



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 08:00 AM UTC

PDB ID : 1N4R / pdb_00001n4r
Title : Protein Geranylgeranyltransferase type-I Complexed with a Geranylgeranylated KKKSKTKCVIL Peptide Product
Authors : Taylor, J.S.; Reid, T.S.; Casey, P.J.; Beese, L.S.
Deposited on : 2002-11-01
Resolution : 2.80 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

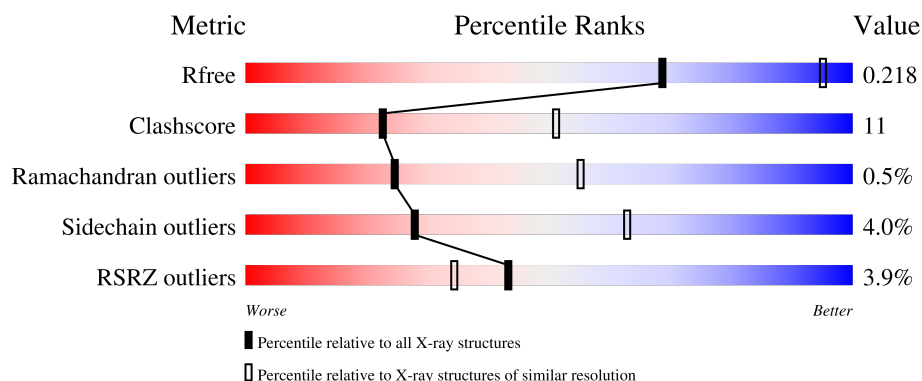
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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 $\leq 5\%$. 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	3% 62% 20% 17%
1	C	377	2% 63% 18% 17%
1	E	377	2% 59% 22% 17%
1	G	377	5% 63% 19% 17%
1	I	377	2% 61% 21% 17%

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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	11	
3	N	11	
3	O	11	
3	P	11	
3	Q	11	
3	R	11	

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	MES	I	905	-	X	-	-
7	CL	G	804	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 33129 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 Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	314	Total	C	N	O	S	0	0	0
			2614	1673	458	478	5			
1	C	314	Total	C	N	O	S	0	0	0
			2648	1691	462	490	5			
1	E	314	Total	C	N	O	S	0	0	0
			2630	1682	460	483	5			
1	G	314	Total	C	N	O	S	0	0	0
			2632	1683	459	485	5			
1	I	314	Total	C	N	O	S	0	0	0
			2654	1693	461	495	5			
1	K	314	Total	C	N	O	S	0	0	0
			2667	1700	466	496	5			

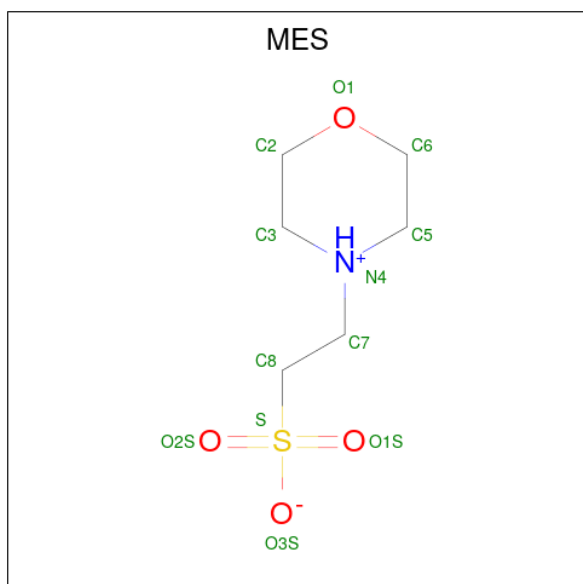
- Molecule 2 is a protein called Geranylgeranyl transferase type-1 subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	346	Total	C	N	O	S	0	0	0
			2689	1702	467	496	24			
2	D	346	Total	C	N	O	S	0	0	0
			2693	1704	467	498	24			
2	F	346	Total	C	N	O	S	0	0	0
			2708	1711	471	502	24			
2	H	346	Total	C	N	O	S	0	0	0
			2670	1692	458	496	24			
2	J	346	Total	C	N	O	S	0	0	0
			2709	1711	471	503	24			
2	L	346	Total	C	N	O	S	0	0	0
			2714	1715	471	504	24			

- Molecule 3 is a protein called Fusion protein consisting of transforming protein p21b and Ras related protein Rap-2b.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	M	6	Total	C	N	O	S	0	0	0
			46	30	7	8	1			
3	N	6	Total	C	N	O	S	0	0	0
			46	30	7	8	1			
3	O	6	Total	C	N	O	S	0	0	0
			46	30	7	8	1			
3	P	6	Total	C	N	O	S	0	0	0
			46	30	7	8	1			
3	Q	6	Total	C	N	O	S	0	0	0
			46	30	7	8	1			
3	R	6	Total	C	N	O	S	0	0	0
			46	30	7	8	1			

- Molecule 4 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
4	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
4	E	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
4	G	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
4	I	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

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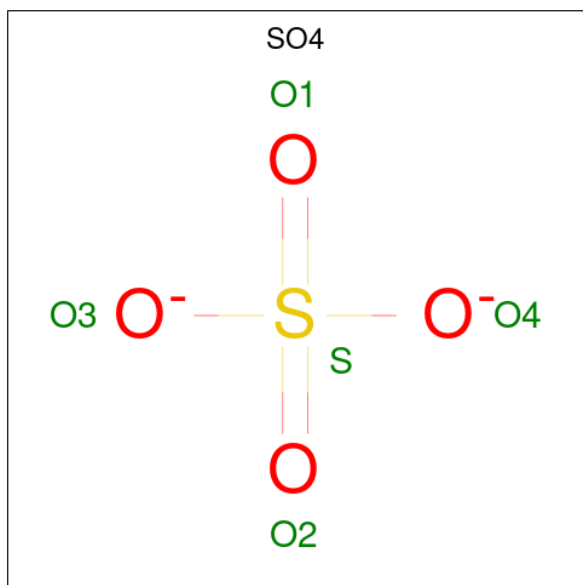
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	K	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 6 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	O	S	0	0
			5	4	1		
6	D	1	Total	O	S	0	0
			5	4	1		

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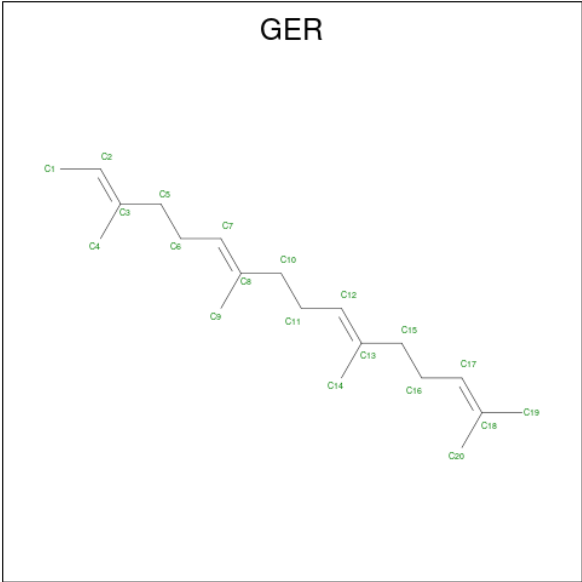
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	F	1	Total	O	S	0	0
			5	4	1		
6	H	1	Total	O	S	0	0
			5	4	1		
6	J	1	Total	O	S	0	0
			5	4	1		
6	L	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	1	Total	Cl	0	0
			1	1		
7	D	1	Total	Cl	0	0
			1	1		
7	F	1	Total	Cl	0	0
			1	1		
7	G	1	Total	Cl	0	0
			1	1		
7	H	1	Total	Cl	0	0
			1	1		
7	J	1	Total	Cl	0	0
			1	1		
7	K	1	Total	Cl	0	0
			1	1		

- Molecule 8 is GERAN-8-YL GERAN (CCD ID: GER) (formula: C₂₀H₃₄).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	M	1	Total C 20 20	0	0
8	N	1	Total C 20 20	0	0
8	O	1	Total C 20 20	0	0
8	P	1	Total C 20 20	0	0
8	Q	1	Total C 20 20	0	0
8	R	1	Total C 20 20	0	0

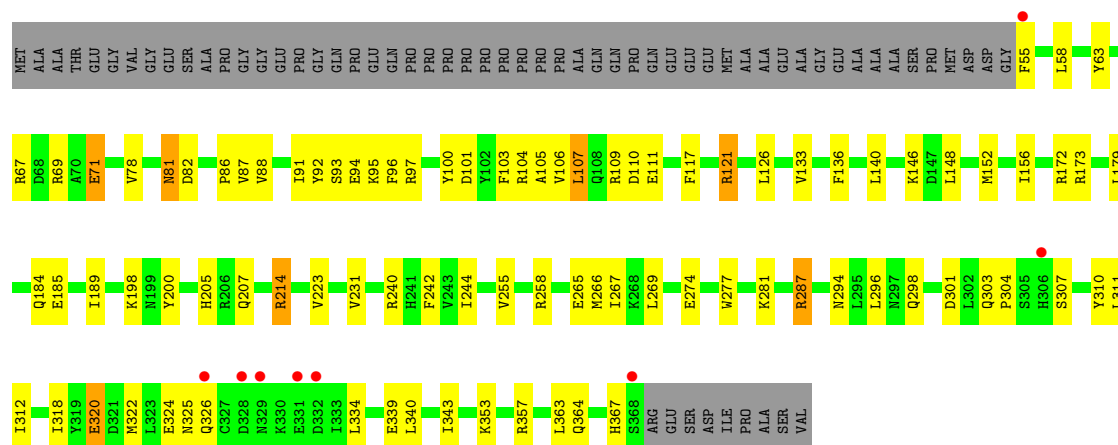
- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	45	Total O 45 45	0	0
9	B	35	Total O 35 35	0	0
9	C	49	Total O 49 49	0	0
9	D	45	Total O 45 45	0	0
9	E	40	Total O 40 40	0	0
9	F	51	Total O 51 51	0	0

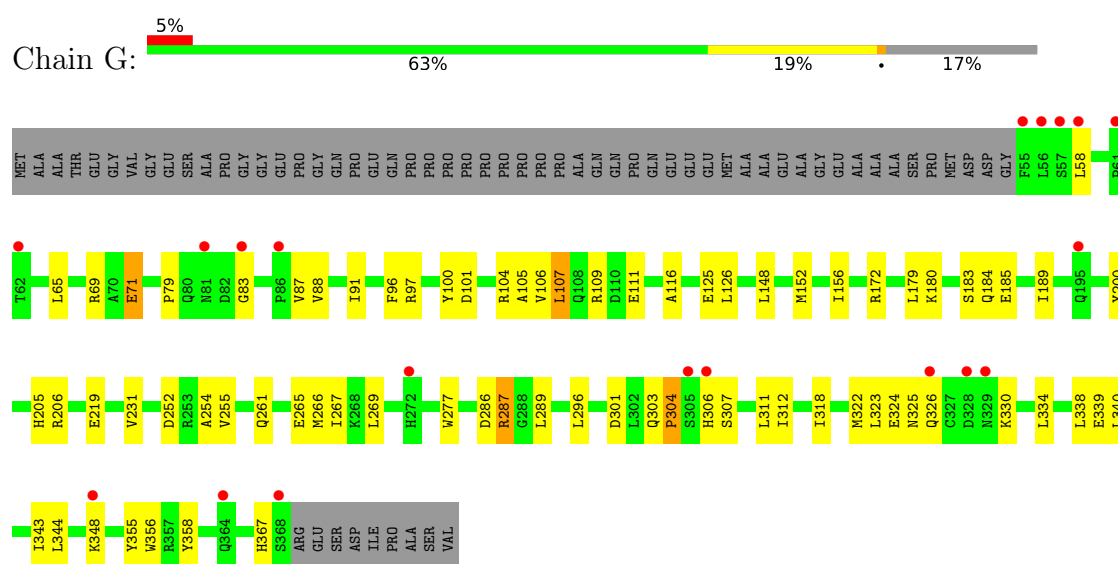
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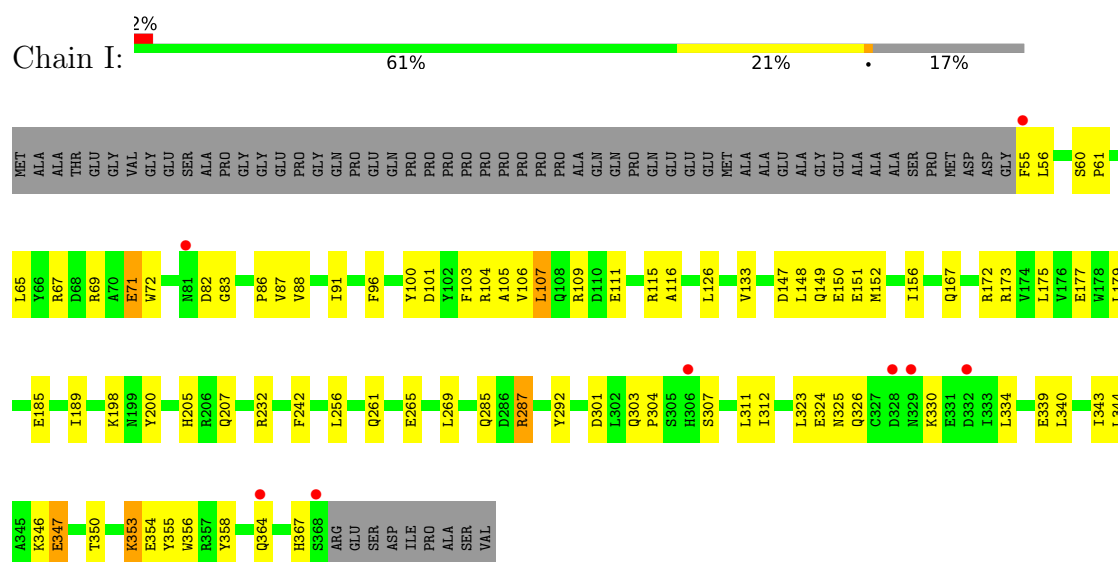
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	G	40	Total 40	O 40	0	0
9	H	23	Total 23	O 23	0	0
9	I	52	Total 52	O 52	0	0
9	J	36	Total 36	O 36	0	0
9	K	101	Total 101	O 101	0	0
9	L	60	Total 60	O 60	0	0
9	M	1	Total 1	O 1	0	0
9	N	3	Total 3	O 3	0	0
9	O	1	Total 1	O 1	0	0
9	Q	3	Total 3	O 3	0	0
9	R	5	Total 5	O 5	0	0



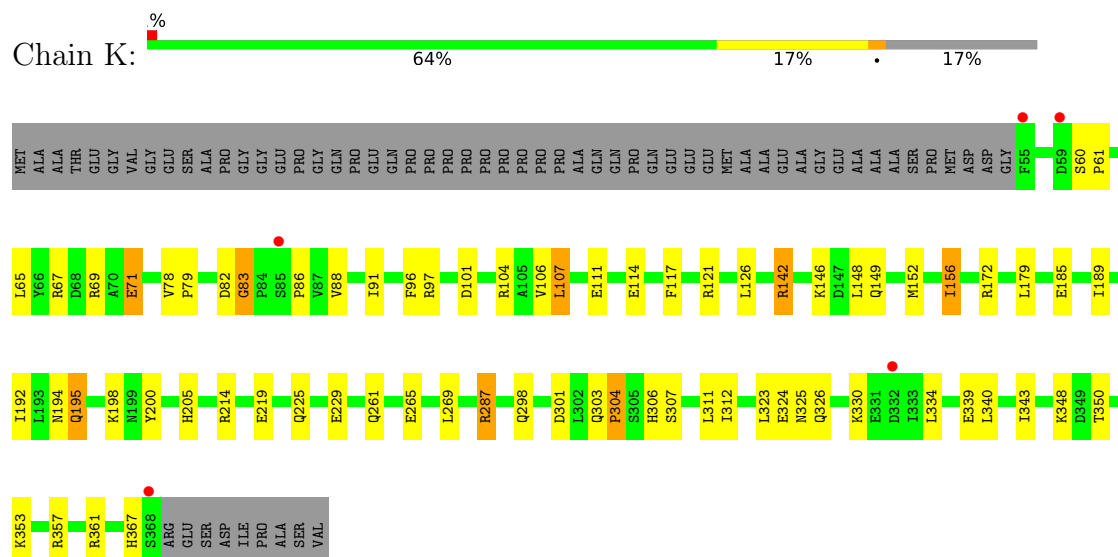
- Molecule 1: Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha



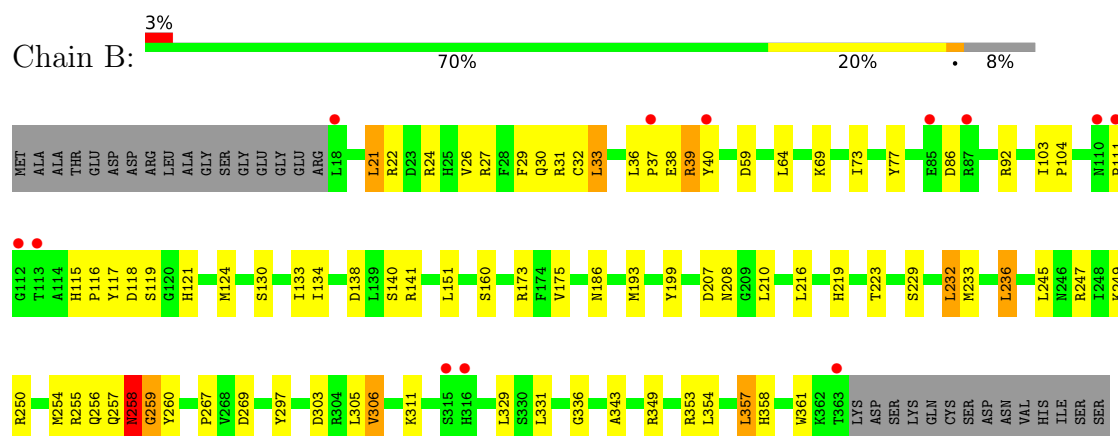
- Molecule 1: Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha



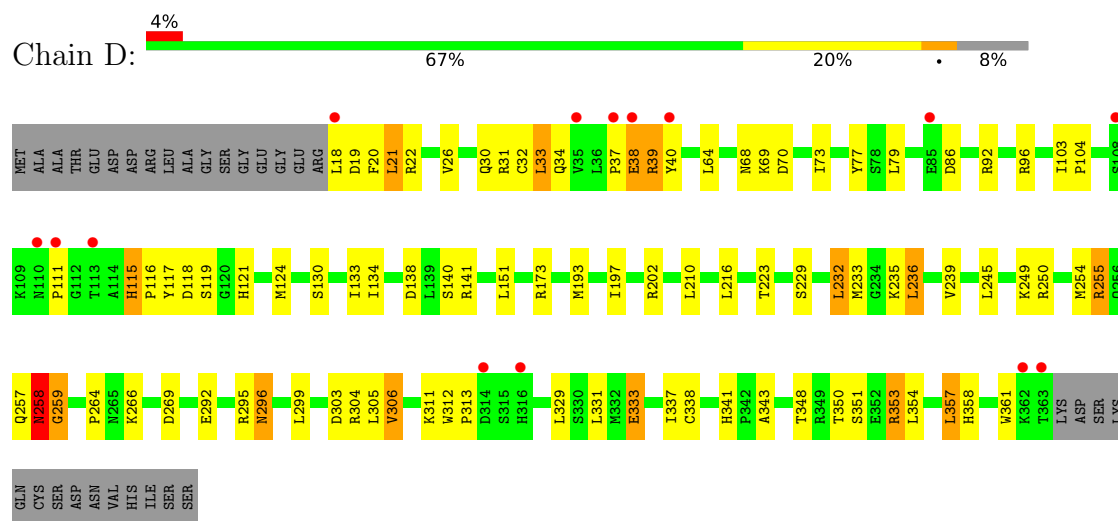
- Molecule 1: Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha



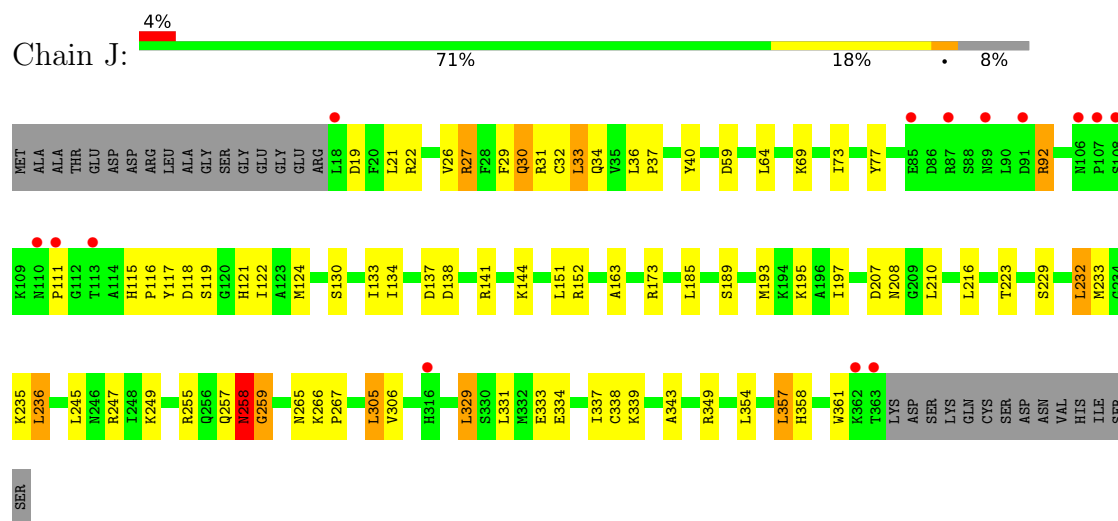
- Molecule 2: Geranylgeranyl transferase type-1 subunit beta



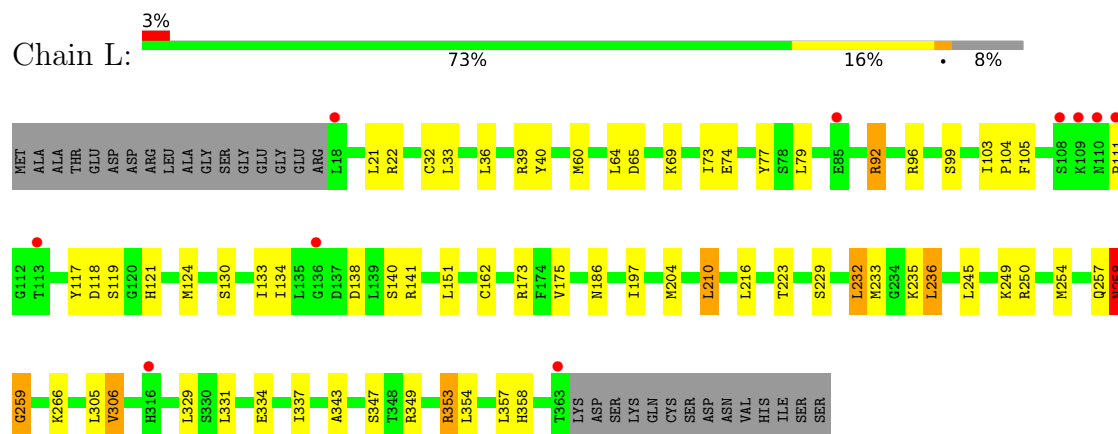
- Molecule 2: Geranylgeranyl transferase type-1 subunit beta



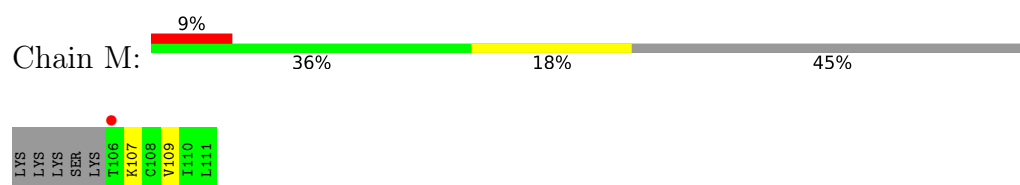
- Molecule 2: Geranylgeranyl transferase type-1 subunit beta



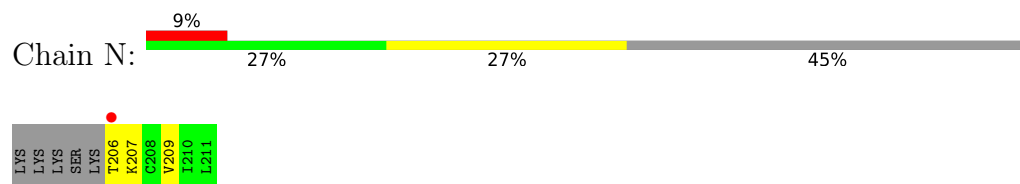
- Molecule 2: Geranylgeranyl transferase type-1 subunit beta



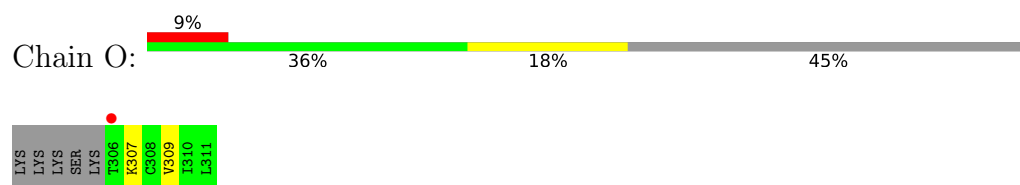
- Molecule 3: Fusion protein consisting of transforming protein p21b and Ras related protein Rap-2b



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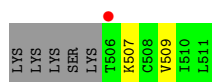
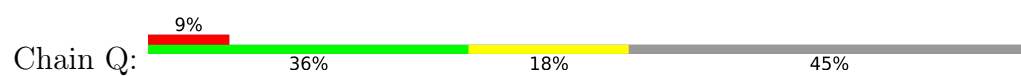
- Molecule 3: Fusion protein consisting of transforming protein p21b and Ras related protein Rap-2b



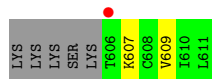
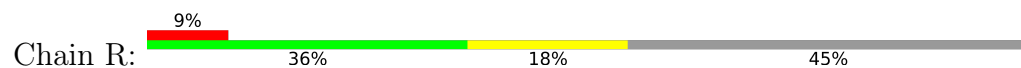
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4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	272.07Å 268.80Å 185.31Å 90.00° 131.55° 90.00°	Depositor
Resolution (Å)	29.86 – 2.80 29.86 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.1 (29.86-2.80) 99.2 (29.86-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 2.61Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.200 , 0.218 0.199 , 0.218	Depositor DCC
R_{free} test set	12102 reflections (4.19%)	wwPDB-VP
Wilson B-factor (Å ²)	51.9	Xtriage
Anisotropy	0.040	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 52.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.085 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	33129	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.61% 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: ZN, CL, SO4, MES, GER

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	0.40	0/2680	0.85	5/3649 (0.1%)
1	C	0.42	0/2714	0.85	6/3690 (0.2%)
1	E	0.42	0/2696	0.84	2/3668 (0.1%)
1	G	0.42	0/2698	0.85	4/3670 (0.1%)
1	I	0.43	0/2720	0.85	6/3698 (0.2%)
1	K	0.45	0/2733	0.86	5/3713 (0.1%)
2	B	0.42	0/2750	0.91	4/3720 (0.1%)
2	D	0.43	0/2754	0.92	8/3725 (0.2%)
2	F	0.43	0/2769	0.92	8/3743 (0.2%)
2	H	0.41	0/2730	0.91	7/3696 (0.2%)
2	J	0.42	0/2770	0.90	3/3745 (0.1%)
2	L	0.46	1/2775 (0.0%)	0.92	7/3750 (0.2%)
3	M	0.57	0/45	0.72	0/58
3	N	0.56	0/45	0.70	0/58
3	O	0.58	0/45	0.74	0/58
3	P	0.55	0/45	0.71	0/58
3	Q	0.57	0/45	0.71	0/58
3	R	0.64	0/45	0.71	0/58
All	All	0.43	1/33059 (0.0%)	0.88	65/44815 (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
2	B	0	1
2	F	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	204	MET	SD-CE	6.44	1.95	1.79

The worst 5 of 65 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	259	GLY	N-CA-C	-9.82	98.40	112.55
2	F	259	GLY	N-CA-C	-9.68	98.61	112.55
2	L	259	GLY	N-CA-C	-9.67	98.62	112.55
2	H	259	GLY	N-CA-C	-9.60	98.73	112.55
2	D	259	GLY	N-CA-C	-9.43	98.97	112.55

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	297	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	2614	0	2499	61	0
1	C	2648	0	2549	54	0
1	E	2630	0	2524	74	0
1	G	2632	0	2527	61	0
1	I	2654	0	2551	56	0
1	K	2667	0	2577	56	0
2	B	2689	0	2585	60	0
2	D	2693	0	2589	65	0
2	F	2708	0	2613	49	0
2	H	2670	0	2551	69	0
2	J	2709	0	2610	49	0
2	L	2714	0	2621	40	0
3	M	46	0	54	1	0
3	N	46	0	54	2	0
3	O	46	0	54	1	0
3	P	46	0	54	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	Q	46	0	54	1	0
3	R	46	0	54	1	0
4	A	12	0	13	3	0
4	C	12	0	13	1	0
4	E	12	0	13	2	0
4	G	12	0	13	2	0
4	I	12	0	13	2	0
4	K	12	0	13	1	0
5	B	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
5	J	1	0	0	0	0
5	L	1	0	0	0	0
6	B	5	0	0	0	0
6	D	5	0	0	0	0
6	F	5	0	0	0	0
6	H	5	0	0	0	0
6	J	5	0	0	0	0
6	L	5	0	0	0	0
7	C	1	0	0	1	0
7	D	1	0	0	0	0
7	F	1	0	0	0	0
7	G	1	0	0	2	0
7	H	1	0	0	0	0
7	J	1	0	0	0	0
7	K	1	0	0	1	0
8	M	20	0	32	1	0
8	N	20	0	32	1	0
8	O	20	0	32	1	0
8	P	20	0	32	1	0
8	Q	20	0	32	1	0
8	R	20	0	32	2	0
9	A	45	0	0	3	0
9	B	35	0	0	1	0
9	C	49	0	0	2	0
9	D	45	0	0	2	0
9	E	40	0	0	2	0
9	F	51	0	0	2	0
9	G	40	0	0	4	0
9	H	23	0	0	0	0
9	I	52	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	J	36	0	0	2	0
9	K	101	0	0	4	0
9	L	60	0	0	0	0
9	M	1	0	0	0	0
9	N	3	0	0	0	0
9	O	1	0	0	0	0
9	Q	3	0	0	0	0
9	R	5	0	0	0	0
All	All	33129	0	31390	673	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 11.

The worst 5 of 673 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:E:156:ILE:HG12	1:E:172:ARG:HH12	1.12	1.14
1:K:156:ILE:HG12	1:K:172:ARG:HH12	0.99	1.14
1:A:156:ILE:HG12	1:A:172:ARG:HH12	1.12	1.12
1:I:156:ILE:HG12	1:I:172:ARG:HH12	1.15	1.11
1:C:156:ILE:HG12	1:C:172:ARG:HH12	1.16	1.09

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%)	288 (92%)	23 (7%)	1 (0%)	36	66
1	C	312/377 (83%)	292 (94%)	20 (6%)	0	100	100
1	E	312/377 (83%)	291 (93%)	21 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	312/377 (83%)	287 (92%)	24 (8%)	1 (0%)	36	66
1	I	312/377 (83%)	290 (93%)	22 (7%)	0	100	100
1	K	312/377 (83%)	292 (94%)	19 (6%)	1 (0%)	36	66
2	B	344/377 (91%)	324 (94%)	18 (5%)	2 (1%)	21	51
2	D	344/377 (91%)	326 (95%)	14 (4%)	4 (1%)	10	34
2	F	344/377 (91%)	323 (94%)	19 (6%)	2 (1%)	21	51
2	H	344/377 (91%)	318 (92%)	22 (6%)	4 (1%)	10	34
2	J	344/377 (91%)	324 (94%)	17 (5%)	3 (1%)	14	41
2	L	344/377 (91%)	325 (94%)	17 (5%)	2 (1%)	21	51
3	M	4/11 (36%)	4 (100%)	0	0	100	100
3	N	4/11 (36%)	4 (100%)	0	0	100	100
3	O	4/11 (36%)	4 (100%)	0	0	100	100
3	P	4/11 (36%)	4 (100%)	0	0	100	100
3	Q	4/11 (36%)	4 (100%)	0	0	100	100
3	R	4/11 (36%)	4 (100%)	0	0	100	100
All	All	3960/4590 (86%)	3704 (94%)	236 (6%)	20 (0%)	24	55

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	111	PRO
2	B	258	ASN
2	D	111	PRO
2	D	258	ASN
2	F	111	PRO

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	276/338 (82%)	269 (98%)	7 (2%)	42	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	285/338 (84%)	276 (97%)	9 (3%)	34	70
1	E	280/338 (83%)	269 (96%)	11 (4%)	28	64
1	G	281/338 (83%)	275 (98%)	6 (2%)	47	79
1	I	287/338 (85%)	279 (97%)	8 (3%)	38	73
1	K	290/338 (86%)	277 (96%)	13 (4%)	24	58
2	B	286/326 (88%)	272 (95%)	14 (5%)	22	55
2	D	287/326 (88%)	272 (95%)	15 (5%)	21	53
2	F	291/326 (89%)	277 (95%)	14 (5%)	23	56
2	H	282/326 (86%)	271 (96%)	11 (4%)	28	64
2	J	291/326 (89%)	275 (94%)	16 (6%)	19	51
2	L	292/326 (90%)	279 (96%)	13 (4%)	24	58
3	M	6/11 (54%)	6 (100%)	0	100	100
3	N	6/11 (54%)	6 (100%)	0	100	100
3	O	6/11 (54%)	6 (100%)	0	100	100
3	P	6/11 (54%)	6 (100%)	0	100	100
3	Q	6/11 (54%)	6 (100%)	0	100	100
3	R	6/11 (54%)	6 (100%)	0	100	100
All	All	3464/4050 (86%)	3327 (96%)	137 (4%)	28	63

5 of 137 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	142	ARG
1	K	287	ARG
2	L	216	LEU
1	E	107	LEU
1	E	81	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 84 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	184	GLN
1	K	108	GLN
1	I	285	GLN
2	J	208	ASN

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Mol	Chain	Res	Type
1	K	234	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 31 ligands modelled in this entry, 13 are monoatomic - leaving 18 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
4	MES	G	904	-	12,12,12	8.99	8 (66%)	15,16,16	2.39	6 (40%)
6	SO4	B	810	-	4,4,4	0.34	0	6,6,6	0.16	0
4	MES	I	905	-	12,12,12	8.91	8 (66%)	15,16,16	2.49	8 (53%)
6	SO4	J	814	-	4,4,4	0.33	0	6,6,6	0.22	0
6	SO4	L	815	-	4,4,4	0.28	0	6,6,6	0.25	0
8	GER	N	1208	3	19,19,19	0.65	0	21,22,22	0.66	0
8	GER	Q	1508	3	19,19,19	0.66	0	21,22,22	0.69	0
6	SO4	H	813	-	4,4,4	0.32	0	6,6,6	0.18	0
8	GER	P	1408	3	19,19,19	0.59	0	21,22,22	0.67	0
8	GER	R	1608	3	19,19,19	0.65	0	21,22,22	0.68	0
6	SO4	F	812	-	4,4,4	0.37	0	6,6,6	0.19	0
4	MES	C	902	-	12,12,12	8.98	8 (66%)	15,16,16	2.36	6 (40%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	SO4	D	811	-	4,4,4	0.34	0	6,6,6	0.19	0
8	GER	O	1308	3	19,19,19	0.67	0	21,22,22	0.69	0
4	MES	E	903	-	12,12,12	9.01	8 (66%)	15,16,16	2.39	6 (40%)
8	GER	M	1108	3	19,19,19	0.70	0	21,22,22	0.66	0
4	MES	A	901	-	12,12,12	9.12	8 (66%)	15,16,16	2.37	5 (33%)
4	MES	K	906	-	12,12,12	9.03	8 (66%)	15,16,16	2.45	6 (40%)

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
4	MES	G	904	-	-	3/6/14/14	0/1/1/1
4	MES	I	905	-	-	3/6/14/14	0/1/1/1
8	GER	N	1208	3	-	3/20/20/20	-
8	GER	Q	1508	3	-	2/20/20/20	-
8	GER	P	1408	3	-	3/20/20/20	-
8	GER	R	1608	3	-	2/20/20/20	-
4	MES	C	902	-	-	3/6/14/14	0/1/1/1
8	GER	O	1308	3	-	2/20/20/20	-
4	MES	E	903	-	-	3/6/14/14	0/1/1/1
8	GER	M	1108	3	-	3/20/20/20	-
4	MES	A	901	-	-	3/6/14/14	0/1/1/1
4	MES	K	906	-	-	3/6/14/14	0/1/1/1

The worst 5 of 48 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	K	906	MES	C8-S	-23.87	1.44	1.77
4	A	901	MES	C8-S	-23.85	1.44	1.77
4	G	904	MES	C8-S	-23.37	1.44	1.77
4	E	903	MES	C8-S	-23.33	1.44	1.77
4	C	902	MES	C8-S	-23.28	1.44	1.77

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	904	MES	O3S-S-C8	4.71	115.23	106.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	905	MES	O3S-S-C8	4.64	115.08	106.00
4	E	903	MES	O3S-S-C8	4.61	115.02	106.00
4	A	901	MES	O3S-S-C8	4.57	114.94	106.00
4	K	906	MES	O3S-S-C8	4.54	114.89	106.00

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	901	MES	C7-C8-S-O1S
4	A	901	MES	C7-C8-S-O2S
4	A	901	MES	C7-C8-S-O3S
4	C	902	MES	C7-C8-S-O1S
4	C	902	MES	C7-C8-S-O3S

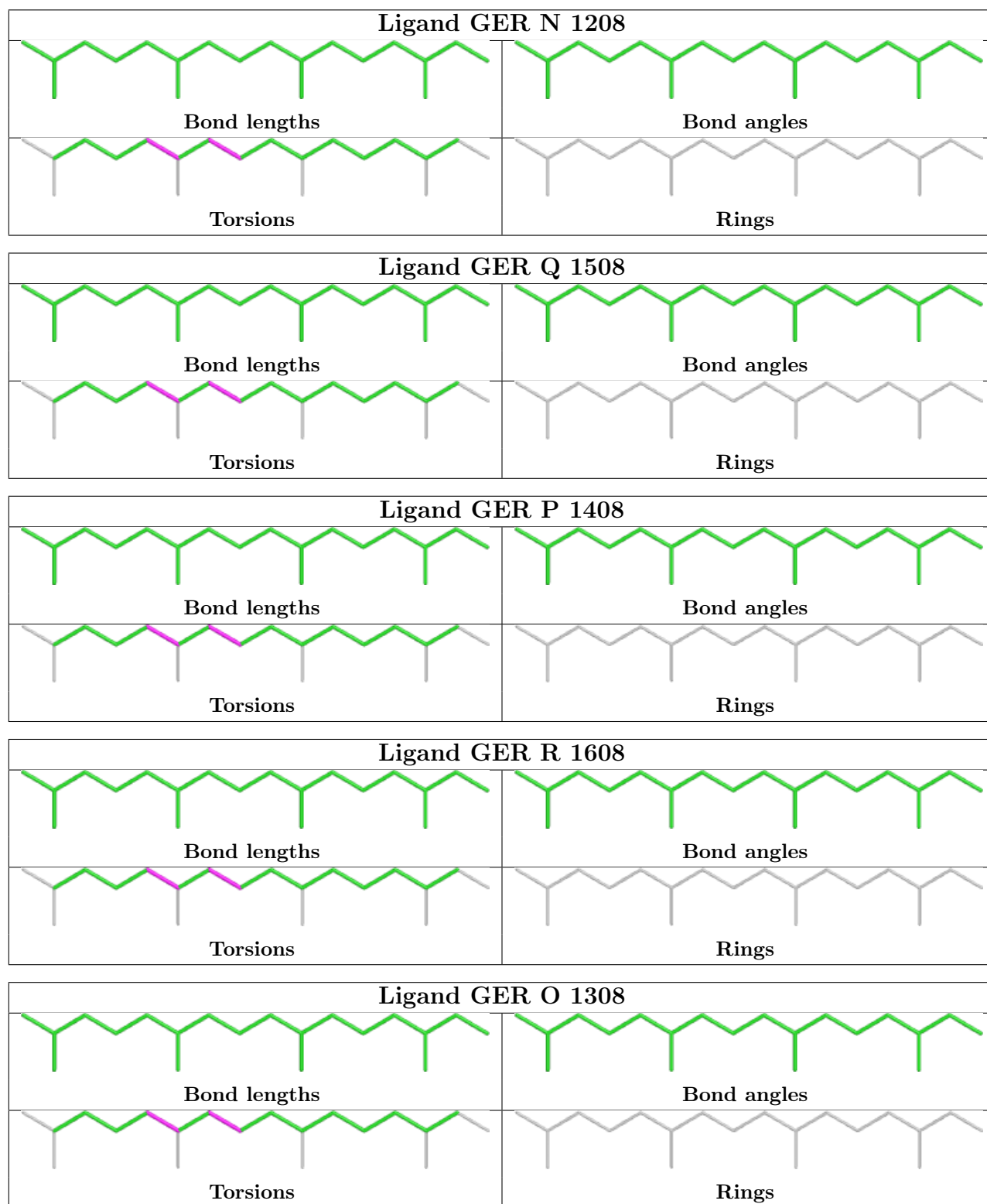
There are no ring outliers.

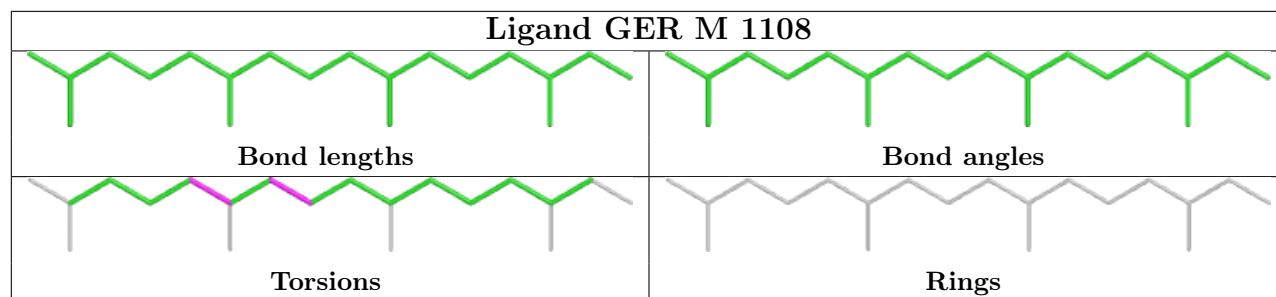
12 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	904	MES	2	0
4	I	905	MES	2	0
8	N	1208	GER	1	0
8	Q	1508	GER	1	0
8	P	1408	GER	1	0
8	R	1608	GER	2	0
4	C	902	MES	1	0
8	O	1308	GER	1	0
4	E	903	MES	2	0
8	M	1108	GER	1	0
4	A	901	MES	3	0
4	K	906	MES	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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%)	0.11	11 (3%) 47 38	36, 57, 91, 105	0
1	C	314/377 (83%)	0.13	7 (2%) 62 52	35, 55, 81, 99	0
1	E	314/377 (83%)	0.16	8 (2%) 58 48	34, 57, 83, 103	0
1	G	314/377 (83%)	0.25	19 (6%) 27 20	38, 58, 85, 104	0
1	I	314/377 (83%)	0.02	8 (2%) 58 48	32, 52, 80, 91	0
1	K	314/377 (83%)	-0.29	5 (1%) 70 61	25, 43, 67, 82	0
2	B	346/377 (91%)	-0.06	12 (3%) 47 38	36, 52, 78, 100	0
2	D	346/377 (91%)	-0.13	14 (4%) 42 33	34, 48, 78, 92	0
2	F	346/377 (91%)	-0.12	14 (4%) 42 33	32, 48, 77, 103	0
2	H	346/377 (91%)	0.54	27 (7%) 19 14	37, 64, 92, 111	0
2	J	346/377 (91%)	-0.07	14 (4%) 42 33	31, 50, 79, 102	0
2	L	346/377 (91%)	-0.34	10 (2%) 53 43	27, 42, 66, 88	0
3	M	6/11 (54%)	0.81	1 (16%) 4 3	52, 58, 82, 89	0
3	N	6/11 (54%)	0.91	1 (16%) 4 3	56, 61, 79, 85	0
3	O	6/11 (54%)	0.68	1 (16%) 4 3	52, 59, 78, 84	0
3	P	6/11 (54%)	1.65	2 (33%) 1 1	64, 68, 89, 92	0
3	Q	6/11 (54%)	0.73	1 (16%) 4 3	51, 56, 72, 79	0
3	R	6/11 (54%)	0.90	1 (16%) 4 3	51, 57, 71, 76	0
All	All	3996/4590 (87%)	0.02	156 (3%) 43 34	25, 52, 83, 111	0

The worst 5 of 156 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	18	LEU	7.4
1	G	55	PHE	7.1
1	C	55	PHE	6.8

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Mol	Chain	Res	Type	RSRZ
2	B	113	THR	6.0
1	E	55	PHE	5.7

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 oligosaccharides 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, 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	B-factors(Å ²)	Q<0.9
4	MES	A	901	12/12	0.89	0.22	96,103,106,106	0
4	MES	G	904	12/12	0.90	0.22	97,101,104,104	0
4	MES	I	905	12/12	0.90	0.22	78,84,88,89	0
4	MES	C	902	12/12	0.91	0.22	86,93,95,96	0
4	MES	K	906	12/12	0.91	0.19	65,77,83,84	0
4	MES	E	903	12/12	0.92	0.19	84,90,94,94	0
6	SO4	D	811	5/5	0.94	0.12	66,66,67,67	0
8	GER	N	1208	20/20	0.94	0.15	49,53,58,59	0
8	GER	O	1308	20/20	0.94	0.15	48,51,58,60	0
8	GER	P	1408	20/20	0.94	0.18	61,66,73,73	0
8	GER	R	1608	20/20	0.94	0.15	47,50,54,54	0
6	SO4	F	812	5/5	0.95	0.10	67,67,68,69	0
8	GER	Q	1508	20/20	0.95	0.14	47,50,55,56	0
8	GER	M	1108	20/20	0.95	0.14	48,52,61,61	0
6	SO4	B	810	5/5	0.96	0.09	67,68,68,69	0
7	CL	J	806	1/1	0.96	0.08	58,58,58,58	0
7	CL	C	801	1/1	0.97	0.16	53,53,53,53	0
7	CL	H	805	1/1	0.97	0.06	60,60,60,60	0
6	SO4	J	814	5/5	0.97	0.07	52,52,54,55	0
7	CL	K	807	1/1	0.97	0.10	44,44,44,44	0
6	SO4	L	815	5/5	0.97	0.08	54,54,56,56	0

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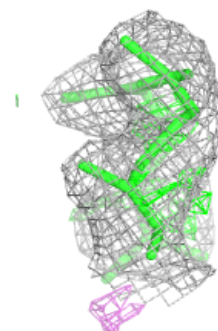
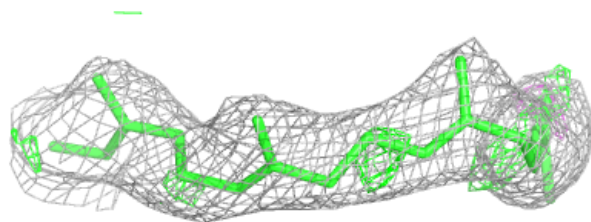
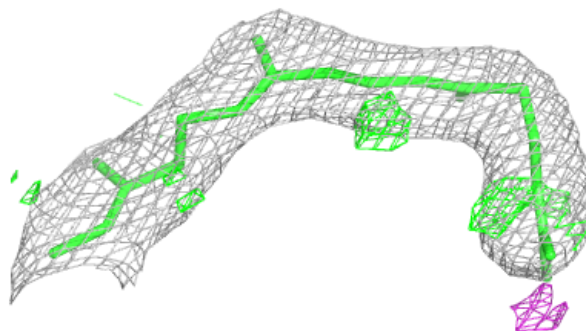
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	ZN	F	378	1/1	0.98	0.08	78,78,78,78	0
7	CL	D	802	1/1	0.98	0.04	45,45,45,45	0
7	CL	G	804	1/1	0.98	0.12	52,52,52,52	0
6	SO4	H	813	5/5	0.98	0.07	68,69,69,70	0
5	ZN	H	378	1/1	0.99	0.07	87,87,87,87	0
7	CL	F	803	1/1	0.99	0.07	51,51,51,51	0
5	ZN	J	378	1/1	0.99	0.05	68,68,68,68	0
5	ZN	L	378	1/1	0.99	0.04	58,58,58,58	0
5	ZN	D	378	1/1	0.99	0.04	66,66,66,66	0
5	ZN	B	378	1/1	0.99	0.06	77,77,77,77	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

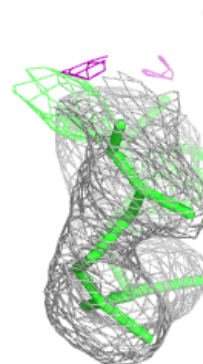
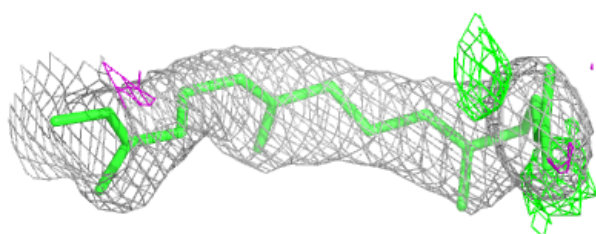
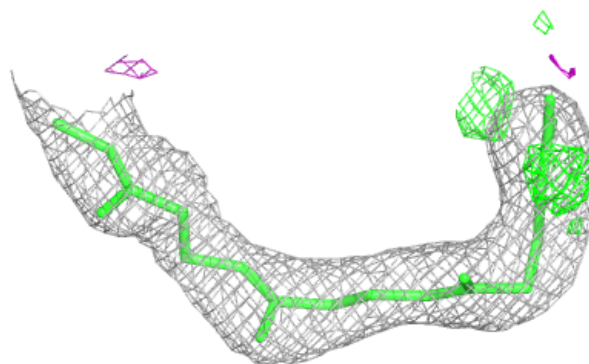
Electron density around GER N 1208:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

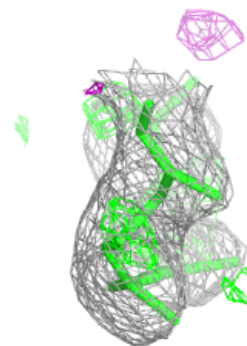
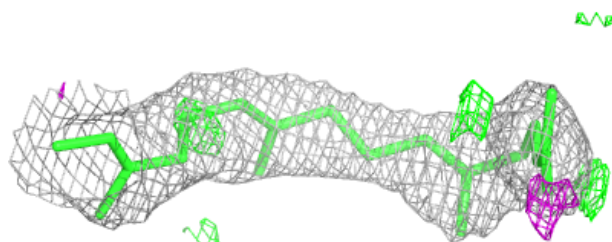
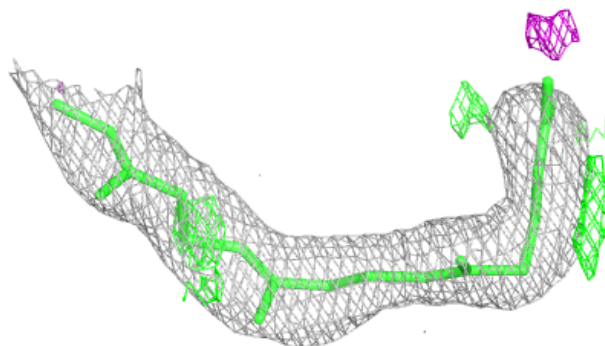


Electron density around GER O 1308:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

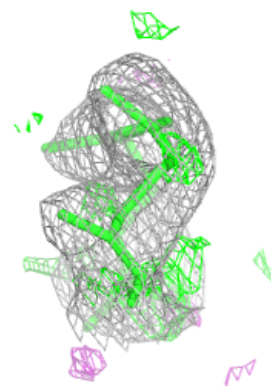
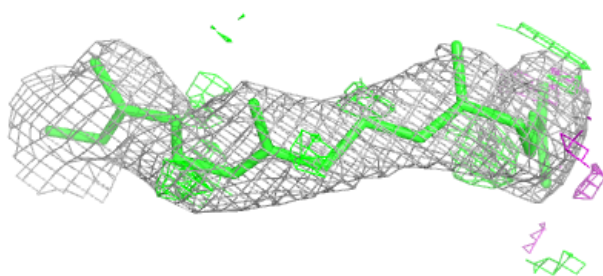
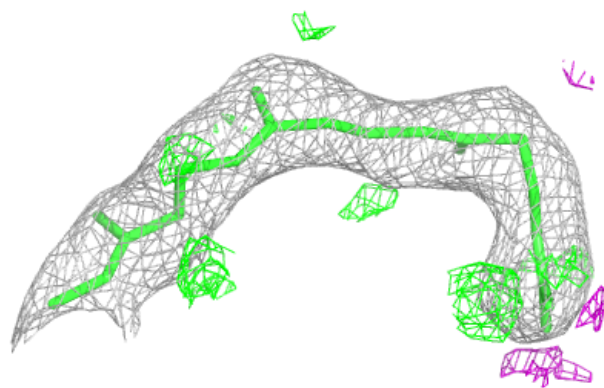
**Electron density around GER P 1408:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

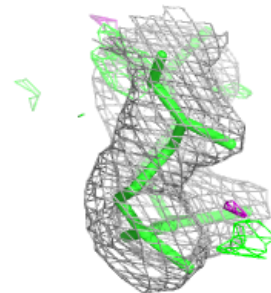
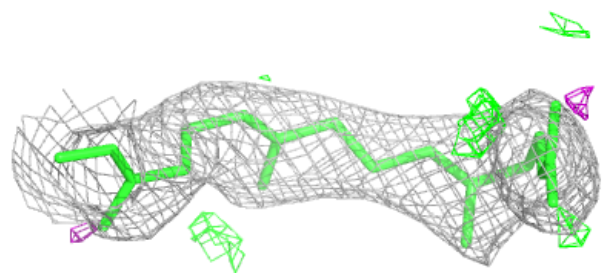
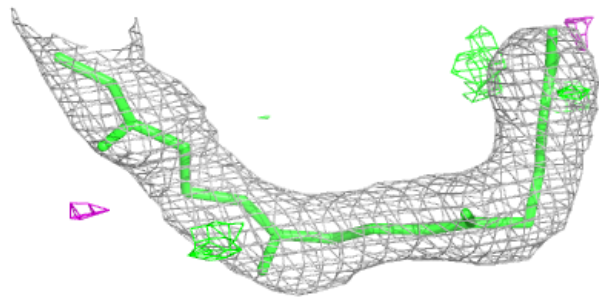


Electron density around GER R 1608:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

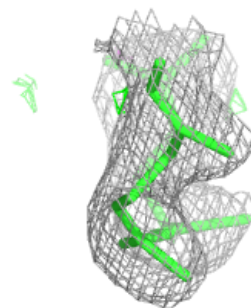
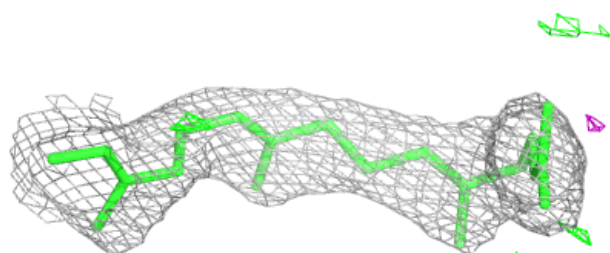
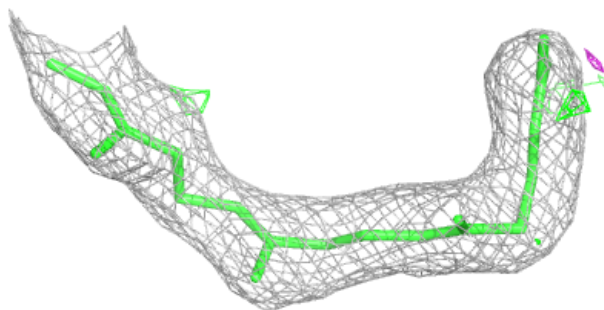
**Electron density around GER Q 1508:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around GER M 1108:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers ⓘ

There are no such residues in this entry.