



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	271.26Å 266.92Å 185.75Å 90.00° 131.91° 90.00°	Depositor
Resolution (Å)	29.96 – 2.90 48.18 – 2.89	Depositor EDS
% Data completeness (in resolution range)	91.4 (29.96-2.90) 91.0 (48.18-2.89)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.34 (at 2.91Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.199 , 0.218 0.196 , 0.214	Depositor DCC
R_{free} test set	9985 reflections (5.05%)	DCC
Wilson B-factor (Å ²)	68.7	Xtriage
Anisotropy	0.064	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 58.2	EDS
Estimated twinning fraction	0.089 for -h-2*k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 199429 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	32873	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.18% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MGM, MES, CL

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	0.35	0/2702	0.53	0/3677
1	C	0.38	0/2721	0.54	0/3698
1	E	0.37	0/2730	0.55	0/3710
1	G	0.37	0/2717	0.54	0/3692
1	I	0.38	0/2714	0.54	0/3690
1	K	0.41	0/2741	0.56	0/3722
2	B	0.38	0/2765	0.60	2/3741 (0.1%)
2	D	0.40	0/2768	0.60	2/3743 (0.1%)
2	F	0.40	0/2779	0.62	2/3757 (0.1%)
2	H	0.39	0/2755	0.60	2/3727 (0.1%)
2	J	0.38	0/2769	0.61	2/3744 (0.1%)
2	L	0.41	0/2781	0.63	2/3759 (0.1%)
3	M	0.47	0/40	0.65	0/51
3	N	0.38	0/40	0.63	0/51
3	O	0.53	0/40	0.58	0/51
3	P	0.43	0/40	0.71	0/51
3	Q	0.55	0/40	0.76	0/51
3	R	0.47	0/40	0.69	0/51
All	All	0.39	0/33182	0.58	12/44966 (0.0%)

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
2	B	0	2
2	D	0	1
2	F	0	2
2	H	0	1
2	J	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	L	0	1
All	All	0	8

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	259	GLY	N-CA-C	-6.08	97.91	113.10
2	D	259	GLY	N-CA-C	-5.77	98.67	113.10
2	L	259	GLY	N-CA-C	-5.71	98.82	113.10
2	F	259	GLY	N-CA-C	-5.68	98.90	113.10
2	H	259	GLY	N-CA-C	-5.68	98.90	113.10

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	272	TYR	Sidechain
2	B	297	TYR	Sidechain
2	D	272	TYR	Sidechain
2	F	272	TYR	Sidechain
2	F	297	TYR	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	2636	0	2526	79	0
1	C	2655	0	2562	70	0
1	E	2664	0	2570	74	0
1	G	2651	0	2563	71	0
1	I	2648	0	2547	64	0
1	K	2675	0	2594	66	0
2	B	2703	0	2606	80	0
2	D	2706	0	2616	77	0
2	F	2717	0	2635	64	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	2694	0	2589	98	0
2	J	2708	0	2613	78	0
2	L	2719	0	2639	65	0
3	M	41	0	47	1	0
3	N	41	0	47	1	0
3	O	41	0	47	2	0
3	P	41	0	47	0	0
3	Q	41	0	47	5	0
3	R	41	0	47	1	0
4	B	1	0	0	0	0
4	D	1	0	0	0	0
4	F	1	0	0	0	0
4	H	1	0	0	0	0
4	J	1	0	0	0	0
4	L	1	0	0	0	0
5	D	1	0	0	0	0
5	F	1	0	0	0	0
5	H	1	0	0	0	0
6	F	12	0	13	0	0
7	B	29	0	34	2	0
7	D	29	0	34	2	0
7	F	29	0	34	4	0
7	H	29	0	34	2	0
7	J	29	0	34	3	0
7	L	29	0	34	3	0
8	A	19	0	0	0	0
8	B	11	0	0	0	0
8	C	16	0	0	0	0
8	D	12	0	0	0	0
8	E	14	0	0	0	0
8	F	26	0	0	0	0
8	G	18	0	0	1	0
8	H	10	0	0	0	0
8	I	14	0	0	0	0
8	J	18	0	0	1	0
8	K	55	0	0	1	0
8	L	37	0	0	0	0
8	M	2	0	0	0	0
8	N	2	0	0	0	0
8	Q	1	0	0	0	0
8	R	1	0	0	0	0
All	All	32873	0	31559	850	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 13.

The worst 5 of 850 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:156:ILE:HG12	1:A:172:ARG:HH12	1.05	1.13
1:G:255:VAL:HG13	1:G:258:ARG:HH12	1.11	1.11
1:E:255:VAL:HG13	1:E:258:ARG:HH21	1.01	1.10
1:K:156:ILE:HG12	1:K:172:ARG:HH12	1.01	1.07
1:I:156:ILE:HG12	1:I:172:ARG:HH12	1.18	1.05

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	312/377 (83%)	287 (92%)	22 (7%)	3 (1%)	19	54
1	C	312/377 (83%)	287 (92%)	22 (7%)	3 (1%)	19	54
1	E	312/377 (83%)	287 (92%)	22 (7%)	3 (1%)	19	54
1	G	312/377 (83%)	288 (92%)	21 (7%)	3 (1%)	19	54
1	I	312/377 (83%)	288 (92%)	21 (7%)	3 (1%)	19	54
1	K	312/377 (83%)	287 (92%)	21 (7%)	4 (1%)	15	46
2	B	344/377 (91%)	326 (95%)	16 (5%)	2 (1%)	30	67
2	D	344/377 (91%)	324 (94%)	19 (6%)	1 (0%)	46	79
2	F	344/377 (91%)	328 (95%)	14 (4%)	2 (1%)	30	67
2	H	344/377 (91%)	318 (92%)	23 (7%)	3 (1%)	21	57
2	J	344/377 (91%)	324 (94%)	16 (5%)	4 (1%)	16	48
2	L	344/377 (91%)	326 (95%)	17 (5%)	1 (0%)	46	79

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	M	3/6 (50%)	3 (100%)	0	0	100	100
3	N	3/6 (50%)	3 (100%)	0	0	100	100
3	O	3/6 (50%)	3 (100%)	0	0	100	100
3	P	3/6 (50%)	3 (100%)	0	0	100	100
3	Q	3/6 (50%)	3 (100%)	0	0	100	100
3	R	3/6 (50%)	3 (100%)	0	0	100	100
All	All	3954/4560 (87%)	3688 (93%)	234 (6%)	32 (1%)	24	60

5 of 32 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	326	GLN
2	B	258	ASN
1	C	326	GLN
2	D	258	ASN
2	F	258	ASN

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	
1	A	282/338 (83%)	270 (96%)	12 (4%)	35	71
1	C	286/338 (85%)	277 (97%)	9 (3%)	47	82
1	E	289/338 (86%)	279 (96%)	10 (4%)	43	78
1	G	285/338 (84%)	278 (98%)	7 (2%)	55	85
1	I	285/338 (84%)	278 (98%)	7 (2%)	55	85
1	K	292/338 (86%)	282 (97%)	10 (3%)	44	79
2	B	291/326 (89%)	279 (96%)	12 (4%)	37	73
2	D	291/326 (89%)	278 (96%)	13 (4%)	34	70
2	F	295/326 (90%)	283 (96%)	12 (4%)	37	73
2	H	288/326 (88%)	276 (96%)	12 (4%)	36	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	J	291/326 (89%)	273 (94%)	18 (6%)	23	55
2	L	295/326 (90%)	282 (96%)	13 (4%)	35	70
3	M	5/6 (83%)	5 (100%)	0	100	100
3	N	5/6 (83%)	5 (100%)	0	100	100
3	O	5/6 (83%)	5 (100%)	0	100	100
3	P	5/6 (83%)	5 (100%)	0	100	100
3	Q	5/6 (83%)	4 (80%)	1 (20%)	1	5
3	R	5/6 (83%)	5 (100%)	0	100	100
All	All	3500/4020 (87%)	3364 (96%)	136 (4%)	39	75

5 of 136 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	232	LEU
2	H	91	ASP
2	L	232	LEU
2	F	255	ARG
1	G	107	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	201	HIS
1	G	325	ASN
1	K	325	ASN
1	G	225	GLN
1	G	285	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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 16 ligands modelled in this entry, 9 are monoatomic - leaving 7 for Mogul analysis.

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	MGM	B	379	-	26,28,28	1.14	2 (7%)	33,37,37	1.92	4 (12%)
7	MGM	D	380	-	26,28,28	1.17	2 (7%)	33,37,37	1.85	3 (9%)
6	MES	F	380	-	11,12,12	6.52	7 (63%)	14,16,16	2.74	5 (35%)
7	MGM	F	381	-	26,28,28	1.31	3 (11%)	33,37,37	1.79	6 (18%)
7	MGM	H	380	-	26,28,28	1.16	3 (11%)	33,37,37	1.81	5 (15%)
7	MGM	J	379	-	26,28,28	1.22	2 (7%)	33,37,37	1.78	7 (21%)
7	MGM	L	379	-	26,28,28	1.29	3 (11%)	33,37,37	1.83	6 (18%)

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
7	MGM	B	379	-	-	0/31/31/31	0/0/0/0
7	MGM	D	380	-	-	0/31/31/31	0/0/0/0
6	MES	F	380	-	-	0/6/14/14	0/1/1/1
7	MGM	F	381	-	-	0/31/31/31	0/0/0/0
7	MGM	H	380	-	-	0/31/31/31	0/0/0/0
7	MGM	J	379	-	-	0/31/31/31	0/0/0/0
7	MGM	L	379	-	-	0/31/31/31	0/0/0/0

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	F	380	MES	C7-C8	-3.54	1.40	1.52
6	F	380	MES	C3-C2	-2.66	1.39	1.50
6	F	380	MES	C5-C6	-2.41	1.40	1.50
6	F	380	MES	C7-N4	-2.37	1.41	1.47
7	H	380	MGM	C5-C6	2.07	1.56	1.53

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	F	380	MES	O3S-S-O2S	-2.84	105.01	111.61
7	J	379	MGM	C10-C8-C9	-2.61	111.42	115.41
7	F	381	MGM	C10-C8-C9	-2.46	111.64	115.41
7	L	379	MGM	C10-C8-C9	-2.46	111.65	115.41
7	B	379	MGM	C10-C8-C9	-2.36	111.80	115.41

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	379	MGM	2	0
7	D	380	MGM	2	0
7	F	381	MGM	4	0
7	H	380	MGM	2	0
7	J	379	MGM	3	0
7	L	379	MGM	3	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, 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	314/377 (83%)	0.24	13 (4%) 41 34	62, 84, 117, 131	0
1	C	314/377 (83%)	0.27	16 (5%) 32 25	61, 81, 110, 131	0
1	E	314/377 (83%)	0.20	9 (2%) 55 49	59, 82, 108, 127	0
1	G	314/377 (83%)	0.34	15 (4%) 34 28	64, 84, 110, 132	0
1	I	314/377 (83%)	0.13	8 (2%) 61 55	55, 80, 111, 125	0
1	K	314/377 (83%)	-0.03	3 (0%) 84 82	53, 68, 95, 107	0
2	B	346/377 (91%)	0.05	7 (2%) 68 64	61, 76, 97, 122	0
2	D	346/377 (91%)	0.05	8 (2%) 64 59	59, 72, 94, 109	0
2	F	346/377 (91%)	0.01	5 (1%) 78 76	55, 69, 95, 117	0
2	H	346/377 (91%)	0.29	14 (4%) 42 35	65, 85, 109, 130	0
2	J	346/377 (91%)	0.00	7 (2%) 68 64	57, 76, 102, 122	0
2	L	346/377 (91%)	-0.06	3 (0%) 85 84	52, 66, 85, 109	0
3	M	5/6 (83%)	0.00	0 100 100	63, 66, 79, 93	1 (20%)
3	N	5/6 (83%)	0.18	0 100 100	67, 69, 78, 93	1 (20%)
3	O	5/6 (83%)	0.41	0 100 100	64, 65, 75, 91	1 (20%)
3	P	5/6 (83%)	0.45	0 100 100	77, 80, 91, 106	1 (20%)
3	Q	5/6 (83%)	0.33	0 100 100	63, 67, 75, 92	1 (20%)
3	R	5/6 (83%)	0.07	0 100 100	59, 60, 73, 88	1 (20%)
All	All	3990/4560 (87%)	0.12	108 (2%) 58 52	52, 77, 105, 132	6 (0%)

The worst 5 of 108 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	361	TRP	6.2
1	E	306	HIS	6.0
1	A	306	HIS	5.8

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Mol	Chain	Res	Type	RSRZ
2	H	108	SER	5.2
1	C	306	HIS	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(Å ²)	Q<0.9
7	MGM	D	380	29/29	0.96	0.26	3.55	66,76,89,90	0
7	MGM	H	380	29/29	0.93	0.29	3.42	76,81,99,101	0
7	MGM	F	381	29/29	0.97	0.24	1.98	59,67,87,89	0
6	MES	F	380	12/12	0.92	0.30	1.78	114,119,120,120	0
7	MGM	L	379	29/29	0.97	0.23	1.54	53,66,76,78	0
7	MGM	J	379	29/29	0.97	0.22	1.48	56,68,79,81	0
7	MGM	B	379	29/29	0.97	0.23	1.29	67,73,89,90	0
4	ZN	D	378	1/1	1.00	0.19	-0.14	72,72,72,72	0
4	ZN	J	378	1/1	1.00	0.16	-0.88	67,67,67,67	0
4	ZN	F	378	1/1	1.00	0.14	-1.17	63,63,63,63	0
4	ZN	B	378	1/1	0.99	0.15	-1.35	66,66,66,66	0
4	ZN	L	378	1/1	1.00	0.16	-1.41	65,65,65,65	0
4	ZN	H	378	1/1	0.99	0.14	-2.02	82,82,82,82	0
5	CL	F	379	1/1	0.96	0.17	-2.04	72,72,72,72	0
5	CL	H	379	1/1	0.96	0.15	-2.26	87,87,87,87	0
5	CL	D	379	1/1	0.94	0.12	-2.48	74,74,74,74	0

6.5 Other polymers [i](#)

There are no such residues in this entry.