



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 12:18 pm BST

PDB ID : 1N4P
Title : Protein Geranylgeranyltransferase type-I Complexed with Geranylgeranyl Diphosphate
Authors : Taylor, J.S.; Reid, T.S.; Casey, P.J.; Beese, L.S.
Deposited on : 2002-11-01
Resolution : 2.65 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
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) : 2.11

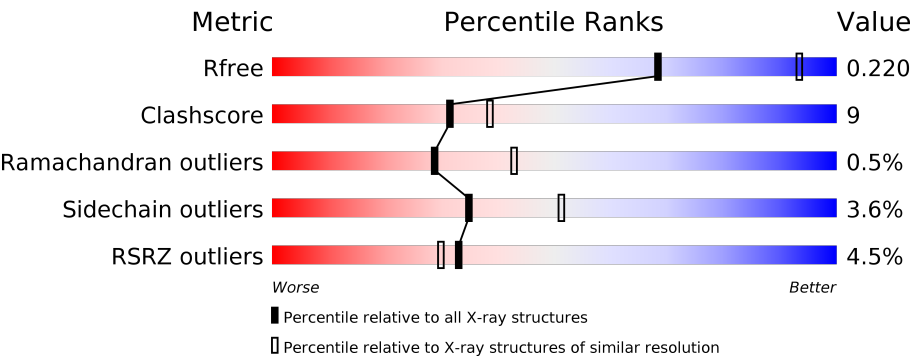
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	1332 (2.68-2.64)
Clashscore	141614	1374 (2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)
RSRZ outliers	127900	1318 (2.68-2.64)

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 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	<div><div>4%</div><div><div></div><div>67%</div><div>15%</div><div>•</div><div>17%</div></div></div>
1	C	377	<div><div>3%</div><div><div></div><div>66%</div><div>17%</div><div>•</div><div>17%</div></div></div>
1	E	377	<div><div>4%</div><div><div></div><div>64%</div><div>17%</div><div>•</div><div>17%</div></div></div>
1	G	377	<div><div>3%</div><div><div></div><div>63%</div><div>20%</div><div>•</div><div>17%</div></div></div>
1	I	377	<div><div>3%</div><div><div></div><div>64%</div><div>18%</div><div>•</div><div>17%</div></div></div>
1	K	377	<div><div>2%</div><div><div></div><div>69%</div><div>14%</div><div>•</div><div>17%</div></div></div>

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Mol	Chain	Length	Quality of chain
2	B	377	<div><div><div>5%</div><div>72%</div><div>19%</div><div>8%</div></div></div>
2	D	377	<div><div><div>4%</div><div>72%</div><div>17%</div><div>8%</div></div></div>
2	F	377	<div><div><div>4%</div><div>76%</div><div>15%</div><div>8%</div></div></div>
2	H	377	<div><div><div>8%</div><div>69%</div><div>21%</div><div>8%</div></div></div>
2	J	377	<div><div><div>4%</div><div>69%</div><div>21%</div><div>8%</div></div></div>
2	L	377	<div><div><div>2%</div><div>73%</div><div>16%</div><div>8%</div></div></div>
3	M	11	<div><div><div>27%</div><div>9%</div><div>27%</div><div>64%</div></div></div>
3	N	11	<div><div><div>18%</div><div>9%</div><div>27%</div><div>64%</div></div></div>

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 33443 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
			2629	1679	463	482	5			
1	C	314	Total	C	N	O	S	0	0	0
			2643	1689	461	488	5			
1	E	314	Total	C	N	O	S	0	0	0
			2642	1686	461	490	5			
1	G	314	Total	C	N	O	S	0	0	0
			2633	1683	459	486	5			
1	I	314	Total	C	N	O	S	0	0	0
			2656	1694	465	492	5			
1	K	314	Total	C	N	O	S	0	0	0
			2671	1703	467	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
			2697	1707	467	499	24			
2	D	346	Total	C	N	O	S	0	0	0
			2713	1715	472	502	24			
2	F	346	Total	C	N	O	S	0	0	0
			2718	1717	474	503	24			
2	H	346	Total	C	N	O	S	0	0	0
			2694	1706	464	500	24			
2	J	346	Total	C	N	O	S	0	0	0
			2711	1713	471	503	24			
2	L	346	Total	C	N	O	S	0	0	0
			2723	1720	473	506	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	4	Total	C	N	O	S	0	0	0
			30	20	4	5	1			
3	N	4	Total	C	N	O	S	0	0	0
			30	20	4	5	1			

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

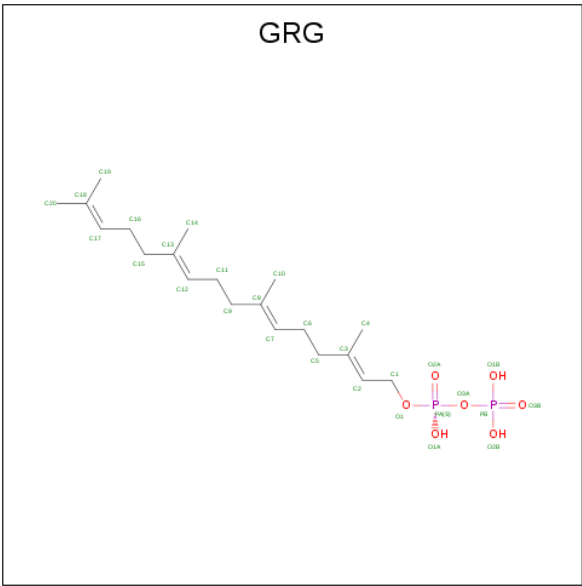
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	J	1	Total	Zn	0	0
			1	1		
4	D	1	Total	Zn	0	0
			1	1		
4	H	1	Total	Zn	0	0
			1	1		
4	B	1	Total	Zn	0	0
			1	1		
4	L	1	Total	Zn	0	0
			1	1		
4	F	1	Total	Zn	0	0
			1	1		

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

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

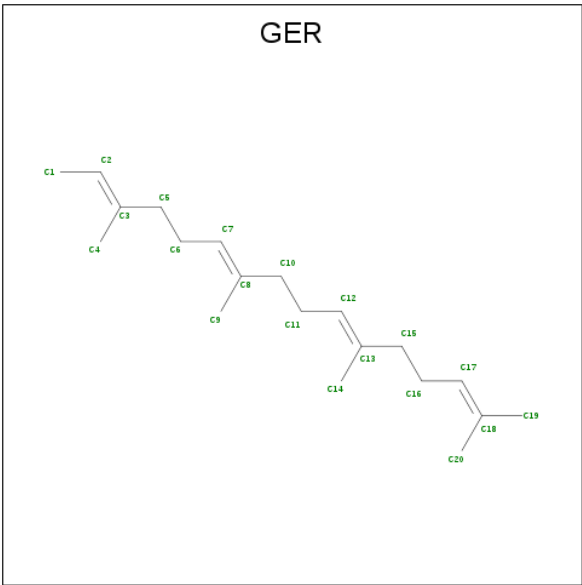
- Molecule 6 is GERANYLGERANYL DIPHOSPHATE (three-letter code: GRG) (formula:

C₂₀H₃₆O₇P₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	O	P	0	0
			29	20	7	2		
6	D	1	Total	C	O	P	0	0
			29	20	7	2		
6	F	1	Total	C	O	P	0	0
			29	20	7	2		
6	H	1	Total	C	O	P	0	0
			29	20	7	2		
6	J	1	Total	C	O	P	0	0
			29	20	7	2		
6	L	1	Total	C	O	P	0	0
			29	20	7	2		

- Molecule 7 is GERAN-8-YL GERAN (three-letter code: GER) (formula: C₂₀H₃₄).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	M	1	Total C 20 20	0	0
7	N	1	Total C 20 20	0	0

- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	71	Total O 71 71	0	0
8	B	63	Total O 63 63	0	0
8	C	80	Total O 80 80	0	0
8	D	94	Total O 94 94	0	0
8	E	64	Total O 64 64	0	0
8	F	92	Total O 92 92	0	0
8	G	58	Total O 58 58	0	0
8	H	48	Total O 48 48	0	0
8	I	87	Total O 87 87	0	0
8	J	73	Total O 73 73	0	0

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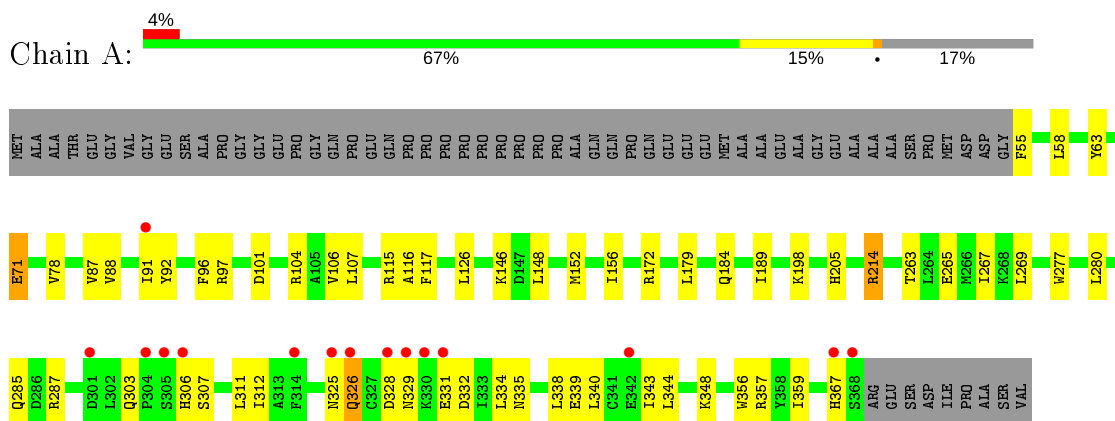
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	K	159	Total 159	O 159	0	0
8	L	134	Total 134	O 134	0	0
8	N	1	Total 1	O 1	0	0

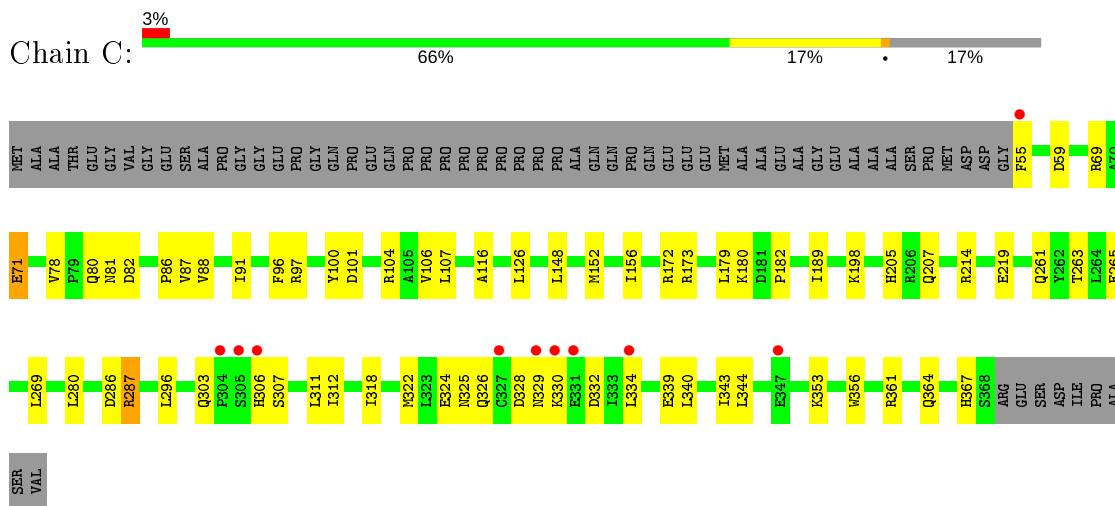
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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 ($\text{RSRZ} > 2$). 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.

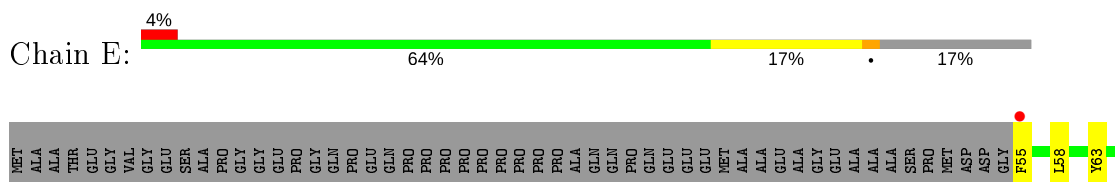
- Molecule 1: Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha

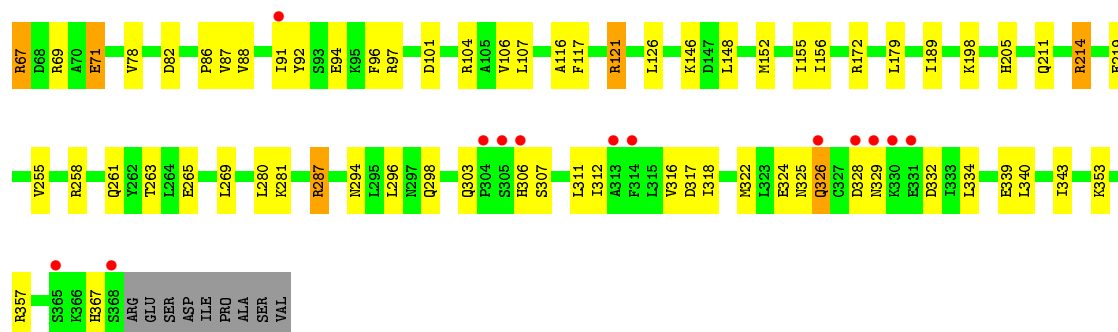


- Molecule 1: Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha

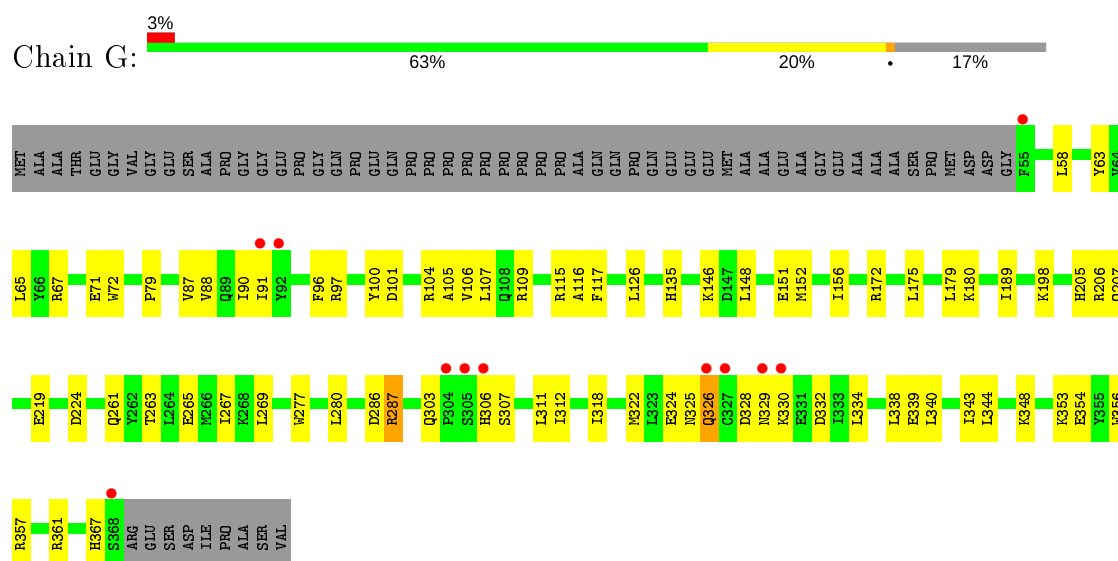


- Molecule 1: Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha

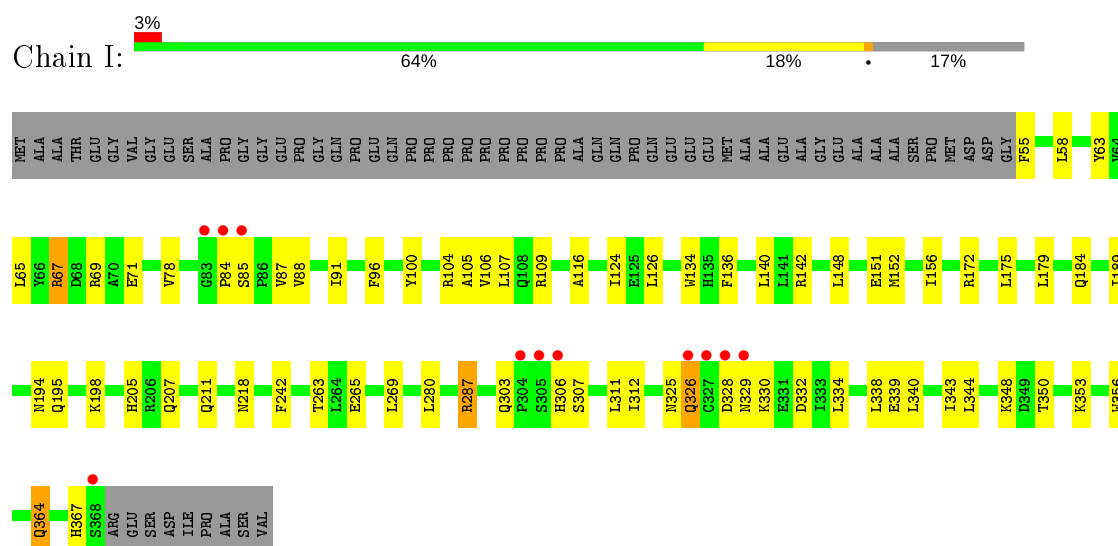




- Molecule 1: Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha

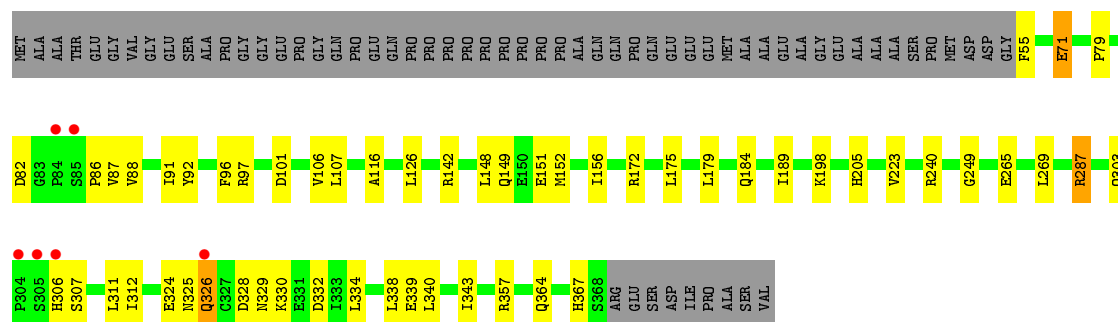


- Molecule 1: Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha

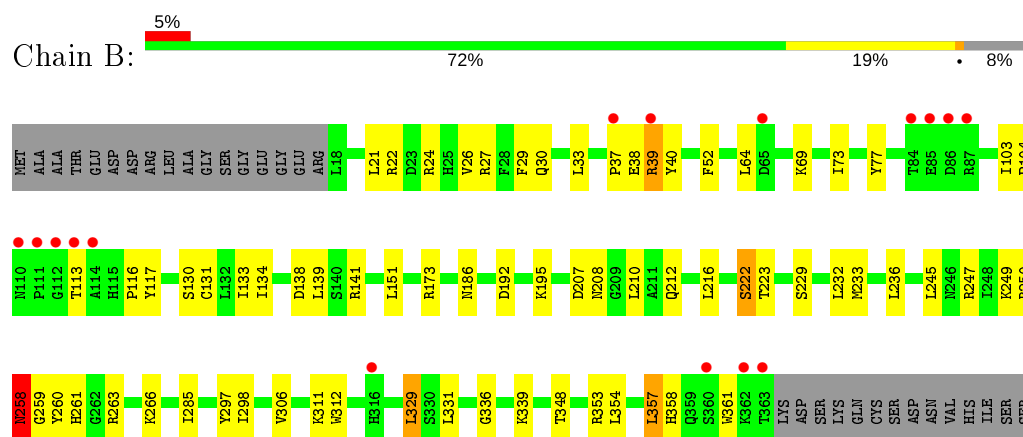


- Molecule 1: Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha

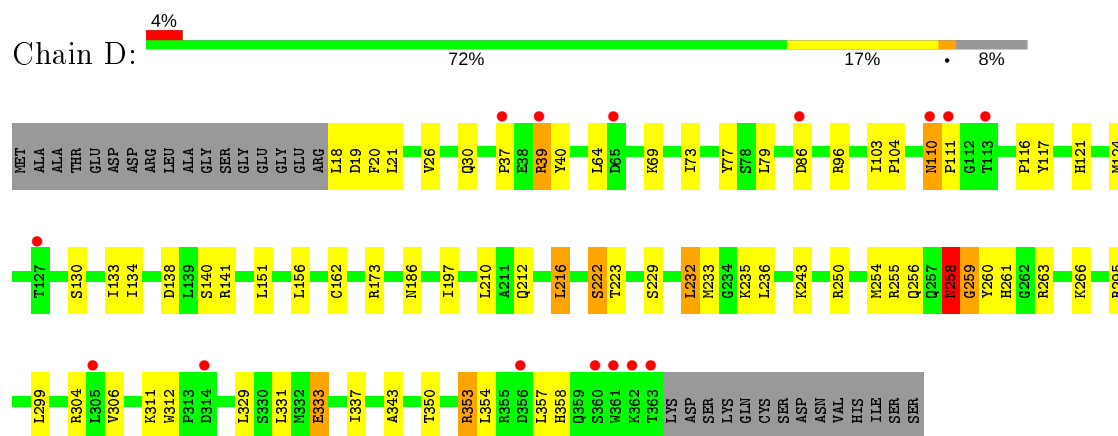




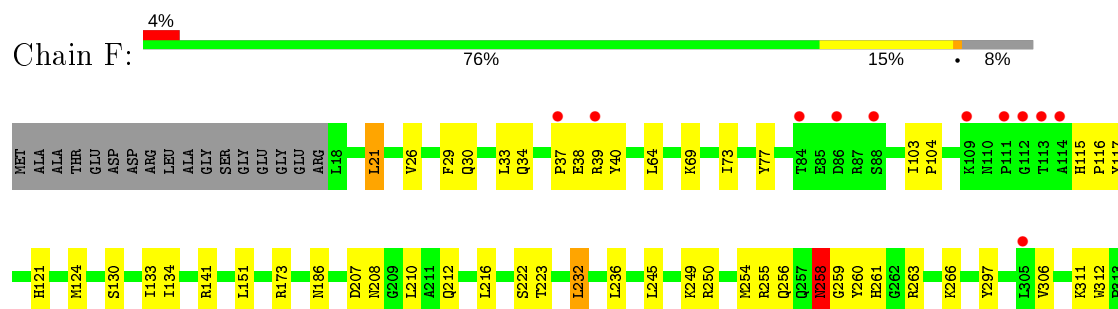
- Molecule 2: Geranylgeranyl transferase type-1 subunit beta



- Molecule 2: Geranylgeranyl transferase type-1 subunit beta

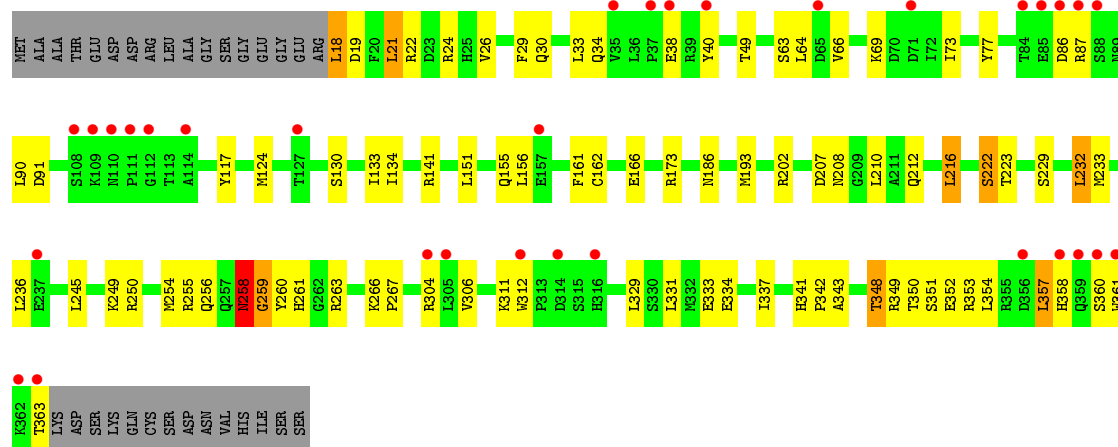


- Molecule 2: Geranylgeranyl transferase type-1 subunit beta

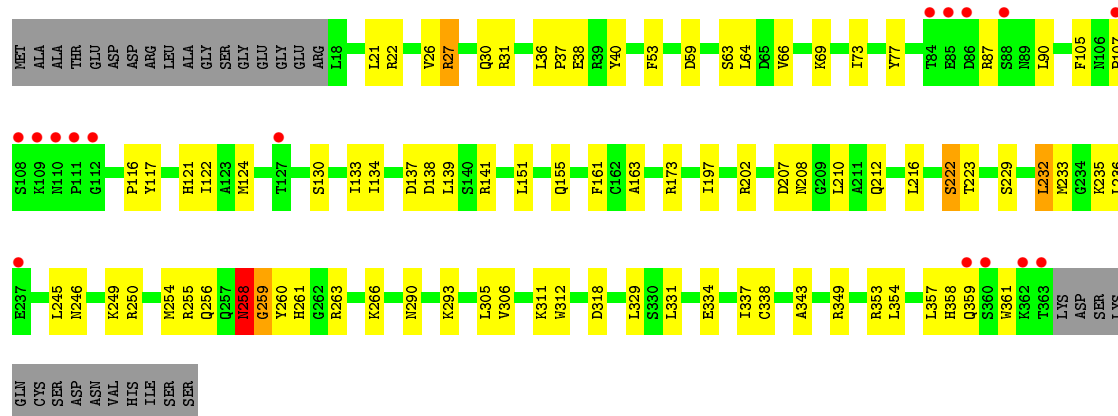




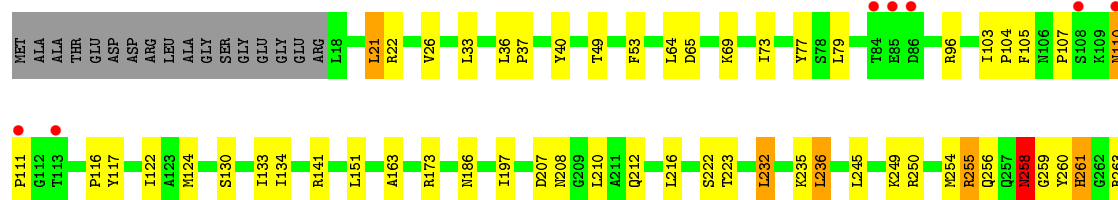
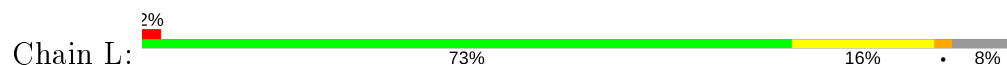
• Molecule 2: Geranylgeranyl transferase type-1 subunit beta



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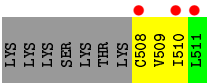


• Molecule 2: Geranylgeranyl transferase type-1 subunit beta

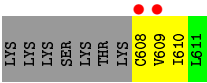




● Molecule 3: Fusion protein consisting of transforming protein p21b and Ras related protein Rap-2b



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4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	272.34Å 271.57Å 185.43Å 90.00° 131.56° 90.00°	Depositor
Resolution (Å)	29.92 – 2.65 29.92 – 2.65	Depositor EDS
% Data completeness (in resolution range)	98.0 (29.92-2.65) 98.7 (29.92-2.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.02 (at 2.64Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.204 , 0.228 0.198 , 0.220	Depositor DCC
R_{free} test set	14292 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	49.7	Xtriage
Anisotropy	0.031	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 54.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.080 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	33443	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.37% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GRG, ZN, CL, 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	0.34	0/2695	0.52	0/3668
1	C	0.36	0/2709	0.53	0/3684
1	E	0.35	0/2708	0.53	0/3684
1	G	0.35	0/2699	0.53	0/3672
1	I	0.36	0/2722	0.53	0/3700
1	K	0.40	0/2737	0.55	0/3717
2	B	0.36	0/2759	0.60	2/3733 (0.1%)
2	D	0.37	0/2775	0.59	2/3752 (0.1%)
2	F	0.38	0/2780	0.60	2/3758 (0.1%)
2	H	0.35	0/2756	0.58	2/3729 (0.1%)
2	J	0.36	0/2773	0.59	2/3750 (0.1%)
2	L	0.40	0/2785	0.61	2/3764 (0.1%)
3	M	0.67	0/29	0.82	0/37
3	N	0.66	0/29	0.81	0/37
All	All	0.37	0/32956	0.56	12/44685 (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	1
2	F	0	1
All	All	0	2

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	259	GLY	N-CA-C	-6.01	98.07	113.10
2	F	259	GLY	N-CA-C	-5.96	98.20	113.10
2	D	259	GLY	N-CA-C	-5.84	98.49	113.10
2	J	259	GLY	N-CA-C	-5.83	98.51	113.10
2	L	259	GLY	N-CA-C	-5.77	98.68	113.10
2	B	259	GLY	N-CA-C	-5.76	98.70	113.10
2	L	258	ASN	N-CA-C	-5.46	96.25	111.00
2	J	258	ASN	N-CA-C	-5.42	96.36	111.00
2	B	258	ASN	N-CA-C	-5.32	96.63	111.00
2	D	258	ASN	N-CA-C	-5.31	96.67	111.00
2	H	258	ASN	N-CA-C	-5.29	96.72	111.00
2	F	258	ASN	N-CA-C	-5.25	96.84	111.00

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	2629	0	2520	48	0
1	C	2643	0	2540	44	0
1	E	2642	0	2534	57	0
1	G	2633	0	2524	55	0
1	I	2656	0	2560	44	0
1	K	2671	0	2588	39	0
2	B	2697	0	2600	50	0
2	D	2713	0	2628	52	0
2	F	2718	0	2635	37	0
2	H	2694	0	2590	67	0
2	J	2711	0	2616	51	0
2	L	2723	0	2643	45	0
3	M	30	0	34	3	0
3	N	30	0	34	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	F	1	0	0	0	0
5	G	1	0	0	1	0
5	H	1	0	0	0	0
5	J	1	0	0	0	0
5	K	1	0	0	1	0
5	L	1	0	0	0	0
6	B	29	0	33	1	0
6	D	29	0	33	1	0
6	F	29	0	33	2	0
6	H	29	0	33	1	0
6	J	29	0	33	1	0
6	L	29	0	33	1	0
7	M	20	0	33	5	0
7	N	20	0	33	5	0
8	A	71	0	0	1	0
8	B	63	0	0	0	0
8	C	80	0	0	3	0
8	D	94	0	0	1	0
8	E	64	0	0	0	0
8	F	92	0	0	2	0
8	G	58	0	0	2	0
8	H	48	0	0	2	0
8	I	87	0	0	4	0
8	J	73	0	0	2	0
8	K	159	0	0	4	0
8	L	134	0	0	2	0
8	N	1	0	0	0	0
All	All	33443	0	31310	573	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 9.

All (573) 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:I:156:ILE:HG12	1:I:172:ARG:HH12	1.10	1.15
1:E:156:ILE:HG12	1:E:172:ARG:HH12	1.09	1.11
1:A:156:ILE:HG12	1:A:172:ARG:HH12	1.03	1.08
1:K:156:ILE:HG12	1:K:172:ARG:HH12	0.99	1.08
1:G:156:ILE:HG12	1:G:172:ARG:HH12	1.17	1.04
1:C:156:ILE:HG12	1:C:172:ARG:HH12	1.17	1.04
2:F:212:GLN:HE21	2:F:222:SER:HB3	1.21	1.01
2:J:212:GLN:HE21	2:J:222:SER:HB3	1.29	0.96
2:H:21:LEU:HD21	2:H:304:ARG:HG2	1.47	0.95
1:K:156:ILE:HG12	1:K:172:ARG:NH1	1.81	0.95
2:F:212:GLN:NE2	2:F:222:SER:HB3	1.86	0.90
1:A:156:ILE:HG12	1:A:172:ARG:NH1	1.86	0.90
1:E:353:LYS:HE2	1:E:357:ARG:HH12	1.38	0.87
5:G:1711:CL:CL	8:G:383:HOH:O	2.31	0.86
2:H:18:LEU:HA	2:H:304:ARG:NH2	1.91	0.85
2:D:173:ARG:HG2	6:D:1722:GRG:H112	1.59	0.84
2:D:212:GLN:HE21	2:D:222:SER:HB3	1.41	0.84
2:L:173:ARG:HG2	6:L:1726:GRG:H112	1.59	0.83
1:E:255:VAL:HG13	1:E:258:ARG:HH21	1.42	0.83
2:B:212:GLN:HE21	2:B:222:SER:HB3	1.44	0.83
1:G:152:MET:O	1:G:156:ILE:HG13	1.79	0.83
2:D:39:ARG:H	2:D:39:ARG:HD2	1.42	0.82
2:D:212:GLN:NE2	2:D:222:SER:HB3	1.95	0.82
2:B:212:GLN:NE2	2:B:222:SER:HB3	1.95	0.82
2:H:348:THR:O	2:H:352:GLU:HG2	1.80	0.81
2:J:173:ARG:HG2	6:J:1725:GRG:H112	1.60	0.81
2:D:37:PRO:HB2	2:D:39:ARG:CD	2.11	0.81
1:A:152:MET:O	1:A:156:ILE:HG13	1.80	0.81
2:B:173:ARG:HG2	6:B:1721:GRG:H112	1.63	0.80
2:F:173:ARG:HG2	6:F:1723:GRG:H112	1.62	0.80
1:I:152:MET:O	1:I:156:ILE:HG13	1.82	0.79
1:E:152:MET:O	1:E:156:ILE:HG13	1.81	0.79
1:E:318:ILE:HG22	1:E:322:MET:HE3	1.65	0.79
1:K:330:LYS:HE2	1:K:367:HIS:HB3	1.66	0.77
2:D:37:PRO:HB2	2:D:39:ARG:HD2	1.67	0.77
2:H:173:ARG:HG2	6:H:1724:GRG:H112	1.67	0.76
2:H:186:ASN:HB2	2:H:358:HIS:CE1	2.20	0.76
1:C:152:MET:O	1:C:156:ILE:HG13	1.83	0.76
1:K:152:MET:O	1:K:156:ILE:HG13	1.85	0.76
1:E:156:ILE:HG12	1:E:172:ARG:NH1	1.94	0.75
1:E:255:VAL:HG13	1:E:258:ARG:NH2	2.01	0.75
2:H:212:GLN:NE2	2:H:222:SER:HB3	2.03	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:609:VAL:HG23	3:N:610:ILE:HG23	1.71	0.73
1:I:156:ILE:HG12	1:I:172:ARG:NH1	1.95	0.73
2:J:212:GLN:NE2	2:J:222:SER:HB3	2.02	0.73
1:G:97:ARG:HG2	1:G:101:ASP:OD2	1.89	0.72
1:K:156:ILE:CG1	1:K:172:ARG:HH12	1.90	0.72
2:H:229:SER:O	2:H:233:MET:HG3	1.90	0.71
1:A:189:ILE:HD11	1:A:205:HIS:HD2	1.56	0.71
1:E:156:ILE:CG1	1:E:172:ARG:HH12	1.98	0.71
5:K:1717:CL:CL	8:K:391:HOH:O	2.43	0.71
3:M:509:VAL:HG23	3:M:510:ILE:HG23	1.71	0.71
1:C:318:ILE:HG22	1:C:322:MET:HE3	1.73	0.70
2:F:133:ILE:HD13	2:F:354:LEU:HD13	1.72	0.70
2:L:212:GLN:HE21	2:L:222:SER:HB3	1.56	0.70
1:E:189:ILE:HD11	1:E:205:HIS:HD2	1.57	0.69
1:A:214:ARG:HG2	1:G:180:LYS:HB2	1.73	0.69
1:G:189:ILE:HD11	1:G:205:HIS:HD2	1.57	0.69
1:C:189:ILE:HD11	1:C:205:HIS:HD2	1.58	0.69
2:B:133:ILE:HD13	2:B:354:LEU:HD13	1.75	0.68
2:D:69:LYS:O	2:D:73:ILE:HG13	1.93	0.68
1:G:312:ILE:HG23	1:G:340:LEU:HD22	1.76	0.68
2:B:69:LYS:O	2:B:73:ILE:HG13	1.93	0.67
2:L:133:ILE:HD13	2:L:354:LEU:HD13	1.75	0.67
1:C:87:VAL:HG12	1:C:88:VAL:HG23	1.75	0.67
2:H:19:ASP:HB2	8:H:1494:HOH:O	1.96	0.66
2:D:37:PRO:HB2	2:D:39:ARG:HD3	1.77	0.66
1:K:91:ILE:O	1:K:91:ILE:HD12	1.95	0.66
1:K:189:ILE:HD11	1:K:205:HIS:HD2	1.60	0.65
2:H:212:GLN:HE21	2:H:222:SER:HB3	1.61	0.65
2:H:69:LYS:O	2:H:73:ILE:HG13	1.97	0.65
2:H:18:LEU:N	2:H:18:LEU:HD22	2.11	0.65
1:I:91:ILE:HD12	1:I:91:ILE:O	1.96	0.65
2:B:245:LEU:O	2:B:249:LYS:HG3	1.97	0.64
2:J:263:ARG:HG3	2:J:266:LYS:HG3	1.78	0.64
1:G:91:ILE:HD12	1:G:91:ILE:O	1.97	0.64
2:B:186:ASN:HB2	2:B:358:HIS:CE1	2.32	0.64
1:E:312:ILE:HG23	1:E:340:LEU:HD22	1.80	0.63
2:H:334:GLU:HB3	2:H:337:ILE:HD12	1.79	0.63
1:K:87:VAL:HG12	1:K:88:VAL:HG23	1.80	0.63
1:E:91:ILE:O	1:E:91:ILE:HD12	1.98	0.63
1:I:156:ILE:CG1	1:I:172:ARG:HH12	2.00	0.63
1:G:87:VAL:HG12	1:G:88:VAL:HG23	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:353:ARG:HH11	2:B:353:ARG:HG2	1.62	0.63
1:G:261:GLN:O	1:G:265:GLU:HG2	1.99	0.63
1:I:189:ILE:HD11	1:I:205:HIS:HD2	1.62	0.63
1:I:87:VAL:HG12	1:I:88:VAL:HG23	1.80	0.63
2:D:263:ARG:HG3	2:D:266:LYS:HG3	1.80	0.62
2:D:295:ARG:CZ	2:D:299:LEU:HD11	2.29	0.62
2:H:21:LEU:CD2	2:H:304:ARG:HG2	2.25	0.62
2:F:69:LYS:O	2:F:73:ILE:HG13	1.99	0.62
1:A:91:ILE:O	1:A:91:ILE:HD12	2.00	0.62
2:H:263:ARG:HG3	2:H:266:LYS:HG3	1.81	0.62
2:B:39:ARG:HB3	2:B:39:ARG:HH11	1.65	0.62
1:A:329:ASN:HB3	1:A:332:ASP:HB3	1.82	0.61
1:E:353:LYS:CE	1:E:357:ARG:HH12	2.10	0.61
2:F:37:PRO:HD2	2:F:40:TYR:CD1	2.34	0.61
2:F:26:VAL:O	2:F:30:GLN:HG3	1.99	0.61
1:G:334:LEU:HD22	1:G:367:HIS:O	2.00	0.61
2:F:263:ARG:HG3	2:F:266:LYS:HG3	1.81	0.61
2:J:133:ILE:HD13	2:J:354:LEU:HD13	1.82	0.61
2:H:87:ARG:HH12	2:H:90:LEU:HD11	1.65	0.61
1:K:312:ILE:HG23	1:K:340:LEU:HD22	1.83	0.61
2:L:197:ILE:HD11	2:L:235:LYS:HD3	1.83	0.61
1:G:101:ASP:HA	1:G:104:ARG:NH1	2.15	0.60
1:C:91:ILE:O	1:C:91:ILE:HD12	2.01	0.60
1:G:100:TYR:O	1:G:104:ARG:HG3	2.01	0.60
1:G:198:LYS:HD3	2:H:266:LYS:HD3	1.81	0.60
1:C:330:LYS:HE2	1:C:367:HIS:HB3	1.83	0.60
1:A:78:VAL:O	1:A:104:ARG:HD2	2.01	0.60
2:B:263:ARG:HG3	2:B:266:LYS:HG3	1.82	0.60
1:G:357:ARG:O	1:G:361:ARG:HG3	2.01	0.60
2:H:232:LEU:HD13	2:H:343:ALA:HB1	1.84	0.60
2:H:21:LEU:HD23	2:H:24:ARG:HE	1.67	0.59
1:I:156:ILE:HD11	1:I:172:ARG:HH22	1.67	0.59
1:A:339:GLU:O	1:A:343:ILE:HG13	2.02	0.59
2:D:39:ARG:H	2:D:39:ARG:CD	2.14	0.59
2:H:193:MET:HE2	2:H:233:MET:HB3	1.85	0.59
1:K:156:ILE:HD11	1:K:172:ARG:HH22	1.68	0.59
2:B:26:VAL:O	2:B:30:GLN:HG3	2.01	0.59
1:A:97:ARG:HG2	1:A:101:ASP:OD2	2.02	0.59
1:K:107:LEU:HD22	2:L:117:TYR:CD2	2.37	0.59
1:C:303:GLN:O	1:C:307:SER:HB2	2.03	0.58
1:I:207:GLN:HG2	1:I:242:PHE:CE2	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:210:LEU:HB2	2:H:223:THR:HA	1.85	0.58
2:J:22:ARG:O	2:J:26:VAL:HG23	2.03	0.58
1:C:198:LYS:HD3	2:D:266:LYS:HD3	1.85	0.58
1:C:180:LYS:HB2	1:E:214:ARG:HG2	1.85	0.58
2:L:232:LEU:HD13	2:L:343:ALA:HB1	1.85	0.58
2:J:210:LEU:HB2	2:J:223:THR:HA	1.84	0.58
1:E:78:VAL:O	1:E:104:ARG:HD2	2.03	0.57
2:L:353:ARG:HD3	2:L:353:ARG:O	2.04	0.57
2:L:210:LEU:HB2	2:L:223:THR:HA	1.86	0.57
2:H:245:LEU:O	2:H:249:LYS:HG3	2.04	0.57
1:C:148:LEU:HB2	1:C:179:LEU:HD21	1.87	0.57
1:G:334:LEU:O	1:G:338:LEU:HG	2.04	0.57
2:J:318:ASP:HB2	7:M:1727:GER:H71	1.87	0.57
1:A:328:ASP:O	1:A:329:ASN:HB2	2.05	0.57
1:I:330:LYS:HE2	1:I:367:HIS:HB3	1.87	0.57
1:A:87:VAL:HG12	1:A:88:VAL:HG23	1.87	0.56
1:A:214:ARG:O	1:A:214:ARG:HG3	2.05	0.56
2:H:22:ARG:HG2	2:H:22:ARG:HH11	1.70	0.56
2:D:210:LEU:HB2	2:D:223:THR:HA	1.86	0.56
1:G:101:ASP:HA	1:G:104:ARG:HH11	1.69	0.56
2:J:338:CYS:SG	2:J:349:ARG:NH2	2.78	0.56
1:K:265:GLU:O	1:K:269:LEU:HD13	2.06	0.56
2:D:37:PRO:HB3	2:D:39:ARG:HH11	1.70	0.56
1:E:82:ASP:HB2	1:E:86:PRO:HB3	1.88	0.56
1:I:107:LEU:HD22	2:J:117:TYR:CD2	2.40	0.56
1:I:329:ASN:HB3	1:I:332:ASP:HB3	1.88	0.56
1:I:312:ILE:HG23	1:I:340:LEU:HD22	1.87	0.56
1:G:156:ILE:HG12	1:G:172:ARG:NH1	2.03	0.56
1:I:148:LEU:HB2	1:I:179:LEU:HD21	1.88	0.56
2:J:232:LEU:HD13	2:J:343:ALA:HB1	1.86	0.56
2:L:263:ARG:HG3	2:L:266:LYS:HG3	1.86	0.56
1:A:265:GLU:O	1:A:269:LEU:HD13	2.06	0.56
1:E:265:GLU:O	1:E:269:LEU:HD13	2.06	0.56
1:E:87:VAL:HG12	1:E:88:VAL:HG23	1.88	0.55
2:B:210:LEU:HB2	2:B:223:THR:HA	1.87	0.55
2:D:18:LEU:HD12	2:D:304:ARG:NH1	2.21	0.55
2:F:37:PRO:HD2	2:F:40:TYR:CE1	2.41	0.55
2:H:353:ARG:O	2:H:357:LEU:HB2	2.05	0.55
2:J:290:ASN:ND2	2:J:293:LYS:HD2	2.22	0.55
1:E:148:LEU:HB2	1:E:179:LEU:HD21	1.87	0.55
1:G:189:ILE:HD11	1:G:205:HIS:CD2	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:90:ILE:HD13	2:H:40:TYR:O	2.07	0.55
1:C:78:VAL:HB	1:C:104:ARG:HB3	1.89	0.55
1:G:148:LEU:HB2	1:G:179:LEU:HD21	1.87	0.55
2:H:64:LEU:HD11	2:H:134:ILE:HG22	1.88	0.55
1:C:334:LEU:HD22	1:C:367:HIS:O	2.07	0.55
2:F:210:LEU:HB2	2:F:223:THR:HA	1.88	0.55
2:B:336:GLY:HA2	2:J:305:LEU:HD13	1.89	0.55
1:C:261:GLN:O	1:C:265:GLU:HG2	2.07	0.55
1:C:82:ASP:HB2	1:C:86:PRO:HB3	1.89	0.55
1:E:261:GLN:O	1:E:265:GLU:HG2	2.06	0.55
2:D:133:ILE:HD13	2:D:354:LEU:HD13	1.89	0.55
1:E:121:ARG:NH1	1:E:121:ARG:HG3	2.21	0.55
1:E:353:LYS:HE2	1:E:357:ARG:NH1	2.17	0.55
1:K:97:ARG:HG2	1:K:101:ASP:OD2	2.07	0.55
2:F:186:ASN:HB2	2:F:358:HIS:NE2	2.22	0.54
1:A:357:ARG:HH11	1:A:357:ARG:HG3	1.72	0.54
1:E:353:LYS:HE3	1:E:357:ARG:HH22	1.73	0.54
2:L:212:GLN:NE2	2:L:222:SER:HB3	2.21	0.54
2:H:349:ARG:O	2:H:352:GLU:HB2	2.07	0.54
1:A:334:LEU:HD22	1:A:367:HIS:O	2.07	0.54
2:H:348:THR:HA	2:H:351:SER:OG	2.07	0.54
1:K:334:LEU:HD22	1:K:367:HIS:O	2.07	0.54
1:E:339:GLU:O	1:E:343:ILE:HG13	2.08	0.54
2:F:232:LEU:HD13	2:F:343:ALA:HB1	1.89	0.54
1:A:303:GLN:O	1:A:307:SER:HB2	2.08	0.54
2:B:250:ARG:O	2:B:254:MET:HG2	2.07	0.54
1:I:198:LYS:HD3	2:J:266:LYS:HD3	1.89	0.54
1:G:91:ILE:HD12	2:H:38:GLU:HB2	1.89	0.54
1:I:195:GLN:NE2	8:I:1500:HOH:O	2.41	0.53
2:J:197:ILE:HD11	2:J:235:LYS:HD3	1.91	0.53
2:D:212:GLN:HE21	2:D:222:SER:CB	2.18	0.53
1:I:344:LEU:HD13	1:I:356:TRP:CE2	2.44	0.53
1:K:198:LYS:HD3	2:L:266:LYS:HD3	1.90	0.53
1:C:339:GLU:O	1:C:343:ILE:HG13	2.09	0.53
1:E:294:ASN:O	1:E:298:GLN:HG3	2.08	0.53
2:H:186:ASN:HB2	2:H:358:HIS:NE2	2.24	0.53
2:H:258:ASN:OD1	2:H:259:GLY:N	2.38	0.53
1:I:334:LEU:HD22	1:I:367:HIS:O	2.09	0.53
2:L:318:ASP:HB2	7:N:1727:GER:H71	1.90	0.53
1:G:328:ASP:O	1:G:329:ASN:HB2	2.09	0.53
1:K:311:LEU:HD23	1:K:311:LEU:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:328:ASP:O	1:C:329:ASN:HB2	2.09	0.52
1:I:339:GLU:O	1:I:343:ILE:HG13	2.08	0.52
3:N:609:VAL:N	7:N:1727:GER:H11	2.23	0.52
2:J:202:ARG:HD2	8:J:384:HOH:O	2.09	0.52
2:B:339:LYS:O	2:B:348:THR:HG23	2.10	0.52
1:A:148:LEU:HB2	1:A:179:LEU:HD21	1.92	0.52
2:B:24:ARG:HD3	2:B:27:ARG:HH22	1.74	0.52
2:B:229:SER:O	2:B:233:MET:HG3	2.09	0.52
2:B:353:ARG:HG2	2:B:353:ARG:NH1	2.22	0.52
2:H:130:SER:O	2:H:134:ILE:HG13	2.10	0.52
1:G:303:GLN:O	1:G:307:SER:HB2	2.10	0.52
1:I:67:ARG:HD2	8:I:927:HOH:O	2.09	0.52
1:G:79:PRO:HA	1:G:101:ASP:OD1	2.11	0.51
1:K:338:LEU:HD11	1:K:364:GLN:HG2	1.92	0.51
2:J:87:ARG:HH12	2:J:90:LEU:HD11	1.75	0.51
1:K:148:LEU:HB2	1:K:179:LEU:HD21	1.92	0.51
1:C:78:VAL:O	1:C:104:ARG:HD2	2.11	0.51
1:E:198:LYS:HD3	2:F:266:LYS:HD3	1.92	0.51
1:I:265:GLU:O	1:I:269:LEU:HD13	2.10	0.51
1:A:189:ILE:HD11	1:A:205:HIS:CD2	2.41	0.51
2:H:267:PRO:HG2	8:H:1609:HOH:O	2.10	0.51
1:I:328:ASP:O	1:I:329:ASN:HB2	2.10	0.51
1:K:311:LEU:HD23	1:K:311:LEU:C	2.30	0.51
1:I:106:VAL:HG11	1:I:116:ALA:HB1	1.93	0.51
2:J:105:PHE:CE2	2:J:107:PRO:HD3	2.46	0.51
2:J:77:TYR:CE1	2:J:141:ARG:HB2	2.45	0.51
3:M:509:VAL:N	7:M:1727:GER:H11	2.25	0.51
1:G:343:ILE:HG22	1:G:348:LYS:HG3	1.93	0.51
2:L:334:GLU:HB3	2:L:337:ILE:HD12	1.93	0.51
1:E:318:ILE:HG22	1:E:322:MET:CE	2.38	0.51
2:F:250:ARG:O	2:F:254:MET:HG2	2.11	0.51
2:J:63:SER:O	2:J:66:VAL:HG22	2.11	0.51
1:K:303:GLN:O	1:K:307:SER:HB2	2.11	0.51
1:G:344:LEU:HD13	1:G:356:TRP:CE2	2.45	0.51
1:I:151:GLU:HG3	1:I:175:LEU:HD11	1.93	0.51
2:B:77:TYR:CZ	2:B:141:ARG:HB2	2.46	0.50
1:A:58:LEU:HD23	1:A:63:TYR:CZ	2.46	0.50
1:I:311:LEU:C	1:I:311:LEU:HD23	2.32	0.50
1:E:214:ARG:O	1:E:214:ARG:HG3	2.12	0.50
1:I:78:VAL:O	1:I:104:ARG:HD2	2.11	0.50
1:K:96:PHE:CE1	1:K:126:LEU:HB3	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:329:ASN:HB3	1:G:332:ASP:HB3	1.94	0.50
1:C:69:ARG:HB3	1:C:71:GLU:OE1	2.12	0.50
2:D:232:LEU:HD13	2:D:343:ALA:HB1	1.92	0.50
2:L:212:GLN:HE21	2:L:212:GLN:HA	1.76	0.50
1:E:92:TYR:O	1:E:97:ARG:NH2	2.45	0.50
1:G:311:LEU:HD23	1:G:311:LEU:C	2.32	0.50
2:D:333:GLU:HA	8:D:740:HOH:O	2.11	0.49
2:F:207:ASP:O	2:F:208:ASN:HB2	2.11	0.49
2:D:333:GLU:O	1:K:357:ARG:NH2	2.45	0.49
2:B:130:SER:O	2:B:134:ILE:HG13	2.11	0.49
2:F:256:GLN:HB2	2:F:260:TYR:CE2	2.47	0.49
2:H:202:ARG:HG3	2:H:202:ARG:HH11	1.77	0.49
2:J:27:ARG:HH12	2:J:30:GLN:NE2	2.09	0.49
2:F:130:SER:O	2:F:134:ILE:HG13	2.12	0.49
1:A:312:ILE:HG23	1:A:340:LEU:HD22	1.95	0.49
1:A:214:ARG:CG	1:A:214:ARG:O	2.59	0.49
2:B:29:PHE:O	2:B:33:LEU:HD22	2.12	0.49
1:C:100:TYR:HB3	1:C:104:ARG:HH21	1.78	0.49
2:D:250:ARG:O	2:D:254:MET:HG2	2.13	0.49
2:F:38:GLU:O	2:F:38:GLU:HG2	2.13	0.49
2:J:334:GLU:HB3	2:J:337:ILE:HD12	1.93	0.49
1:G:135:HIS:CD2	2:H:166:GLU:HG2	2.48	0.49
2:B:207:ASP:O	2:B:208:ASN:HB2	2.13	0.49
2:L:333:GLU:HA	8:L:1050:HOH:O	2.13	0.49
2:B:22:ARG:HH11	2:B:22:ARG:HG2	1.77	0.49
2:D:186:ASN:HB2	2:D:358:HIS:CE1	2.48	0.49
1:K:189:ILE:HD11	1:K:205:HIS:CD2	2.45	0.49
1:C:106:VAL:HG11	1:C:116:ALA:HB1	1.94	0.49
1:G:65:LEU:HD12	1:G:67:ARG:HH11	1.77	0.49
2:L:256:GLN:HB2	2:L:260:TYR:CE2	2.48	0.49
2:B:105:PHE:CE2	2:B:107:PRO:HD3	2.47	0.48
1:I:100:TYR:O	1:I:104:ARG:HG3	2.12	0.48
1:A:325:ASN:O	1:A:326:GLN:C	2.52	0.48
1:G:97:ARG:HH11	1:G:97:ARG:HB3	1.78	0.48
1:E:67:ARG:NH2	1:E:94:GLU:OE1	2.43	0.48
1:E:303:GLN:O	1:E:307:SER:HB2	2.14	0.48
1:G:339:GLU:O	1:G:343:ILE:HG13	2.13	0.48
1:I:84:PRO:HG2	1:I:85:SER:H	1.79	0.48
2:F:212:GLN:HE21	2:F:222:SER:CB	2.08	0.48
2:H:256:GLN:HB2	2:H:260:TYR:CE2	2.49	0.48
1:A:156:ILE:HD11	1:A:172:ARG:HH22	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:22:ARG:O	2:H:26:VAL:HG23	2.14	0.48
1:I:303:GLN:O	1:I:307:SER:HB2	2.14	0.48
1:C:265:GLU:O	1:C:269:LEU:HD13	2.13	0.48
1:I:338:LEU:HD11	1:I:364:GLN:HG2	1.96	0.48
2:J:358:HIS:O	2:J:361:TRP:HB2	2.14	0.48
2:B:38:GLU:HG2	2:B:38:GLU:O	2.14	0.48
1:A:117:PHE:CE2	1:A:146:LYS:HE2	2.49	0.48
1:E:69:ARG:HB3	1:E:71:GLU:OE1	2.14	0.48
1:E:121:ARG:HH11	1:E:121:ARG:HG3	1.78	0.48
2:H:193:MET:HE2	2:H:233:MET:CG	2.44	0.48
1:E:296:LEU:HD22	1:E:322:MET:CE	2.44	0.47
1:G:219:GLU:OE1	1:G:219:GLU:HA	2.14	0.47
1:A:184:GLN:HB2	8:A:379:HOH:O	2.14	0.47
1:C:311:LEU:HD23	1:C:311:LEU:C	2.34	0.47
2:D:197:ILE:HD11	2:D:235:LYS:HD3	1.95	0.47
2:D:79:LEU:O	2:D:96:ARG:HG3	2.14	0.47
2:J:130:SER:O	2:J:134:ILE:HG13	2.14	0.47
2:L:105:PHE:CE2	2:L:107:PRO:HD3	2.49	0.47
2:L:110:ASN:HB3	2:L:111:PRO:HD2	1.96	0.47
1:E:96:PHE:CE1	1:E:126:LEU:HB3	2.49	0.47
1:I:184:GLN:HB2	8:I:378:HOH:O	2.15	0.47
1:I:189:ILE:HD11	1:I:205:HIS:CD2	2.47	0.47
2:J:229:SER:O	2:J:233:MET:HG3	2.14	0.47
2:B:256:GLN:HB2	2:B:260:TYR:CE2	2.50	0.47
1:C:173:ARG:NH1	8:C:412:HOH:O	2.46	0.47
1:G:265:GLU:O	1:G:269:LEU:HD13	2.14	0.47
1:E:106:VAL:HG11	1:E:116:ALA:HB1	1.96	0.47
1:E:58:LEU:HD23	1:E:63:TYR:CE2	2.50	0.47
2:H:311:LYS:HG3	2:H:312:TRP:CD2	2.49	0.47
2:J:258:ASN:OD1	2:J:259:GLY:N	2.42	0.47
1:G:117:PHE:CE2	1:G:146:LYS:HE2	2.49	0.47
2:J:69:LYS:O	2:J:73:ILE:HG13	2.13	0.47
1:K:249:GLY:HA3	8:K:640:HOH:O	2.14	0.47
1:C:312:ILE:HG23	1:C:340:LEU:HD22	1.97	0.47
2:F:311:LYS:HG3	2:F:312:TRP:CD2	2.50	0.47
1:G:156:ILE:HD11	1:G:172:ARG:HH22	1.80	0.47
2:D:37:PRO:CB	2:D:39:ARG:HH11	2.27	0.47
1:E:312:ILE:O	1:E:316:VAL:HG23	2.15	0.46
1:C:214:ARG:HG2	1:C:214:ARG:O	2.14	0.46
1:E:156:ILE:HD11	1:E:172:ARG:HH22	1.79	0.46
2:D:130:SER:O	2:D:134:ILE:HG13	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:250:ARG:O	2:H:254:MET:HG2	2.16	0.46
2:B:212:GLN:HE21	2:B:222:SER:CB	2.20	0.46
1:E:334:LEU:HD22	1:E:367:HIS:O	2.15	0.46
2:H:30:GLN:OE1	2:H:66:VAL:HB	2.16	0.46
1:I:65:LEU:O	1:I:69:ARG:HG3	2.15	0.46
2:L:53:PHE:HE1	7:N:1727:GER:H42	1.80	0.46
1:C:96:PHE:CE1	1:C:126:LEU:HB3	2.50	0.46
2:B:22:ARG:O	2:B:26:VAL:HG23	2.16	0.46
1:G:325:ASN:O	1:G:326:GLN:C	2.54	0.46
2:H:29:PHE:O	2:H:33:LEU:HD22	2.15	0.46
1:K:71:GLU:H	1:K:71:GLU:CD	2.18	0.46
1:C:189:ILE:HD11	1:C:205:HIS:CD2	2.44	0.46
2:D:311:LYS:HG3	2:D:312:TRP:CD2	2.50	0.46
1:G:106:VAL:HG11	1:G:116:ALA:HB1	1.97	0.46
2:L:133:ILE:CD1	2:L:354:LEU:HD13	2.42	0.46
2:B:357:LEU:HD22	2:B:361:TRP:CE2	2.51	0.46
2:D:138:ASP:OD1	2:D:140:SER:HB3	2.15	0.46
2:H:22:ARG:HG2	2:H:22:ARG:NH1	2.29	0.46
1:A:198:LYS:HD3	2:B:266:LYS:HD3	1.97	0.46
1:A:344:LEU:HD13	1:A:356:TRP:CE2	2.51	0.46
2:B:311:LYS:HG3	2:B:312:TRP:CD2	2.51	0.46
1:E:263:THR:HG21	1:E:280:LEU:HB2	1.98	0.46
2:H:193:MET:HE2	2:H:233:MET:CB	2.46	0.46
1:A:106:VAL:HG11	1:A:116:ALA:HB1	1.97	0.46
1:C:80:GLN:N	1:C:104:ARG:NH1	2.64	0.46
1:A:285:GLN:NE2	2:B:247:ARG:NH1	2.63	0.45
1:C:219:GLU:OE1	1:C:219:GLU:HA	2.16	0.45
1:K:106:VAL:HG11	1:K:116:ALA:HB1	1.98	0.45
2:B:37:PRO:HD2	2:B:40:TYR:CE1	2.51	0.45
1:G:96:PHE:CE1	1:G:126:LEU:HB3	2.51	0.45
1:I:263:THR:HG21	1:I:280:LEU:HB2	1.98	0.45
2:L:22:ARG:NH1	2:L:22:ARG:HG2	2.30	0.45
1:C:97:ARG:HG2	1:C:101:ASP:OD2	2.15	0.45
2:H:26:VAL:O	2:H:30:GLN:HG3	2.17	0.45
1:I:325:ASN:O	1:I:326:GLN:C	2.54	0.45
2:L:77:TYR:CZ	2:L:141:ARG:HB2	2.51	0.45
2:F:245:LEU:O	2:F:249:LYS:HG3	2.16	0.45
1:G:58:LEU:HD23	1:G:63:TYR:CZ	2.51	0.45
2:J:77:TYR:CZ	2:J:141:ARG:HB2	2.51	0.45
1:A:357:ARG:NH1	1:A:357:ARG:HG3	2.31	0.45
1:E:287:ARG:HG2	1:E:287:ARG:H	1.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:263:THR:HG21	1:A:280:LEU:HB2	1.98	0.45
2:J:311:LYS:HE2	2:J:312:TRP:CZ2	2.52	0.45
2:J:38:GLU:O	2:J:38:GLU:HG2	2.17	0.45
1:A:96:PHE:CE1	1:A:126:LEU:HB3	2.52	0.45
2:D:64:LEU:HD11	2:D:134:ILE:HG22	1.98	0.45
1:G:105:ALA:O	1:G:109:ARG:HG3	2.16	0.45
2:L:103:ILE:HG23	2:L:104:PRO:HD2	1.98	0.45
2:L:22:ARG:HH11	2:L:22:ARG:HG2	1.81	0.45
1:E:281:LYS:NZ	1:E:317:ASP:OD1	2.37	0.45
2:H:21:LEU:CD1	2:H:21:LEU:N	2.79	0.45
1:I:218:ASN:HB3	8:I:1242:HOH:O	2.16	0.45
2:B:311:LYS:HE2	2:B:312:TRP:CZ2	2.51	0.45
1:E:107:LEU:HD22	2:F:117:TYR:CD2	2.52	0.45
1:G:286:ASP:HB2	8:G:618:HOH:O	2.16	0.45
1:G:318:ILE:HG22	1:G:322:MET:CE	2.47	0.45
2:H:156:LEU:HD21	2:H:162:CYS:SG	2.57	0.45
1:K:325:ASN:O	1:K:326:GLN:C	2.55	0.45
1:A:91:ILE:HD11	2:B:38:GLU:H	1.81	0.45
1:E:91:ILE:HD12	2:F:38:GLU:HB2	1.99	0.45
1:A:71:GLU:O	1:A:115:ARG:NH1	2.50	0.44
2:B:103:ILE:HG23	2:B:104:PRO:HD2	1.99	0.44
1:I:105:ALA:O	1:I:109:ARG:HG3	2.17	0.44
1:A:58:LEU:HD23	1:A:63:TYR:CE2	2.52	0.44
1:A:198:LYS:CD	2:B:266:LYS:HD3	2.47	0.44
2:D:133:ILE:HG22	2:D:350:THR:HG23	1.98	0.44
2:J:256:GLN:HB2	2:J:260:TYR:CE2	2.52	0.44
1:C:344:LEU:HD13	1:C:356:TRP:CE2	2.52	0.44
2:D:19:ASP:OD2	2:D:19:ASP:N	2.44	0.44
1:E:189:ILE:HD11	1:E:205:HIS:CD2	2.44	0.44
1:E:328:ASP:O	1:E:329:ASN:HB2	2.18	0.44
1:C:263:THR:HG21	1:C:280:LEU:HB2	1.98	0.44
2:D:295:ARG:NH2	2:D:299:LEU:HD11	2.33	0.44
2:J:207:ASP:O	2:J:208:ASN:HB2	2.18	0.44
2:D:103:ILE:HG23	2:D:104:PRO:HD2	1.99	0.44
2:D:229:SER:O	2:D:233:MET:HG3	2.18	0.44
1:I:58:LEU:HD23	1:I:63:TYR:CZ	2.52	0.44
3:N:608:CYS:HA	7:N:1727:GER:C2	2.48	0.44
1:G:353:LYS:HG2	1:G:354:GLU:N	2.32	0.44
2:L:212:GLN:NE2	2:L:212:GLN:HA	2.33	0.44
3:M:508:CYS:HA	7:M:1727:GER:C2	2.48	0.44
1:A:334:LEU:O	1:A:338:LEU:HG	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:24:ARG:HG3	2:H:24:ARG:HH11	1.83	0.44
2:H:311:LYS:HE2	2:H:312:TRP:CZ2	2.52	0.44
2:J:116:PRO:HB2	2:J:117:TYR:CD2	2.53	0.44
1:G:107:LEU:HD22	2:H:117:TYR:CD2	2.53	0.44
2:H:360:SER:O	2:H:363:THR:HG23	2.18	0.44
2:H:77:TYR:CZ	2:H:141:ARG:HB2	2.53	0.44
2:L:207:ASP:O	2:L:208:ASN:HB2	2.18	0.44
2:B:116:PRO:HB2	2:B:117:TYR:CD2	2.53	0.43
1:C:207:GLN:OE1	2:D:216:LEU:HD13	2.18	0.43
2:D:295:ARG:NH1	2:D:299:LEU:CD1	2.81	0.43
2:H:24:ARG:HG3	2:H:24:ARG:NH1	2.32	0.43
1:K:92:TYR:O	1:K:97:ARG:NH2	2.52	0.43
1:K:79:PRO:HA	1:K:101:ASP:OD1	2.19	0.43
2:L:130:SER:O	2:L:134:ILE:HG13	2.18	0.43
1:G:263:THR:HG21	1:G:280:LEU:HB2	2.00	0.43
1:I:96:PHE:CE1	1:I:126:LEU:HB3	2.53	0.43
2:J:311:LYS:HG3	2:J:312:TRP:CD2	2.53	0.43
1:E:117:PHE:CE2	1:E:146:LYS:HE2	2.54	0.43
1:E:121:ARG:HH11	1:E:121:ARG:CG	2.32	0.43
2:F:29:PHE:O	2:F:33:LEU:HD22	2.19	0.43
2:F:333:GLU:HA	8:F:875:HOH:O	2.18	0.43
2:H:207:ASP:O	2:H:208:ASN:HB2	2.18	0.43
1:K:328:ASP:O	1:K:329:ASN:HB2	2.18	0.43
2:B:22:ARG:HG2	2:B:22:ARG:NH1	2.34	0.43
2:D:116:PRO:HB2	2:D:117:TYR:CD2	2.53	0.43
1:G:330:LYS:HE2	1:G:367:HIS:HB3	2.00	0.43
1:K:151:GLU:HG3	1:K:175:LEU:HD11	2.00	0.43
2:L:245:LEU:O	2:L:249:LYS:HG3	2.19	0.43
2:D:110:ASN:HB3	2:D:111:PRO:HD2	2.01	0.43
1:E:296:LEU:HD22	1:E:322:MET:HE1	2.00	0.43
2:F:21:LEU:N	2:F:21:LEU:CD1	2.82	0.43
2:F:30:GLN:O	2:F:34:GLN:HG3	2.19	0.43
1:K:223:VAL:HG11	1:K:240:ARG:HB2	2.01	0.43
2:L:311:LYS:HG3	2:L:312:TRP:CD2	2.54	0.43
1:A:340:LEU:HD23	1:A:343:ILE:HD12	2.01	0.43
2:B:64:LEU:HD11	2:B:134:ILE:HG22	2.01	0.43
1:G:72:TRP:CZ2	1:G:115:ARG:HB2	2.53	0.43
2:H:18:LEU:N	2:H:18:LEU:CD2	2.81	0.43
2:J:53:PHE:HE1	7:M:1727:GER:H42	1.84	0.43
2:L:250:ARG:O	2:L:254:MET:HG2	2.19	0.43
2:B:192:ASP:OD1	2:B:195:LYS:HE3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:103:ILE:HG23	2:F:104:PRO:HD2	2.00	0.43
2:H:193:MET:HG3	2:H:233:MET:HE1	2.01	0.43
1:K:339:GLU:O	1:K:343:ILE:HG13	2.19	0.43
2:L:122:ILE:HG22	2:L:163:ALA:HA	2.01	0.43
2:L:21:LEU:HG	8:L:632:HOH:O	2.19	0.43
1:C:361:ARG:HD3	8:C:1272:HOH:O	2.19	0.43
1:E:97:ARG:HG2	1:E:101:ASP:OD2	2.18	0.43
1:C:296:LEU:HD22	1:C:322:MET:CE	2.49	0.42
2:D:311:LYS:HE2	2:D:312:TRP:CZ2	2.54	0.42
2:D:77:TYR:CZ	2:D:141:ARG:HB2	2.54	0.42
1:E:325:ASN:O	1:E:326:GLN:C	2.56	0.42
2:F:116:PRO:HB2	2:F:117:TYR:CD2	2.54	0.42
1:G:267:ILE:HD13	1:G:277:TRP:CE2	2.54	0.42
1:C:286:ASP:HB2	8:C:621:HOH:O	2.18	0.42
2:D:86:ASP:N	2:D:86:ASP:OD2	2.48	0.42
1:E:329:ASN:HB3	1:E:332:ASP:HB3	2.00	0.42
2:H:354:LEU:HD11	2:H:358:HIS:NE2	2.34	0.42
2:J:36:LEU:HA	2:J:37:PRO:HD3	1.89	0.42
1:C:107:LEU:HD22	2:D:117:TYR:CD2	2.53	0.42
2:D:243:LYS:HE2	2:D:243:LYS:HB3	1.87	0.42
2:D:256:GLN:HB2	2:D:260:TYR:CE2	2.53	0.42
2:L:22:ARG:O	2:L:26:VAL:HG23	2.18	0.42
1:C:156:ILE:HD11	1:C:172:ARG:HH22	1.84	0.42
6:F:1723:GRG:HC62	6:F:1723:GRG:H101	1.91	0.42
1:K:329:ASN:HB3	1:K:332:ASP:HB3	2.02	0.42
1:A:267:ILE:HD13	1:A:277:TRP:CE2	2.55	0.42
1:A:348:LYS:HA	1:A:348:LYS:HD3	1.82	0.42
1:A:71:GLU:CD	1:A:71:GLU:H	2.17	0.42
1:G:318:ILE:HG22	1:G:322:MET:HE3	2.02	0.42
1:I:287:ARG:H	1:I:287:ARG:HG2	1.59	0.42
2:L:186:ASN:HB2	2:L:358:HIS:CE1	2.55	0.42
2:L:79:LEU:O	2:L:96:ARG:HG3	2.19	0.42
2:D:121:HIS:HB3	2:D:124:MET:HG2	2.02	0.42
2:D:20:PHE:CZ	2:D:337:ILE:HD11	2.55	0.42
2:F:121:HIS:HB3	2:F:124:MET:HG2	2.02	0.42
2:F:311:LYS:HE2	2:F:312:TRP:CZ2	2.54	0.42
2:B:21:LEU:CD1	2:B:21:LEU:N	2.83	0.42
2:F:353:ARG:NE	8:F:739:HOH:O	2.52	0.42
1:A:311:LEU:HD23	1:A:311:LEU:C	2.40	0.42
2:L:311:LYS:HE2	2:L:312:TRP:CZ2	2.55	0.42
1:A:359:ILE:HD13	1:A:359:ILE:HA	1.92	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:115:HIS:HA	2:F:116:PRO:HD3	1.91	0.42
2:H:63:SER:O	2:H:66:VAL:HG22	2.20	0.42
2:H:87:ARG:HB3	2:H:87:ARG:NH1	2.35	0.42
2:J:122:ILE:HG22	2:J:163:ALA:HA	2.01	0.42
2:F:77:TYR:CZ	2:F:141:ARG:HB2	2.54	0.41
2:J:59:ASP:OD2	2:J:349:ARG:NH1	2.53	0.41
2:D:37:PRO:HD2	2:D:40:TYR:CE1	2.55	0.41
1:E:219:GLU:HA	1:E:219:GLU:OE1	2.19	0.41
2:L:69:LYS:O	2:L:73:ILE:HG13	2.20	0.41
1:E:214:ARG:O	1:E:214:ARG:CG	2.68	0.41
2:J:138:ASP:O	2:J:139:LEU:HB2	2.20	0.41
1:K:82:ASP:HB2	1:K:86:PRO:HB3	2.03	0.41
2:F:37:PRO:HD2	2:F:40:TYR:HD1	1.85	0.41
1:G:287:ARG:HG2	1:G:287:ARG:H	1.54	0.41
2:B:37:PRO:HD2	2:B:40:TYR:CD1	2.55	0.41
2:B:77:TYR:CE1	2:B:141:ARG:HB2	2.55	0.41
1:C:325:ASN:O	1:C:326:GLN:C	2.59	0.41
1:E:311:LEU:HD23	1:E:311:LEU:C	2.41	0.41
2:J:155:GLN:HB2	2:J:161:PHE:CE2	2.56	0.41
2:J:246:ASN:ND2	8:J:395:HOH:O	2.54	0.41
2:D:26:VAL:O	2:D:30:GLN:HG3	2.21	0.41
2:D:353:ARG:NH1	2:D:357:LEU:HG	2.35	0.41
7:M:1727:GER:H112	7:M:1727:GER:H91	1.88	0.41
1:C:329:ASN:HB3	1:C:332:ASP:HB3	2.01	0.41
1:E:155:ILE:HD12	1:E:155:ILE:HA	1.94	0.41
1:I:136:PHE:CE2	1:I:140:LEU:HD11	2.55	0.41
1:I:344:LEU:HA	1:I:348:LYS:HB2	2.02	0.41
2:J:359:GLN:C	2:J:361:TRP:H	2.24	0.41
2:J:37:PRO:HD2	2:J:40:TYR:CE1	2.55	0.41
1:K:149:GLN:HG3	8:K:1048:HOH:O	2.20	0.41
2:L:116:PRO:HB2	2:L:117:TYR:CD2	2.56	0.41
1:A:92:TYR:O	1:A:97:ARG:NH2	2.54	0.41
1:C:100:TYR:HB3	1:C:104:ARG:NH2	2.36	0.41
2:H:49:THR:HG23	2:H:124:MET:SD	2.61	0.41
2:J:121:HIS:HB3	2:J:124:MET:HG2	2.03	0.41
2:L:37:PRO:HD2	2:L:40:TYR:CD1	2.56	0.41
1:E:353:LYS:CE	1:E:357:ARG:HH22	2.34	0.41
2:F:64:LEU:HD23	2:F:64:LEU:HA	1.84	0.41
2:H:30:GLN:O	2:H:34:GLN:HG3	2.21	0.41
2:H:352:GLU:HA	2:H:352:GLU:OE2	2.20	0.41
1:C:353:LYS:HE3	1:K:339:GLU:HG3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:138:ASP:O	2:B:139:LEU:HB2	2.20	0.41
2:D:37:PRO:HD2	2:D:40:TYR:CD1	2.55	0.41
1:G:189:ILE:HG21	1:G:206:ARG:HB2	2.03	0.41
2:H:133:ILE:HG22	2:H:350:THR:HG23	2.02	0.41
2:H:341:HIS:HA	2:H:342:PRO:HD2	1.81	0.41
2:J:250:ARG:O	2:J:254:MET:HG2	2.20	0.41
2:L:236:LEU:HD22	2:L:245:LEU:HD21	2.03	0.41
2:L:255:ARG:HD3	2:L:261:HIS:CD2	2.55	0.41
2:L:36:LEU:HA	2:L:37:PRO:HD3	1.93	0.41
2:L:40:TYR:CE2	7:N:1727:GER:H101	2.56	0.41
1:A:331:GLU:O	1:A:335:ASN:ND2	2.54	0.41
2:B:52:PHE:HA	2:B:131:CYS:SG	2.61	0.41
2:J:245:LEU:O	2:J:249:LYS:HG3	2.21	0.41
2:J:77:TYR:HE2	2:J:137:ASP:OD2	2.04	0.41
1:K:184:GLN:HB2	8:K:382:HOH:O	2.20	0.41
2:B:249:LYS:HB3	2:B:285:ILE:HD13	2.03	0.40
2:D:156:LEU:HD21	2:D:162:CYS:SG	2.61	0.40
1:G:207:GLN:OE1	2:H:216:LEU:HD13	2.21	0.40
1:C:287:ARG:H	1:C:287:ARG:HG2	1.64	0.40
2:D:258:ASN:OD1	2:D:259:GLY:N	2.42	0.40
1:K:287:ARG:HG2	1:K:287:ARG:H	1.63	0.40
2:L:49:THR:HG23	2:L:124:MET:SD	2.61	0.40
2:B:64:LEU:HB3	2:B:69:LYS:HE2	2.03	0.40
1:G:58:LEU:HD23	1:G:63:TYR:CE2	2.56	0.40
1:I:350:THR:O	1:I:353:LYS:HB3	2.21	0.40
2:J:133:ILE:CD1	2:J:354:LEU:HD13	2.49	0.40
2:L:64:LEU:HD23	2:L:64:LEU:HA	1.90	0.40
1:A:156:ILE:CD1	1:A:172:ARG:HH22	2.35	0.40
2:B:298:ILE:HD12	2:B:329:LEU:HD13	2.04	0.40
1:G:151:GLU:HG3	1:G:175:LEU:HD11	2.02	0.40
1:A:107:LEU:HD22	2:B:117:TYR:CD2	2.56	0.40
2:F:64:LEU:HD11	2:F:134:ILE:HG22	2.04	0.40
2:H:155:GLN:HB2	2:H:161:PHE:CE2	2.56	0.40
2:H:357:LEU:HD22	2:H:361:TRP:CZ2	2.56	0.40
2:H:86:ASP:N	2:H:86:ASP:OD2	2.50	0.40
1:I:124:ILE:HD13	1:I:134:TRP:CH2	2.57	0.40
2:J:30:GLN:HE21	2:J:30:GLN:HB3	1.65	0.40
2:J:37:PRO:HD2	2:J:40:TYR:CD1	2.57	0.40
2:J:64:LEU:HB3	2:J:69:LYS:HE2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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%)	23 (7%)	2 (1%)	25	37
1	C	312/377 (83%)	289 (93%)	22 (7%)	1 (0%)	41	56
1	E	312/377 (83%)	289 (93%)	21 (7%)	2 (1%)	25	37
1	G	312/377 (83%)	291 (93%)	19 (6%)	2 (1%)	25	37
1	I	312/377 (83%)	289 (93%)	21 (7%)	2 (1%)	25	37
1	K	312/377 (83%)	293 (94%)	17 (5%)	2 (1%)	25	37
2	B	344/377 (91%)	329 (96%)	14 (4%)	1 (0%)	41	56
2	D	344/377 (91%)	329 (96%)	13 (4%)	2 (1%)	25	37
2	F	344/377 (91%)	328 (95%)	15 (4%)	1 (0%)	41	56
2	H	344/377 (91%)	323 (94%)	19 (6%)	2 (1%)	25	37
2	J	344/377 (91%)	324 (94%)	19 (6%)	1 (0%)	41	56
2	L	344/377 (91%)	330 (96%)	13 (4%)	1 (0%)	41	56
3	M	2/11 (18%)	2 (100%)	0	0	100	100
3	N	2/11 (18%)	2 (100%)	0	0	100	100
All	All	3940/4546 (87%)	3705 (94%)	216 (6%)	19 (0%)	29	43

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	258	ASN
1	G	306	HIS
1	G	326	GLN
2	H	258	ASN
1	I	306	HIS
2	J	258	ASN
1	K	306	HIS
2	L	258	ASN
1	A	306	HIS

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Mol	Chain	Res	Type
1	A	326	GLN
2	D	258	ASN
2	F	258	ASN
1	I	326	GLN
1	K	326	GLN
1	C	306	HIS
2	D	333	GLU
1	E	306	HIS
2	H	333	GLU
1	E	326	GLN

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	280/338 (83%)	276 (99%)	4 (1%)	67	81
1	C	283/338 (84%)	275 (97%)	8 (3%)	43	61
1	E	284/338 (84%)	276 (97%)	8 (3%)	43	61
1	G	281/338 (83%)	277 (99%)	4 (1%)	67	81
1	I	287/338 (85%)	279 (97%)	8 (3%)	43	61
1	K	291/338 (86%)	286 (98%)	5 (2%)	60	77
2	B	289/326 (89%)	275 (95%)	14 (5%)	25	39
2	D	293/326 (90%)	278 (95%)	15 (5%)	24	37
2	F	294/326 (90%)	281 (96%)	13 (4%)	28	43
2	H	288/326 (88%)	272 (94%)	16 (6%)	21	33
2	J	292/326 (90%)	276 (94%)	16 (6%)	21	33
2	L	296/326 (91%)	281 (95%)	15 (5%)	24	37
3	M	4/11 (36%)	4 (100%)	0	100	100
3	N	4/11 (36%)	4 (100%)	0	100	100
All	All	3466/4006 (86%)	3340 (96%)	126 (4%)	35	51

All (126) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	PHE
1	A	71	GLU
1	A	214	ARG
1	A	287	ARG
2	B	39	ARG
2	B	113	THR
2	B	151	LEU
2	B	216	LEU
2	B	222	SER
2	B	232	LEU
2	B	236	LEU
2	B	255	ARG
2	B	258	ASN
2	B	261	HIS
2	B	306	VAL
2	B	329	LEU
2	B	331	LEU
2	B	357	LEU
1	C	55	PHE
1	C	59	ASP
1	C	71	GLU
1	C	81	ASN
1	C	182	PRO
1	C	287	ARG
1	C	324	GLU
1	C	364	GLN
2	D	21	LEU
2	D	39	ARG
2	D	110	ASN
2	D	151	LEU
2	D	216	LEU
2	D	222	SER
2	D	232	LEU
2	D	236	LEU
2	D	255	ARG
2	D	258	ASN
2	D	261	HIS
2	D	306	VAL
2	D	329	LEU
2	D	331	LEU
2	D	353	ARG
1	E	55	PHE

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Mol	Chain	Res	Type
1	E	67	ARG
1	E	71	GLU
1	E	121	ARG
1	E	211	GLN
1	E	214	ARG
1	E	287	ARG
1	E	324	GLU
2	F	21	LEU
2	F	39	ARG
2	F	151	LEU
2	F	216	LEU
2	F	232	LEU
2	F	236	LEU
2	F	255	ARG
2	F	258	ASN
2	F	261	HIS
2	F	306	VAL
2	F	329	LEU
2	F	331	LEU
2	F	353	ARG
1	G	71	GLU
1	G	224	ASP
1	G	287	ARG
1	G	324	GLU
2	H	18	LEU
2	H	21	LEU
2	H	91	ASP
2	H	151	LEU
2	H	216	LEU
2	H	222	SER
2	H	232	LEU
2	H	236	LEU
2	H	255	ARG
2	H	258	ASN
2	H	261	HIS
2	H	306	VAL
2	H	329	LEU
2	H	331	LEU
2	H	348	THR
2	H	357	LEU
1	I	55	PHE
1	I	67	ARG

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Mol	Chain	Res	Type
1	I	71	GLU
1	I	142	ARG
1	I	194	ASN
1	I	211	GLN
1	I	287	ARG
1	I	364	GLN
2	J	21	LEU
2	J	27	ARG
2	J	31	ARG
2	J	151	LEU
2	J	216	LEU
2	J	222	SER
2	J	232	LEU
2	J	236	LEU
2	J	255	ARG
2	J	258	ASN
2	J	261	HIS
2	J	306	VAL
2	J	329	LEU
2	J	331	LEU
2	J	353	ARG
2	J	357	LEU
1	K	55	PHE
1	K	71	GLU
1	K	142	ARG
1	K	287	ARG
1	K	324	GLU
2	L	21	LEU
2	L	33	LEU
2	L	65	ASP
2	L	110	ASN
2	L	151	LEU
2	L	216	LEU
2	L	232	LEU
2	L	236	LEU
2	L	255	ARG
2	L	258	ASN
2	L	261	HIS
2	L	306	VAL
2	L	329	LEU
2	L	331	LEU
2	L	353	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	89	GLN
1	A	201	HIS
1	A	278	ASN
1	A	329	ASN
1	A	335	ASN
2	B	212	GLN
1	C	108	GLN
1	C	184	GLN
1	C	218	ASN
1	C	298	GLN
1	C	335	ASN
1	C	364	GLN
2	D	212	GLN
2	D	246	ASN
1	E	184	GLN
1	E	201	HIS
1	E	298	GLN
2	F	212	GLN
2	F	246	ASN
1	G	80	GLN
1	G	89	GLN
1	G	162	GLN
1	G	201	HIS
1	G	297	ASN
1	G	325	ASN
2	H	212	GLN
2	H	296	ASN
1	I	89	GLN
1	I	135	HIS
1	I	285	GLN
1	I	364	GLN
2	J	30	GLN
2	J	208	ASN
2	J	212	GLN
2	J	246	ASN
1	K	135	HIS
1	K	218	ASN
1	K	298	GLN
2	L	212	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 23 ligands modelled in this entry, 15 are monoatomic - leaving 8 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$
6	GRG	B	1721	-	26,28,28	0.75	0	33,37,37	0.83	1 (3%)
6	GRG	L	1726	-	26,28,28	0.72	0	33,37,37	0.82	1 (3%)
6	GRG	J	1725	-	26,28,28	0.74	0	33,37,37	0.80	1 (3%)
7	GER	N	1727	-	19,19,19	0.87	0	22,22,22	0.68	0
7	GER	M	1727	-	19,19,19	0.84	0	22,22,22	0.66	0
6	GRG	F	1723	-	26,28,28	0.75	0	33,37,37	0.79	1 (3%)
6	GRG	H	1724	-	26,28,28	0.72	0	33,37,37	0.83	1 (3%)
6	GRG	D	1722	-	26,28,28	0.79	0	33,37,37	0.81	1 (3%)

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
6	GRG	B	1721	-	-	8/31/31/31	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	GRG	L	1726	-	-	6/31/31/31	-
6	GRG	J	1725	-	-	8/31/31/31	-
7	GER	N	1727	-	-	9/20/20/20	-
7	GER	M	1727	-	-	9/20/20/20	-
6	GRG	F	1723	-	-	6/31/31/31	-
6	GRG	H	1724	-	-	9/31/31/31	-
6	GRG	D	1722	-	-	7/31/31/31	-

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	L	1726	GRG	O1B-PB-O3A	2.61	113.40	104.64
6	B	1721	GRG	O1B-PB-O3A	2.58	113.30	104.64
6	H	1724	GRG	O1B-PB-O3A	2.56	113.24	104.64
6	D	1722	GRG	O1B-PB-O3A	2.53	113.12	104.64
6	J	1725	GRG	O1B-PB-O3A	2.45	112.86	104.64
6	F	1723	GRG	O1B-PB-O3A	2.38	112.61	104.64

There are no chirality outliers.

All (62) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	L	1726	GRG	PA-O3A-PB-O1B
6	H	1724	GRG	PA-O3A-PB-O1B
6	B	1721	GRG	PA-O3A-PB-O1B
6	D	1722	GRG	PA-O3A-PB-O1B
6	J	1725	GRG	PA-O3A-PB-O1B
6	F	1723	GRG	PA-O3A-PB-O1B
7	M	1727	GER	C11-C10-C8-C9
7	N	1727	GER	C11-C10-C8-C9
7	M	1727	GER	C11-C10-C8-C7
7	N	1727	GER	C11-C10-C8-C7
7	M	1727	GER	C4-C3-C5-C6
7	M	1727	GER	C14-C13-C15-C16
7	N	1727	GER	C14-C13-C15-C16
7	M	1727	GER	C12-C13-C15-C16
7	N	1727	GER	C12-C13-C15-C16
7	N	1727	GER	C4-C3-C5-C6

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Mol	Chain	Res	Type	Atoms
7	M	1727	GER	C13-C15-C16-C17
7	M	1727	GER	C2-C3-C5-C6
7	N	1727	GER	C13-C15-C16-C17
7	N	1727	GER	C2-C3-C5-C6
6	L	1726	GRG	C14-C13-C15-C16
6	J	1725	GRG	C14-C13-C15-C16
6	F	1723	GRG	C14-C13-C15-C16
6	F	1723	GRG	C10-C8-C9-C11
6	H	1724	GRG	C14-C13-C15-C16
6	B	1721	GRG	C14-C13-C15-C16
6	D	1722	GRG	C14-C13-C15-C16
6	L	1726	GRG	C10-C8-C9-C11
6	H	1724	GRG	C10-C8-C9-C11
6	B	1721	GRG	C10-C8-C9-C11
6	D	1722	GRG	C10-C8-C9-C11
6	J	1725	GRG	C10-C8-C9-C11
6	L	1726	GRG	PA-O3A-PB-O3B
6	H	1724	GRG	PA-O3A-PB-O3B
6	B	1721	GRG	PA-O3A-PB-O3B
6	J	1725	GRG	PA-O3A-PB-O3B
6	L	1726	GRG	PA-O3A-PB-O2B
6	H	1724	GRG	PA-O3A-PB-O2B
6	B	1721	GRG	PA-O3A-PB-O2B
6	D	1722	GRG	PA-O3A-PB-O2B
6	J	1725	GRG	PA-O3A-PB-O2B
6	F	1723	GRG	PA-O3A-PB-O2B
6	H	1724	GRG	C12-C13-C15-C16
6	L	1726	GRG	C9-C11-C12-C13
6	H	1724	GRG	C9-C11-C12-C13
7	M	1727	GER	C10-C11-C12-C13
7	M	1727	GER	C15-C16-C17-C18
6	B	1721	GRG	C9-C11-C12-C13
7	N	1727	GER	C10-C11-C12-C13
7	N	1727	GER	C15-C16-C17-C18
6	D	1722	GRG	C9-C11-C12-C13
6	J	1725	GRG	C9-C11-C12-C13
6	F	1723	GRG	C9-C11-C12-C13
6	B	1721	GRG	C12-C13-C15-C16
6	D	1722	GRG	C12-C13-C15-C16
6	H	1724	GRG	C4-C3-C5-C6
6	J	1725	GRG	C12-C13-C15-C16
6	F	1723	GRG	C12-C13-C15-C16

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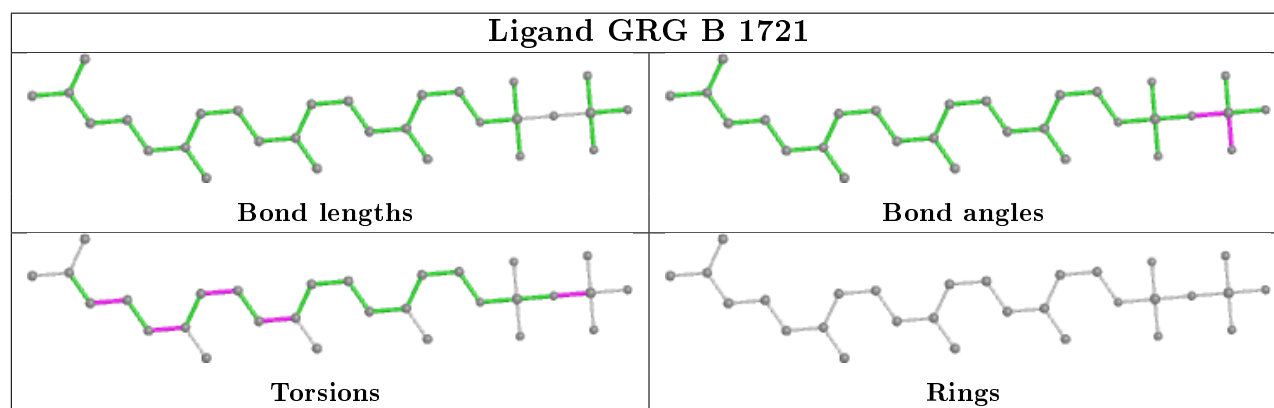
Mol	Chain	Res	Type	Atoms
6	H	1724	GRG	C15-C16-C17-C18
6	B	1721	GRG	C15-C16-C17-C18
6	D	1722	GRG	C15-C16-C17-C18
6	J	1725	GRG	C15-C16-C17-C18

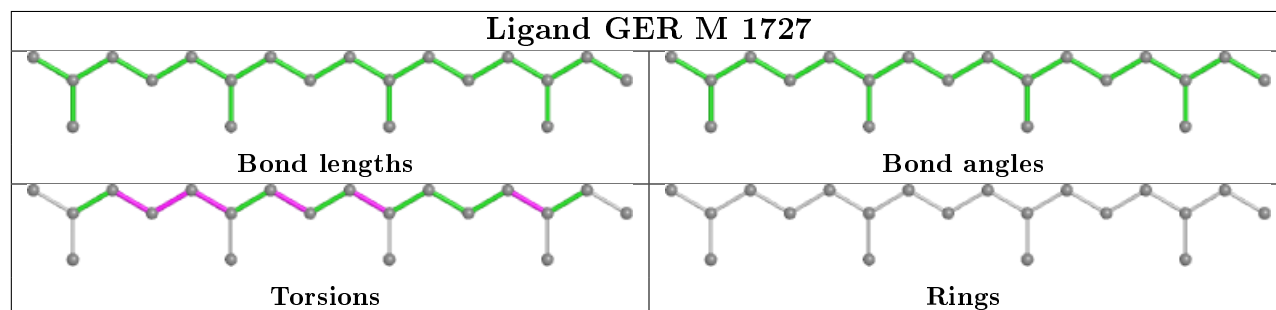
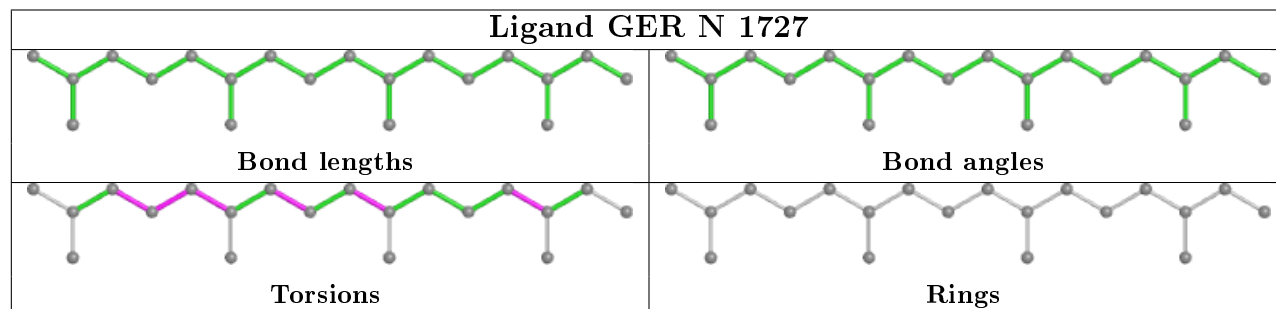
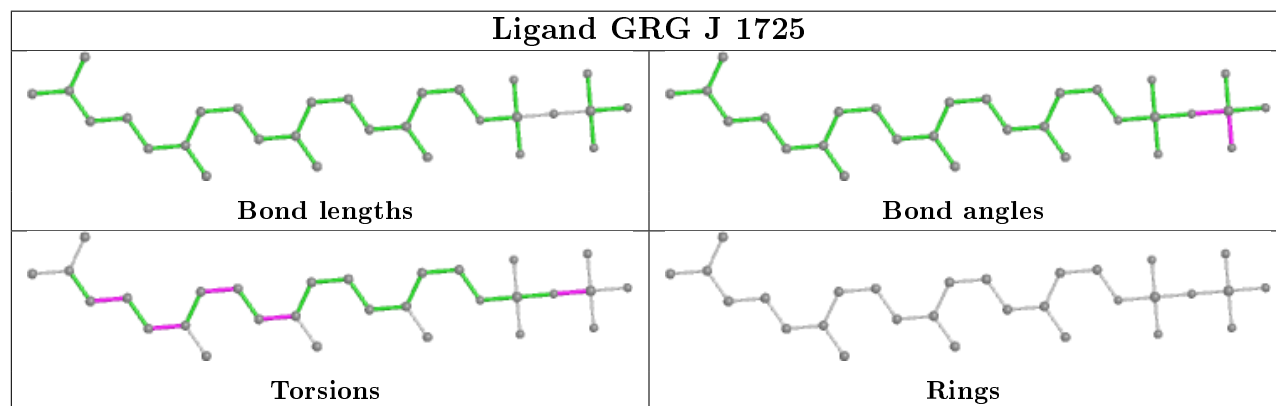
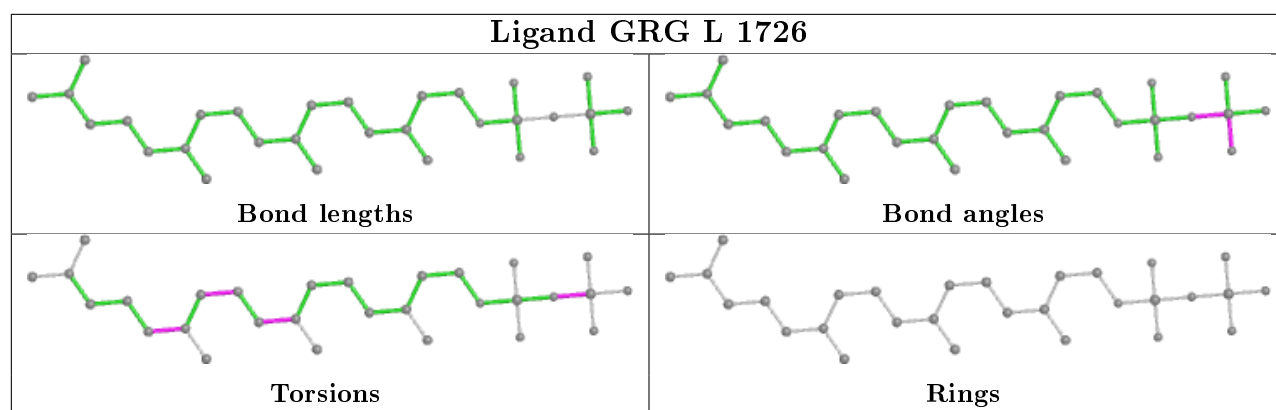
There are no ring outliers.

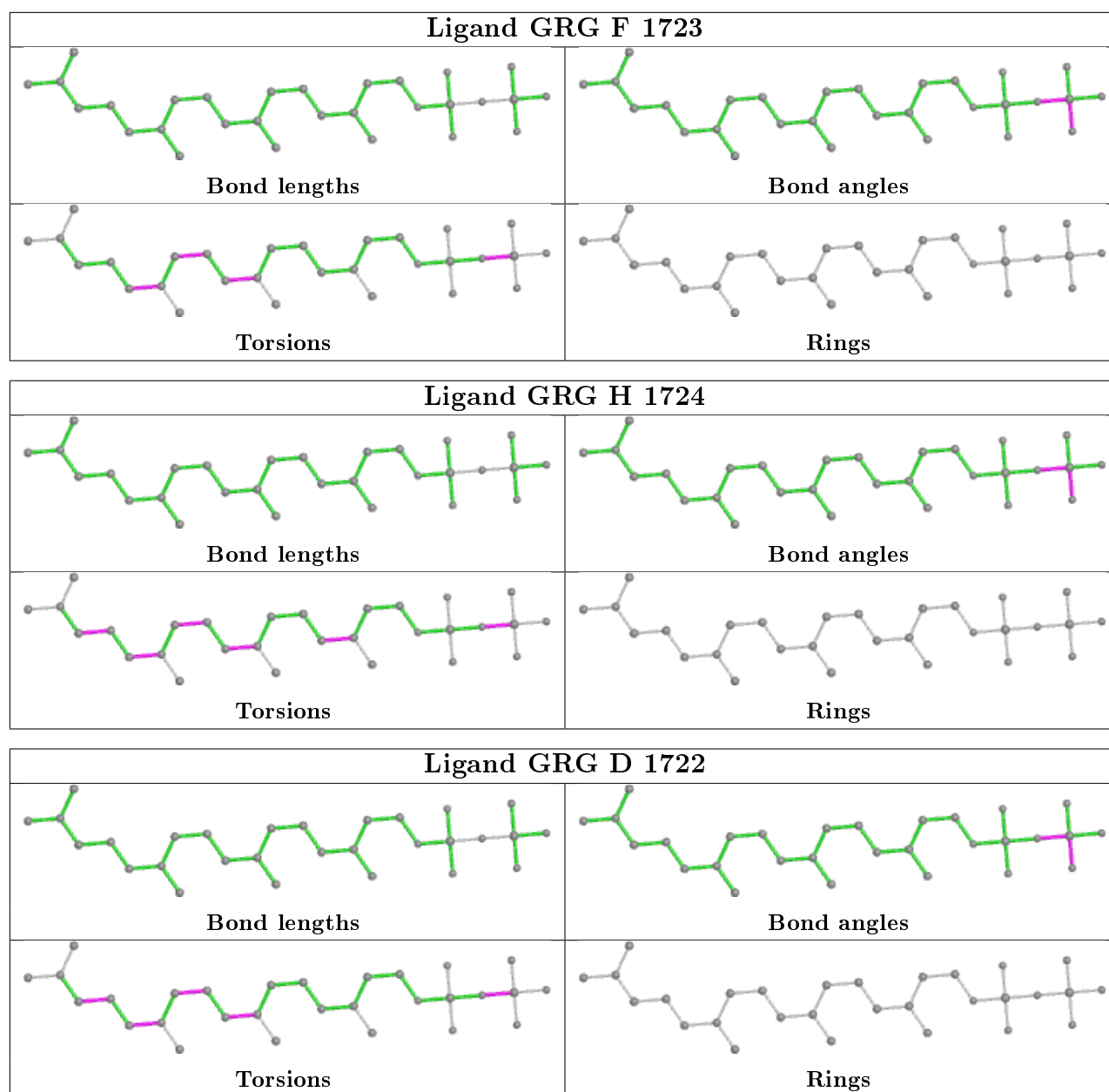
8 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	1721	GRG	1	0
6	L	1726	GRG	1	0
6	J	1725	GRG	1	0
7	N	1727	GER	5	0
7	M	1727	GER	5	0
6	F	1723	GRG	2	0
6	H	1724	GRG	1	0
6	D	1722	GRG	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%)	0.02	15 (4%)	30	27	35, 57, 92, 110	0
1	C	314/377 (83%)	-0.05	10 (3%)	47	44	33, 54, 80, 97	0
1	E	314/377 (83%)	0.16	14 (4%)	33	30	35, 59, 86, 103	0
1	G	314/377 (83%)	0.13	11 (3%)	44	40	35, 59, 87, 102	0
1	I	314/377 (83%)	-0.03	11 (3%)	44	40	29, 52, 84, 95	0
1	K	314/377 (83%)	-0.23	6 (1%)	66	63	23, 41, 67, 81	0
2	B	346/377 (91%)	-0.01	17 (4%)	29	26	35, 52, 75, 100	0
2	D	346/377 (91%)	0.01	15 (4%)	35	31	32, 46, 71, 95	0
2	F	346/377 (91%)	0.00	16 (4%)	32	29	34, 47, 74, 101	0
2	H	346/377 (91%)	0.41	32 (9%)	9	7	36, 65, 95, 112	0
2	J	346/377 (91%)	0.09	16 (4%)	32	29	30, 50, 80, 104	0
2	L	346/377 (91%)	-0.05	9 (2%)	56	52	25, 40, 65, 93	0
3	M	4/11 (36%)	2.72	3 (75%)	0	0	60, 65, 73, 79	4 (100%)
3	N	4/11 (36%)	2.34	2 (50%)	0	0	59, 65, 74, 80	4 (100%)
All	All	3968/4546 (87%)	0.04	177 (4%)	33	30	23, 52, 84, 112	8 (0%)

All (177) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	306	HIS	6.0
1	G	306	HIS	5.4
1	G	305	SER	5.3
2	D	363	THR	5.1
2	H	363	THR	5.1
1	C	304	PRO	4.7
2	B	363	THR	4.7
2	J	108	SER	4.7

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Mol	Chain	Res	Type	RSRZ
1	G	304	PRO	4.7
2	F	112	GLY	4.6
2	H	112	GLY	4.6
1	E	306	HIS	4.6
1	E	91	ILE	4.6
1	G	55	PHE	4.5
2	H	361	TRP	4.5
2	H	65	ASP	4.3
2	H	304	ARG	4.2
1	C	305	SER	4.2
1	A	304	PRO	4.2
2	J	111	PRO	4.1
2	H	111	PRO	4.0
2	F	113	THR	4.0
2	J	86	ASP	3.9
3	M	508	CYS	3.8
2	F	363	THR	3.8
1	I	328	ASP	3.8
2	H	86	ASP	3.7
2	J	84	THR	3.7
2	H	360	SER	3.7
1	I	306	HIS	3.7
2	H	38	GLU	3.7
2	F	88	SER	3.6
1	E	304	PRO	3.6
1	A	306	HIS	3.6
2	L	363	THR	3.6
2	B	113	THR	3.5
2	D	110	ASN	3.5
2	H	108	SER	3.5
1	I	305	SER	3.4
2	H	88	SER	3.4
2	D	111	PRO	3.4
2	B	86	ASP	3.4
2	H	362	LYS	3.4
2	L	113	THR	3.3
1	K	306	HIS	3.3
1	A	328	ASP	3.3
2	L	86	ASP	3.2
2	B	37	PRO	3.2
1	A	91	ILE	3.2
1	E	368	SER	3.2

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Mol	Chain	Res	Type	RSRZ
2	H	314	ASP	3.1
2	H	305	LEU	3.1
2	B	362	LYS	3.1
2	J	363	THR	3.1
1	G	91	ILE	3.1
2	J	112	GLY	3.1
3	M	510	ILE	3.0
1	I	368	SER	3.0
2	D	362	LYS	3.0
1	E	328	ASP	3.0
2	L	111	PRO	3.0
1	I	304	PRO	3.0
1	K	305	SER	3.0
2	B	111	PRO	3.0
2	F	37	PRO	3.0
1	E	305	SER	2.9
1	E	314	PHE	2.9
2	L	84	THR	2.9
1	A	329	ASN	2.9
1	G	329	ASN	2.9
2	J	110	ASN	2.9
2	B	110	ASN	2.9
1	E	331	GLU	2.9
3	N	609	VAL	2.9
1	E	326	GLN	2.8
2	F	111	PRO	2.9
2	H	84	THR	2.8
2	H	40	TYR	2.8
1	C	55	PHE	2.8
2	H	71	ASP	2.8
1	C	329	ASN	2.8
1	G	330	LYS	2.8
2	J	85	GLU	2.8
2	H	87	ARG	2.8
3	M	511	LEU	2.8
2	L	110	ASN	2.8
1	E	55	PHE	2.7
2	J	360	SER	2.7
1	G	326	GLN	2.7
2	J	88	SER	2.7
2	H	37	PRO	2.7
2	H	316	HIS	2.7

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Mol	Chain	Res	Type	RSRZ
3	N	608	CYS	2.6
1	I	83	GLY	2.6
1	I	329	ASN	2.6
2	D	65	ASP	2.6
2	B	84	THR	2.6
2	F	84	THR	2.6
2	H	110	ASN	2.6
2	H	35	VAL	2.6
2	L	108	SER	2.6
1	I	84	PRO	2.6
1	E	313	ALA	2.6
2	F	86	ASP	2.6
2	H	85	GLU	2.6
1	C	327	CYS	2.5
2	F	39	ARG	2.5
1	C	330	LYS	2.5
1	A	301	ASP	2.5
2	D	305	LEU	2.5
2	B	360	SER	2.5
2	H	127	THR	2.5
2	B	114	ALA	2.5
2	J	237	GLU	2.5
2	F	362	LYS	2.5
1	E	365	SER	2.5
1	G	92	TYR	2.5
1	A	326	GLN	2.4
1	A	305	SER	2.4
1	I	326	GLN	2.4
1	A	330	LYS	2.4
1	A	331	GLU	2.4
2	D	113	THR	2.4
1	C	331	GLU	2.4
2	J	109	LYS	2.4
2	H	114	ALA	2.3
1	E	330	LYS	2.3
2	D	314	ASP	2.3
2	F	314	ASP	2.3
2	D	37	PRO	2.3
2	D	86	ASP	2.3
2	H	356	ASP	2.3
2	L	85	GLU	2.3
1	A	342	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	314	PHE	2.3
1	K	304	PRO	2.3
2	B	87	ARG	2.3
1	A	368	SER	2.2
2	D	360	SER	2.2
1	A	367	HIS	2.2
1	C	347	GLU	2.2
1	G	327	CYS	2.2
1	K	85	SER	2.2
2	F	305	LEU	2.2
2	B	112	GLY	2.2
2	J	107	PRO	2.2
2	H	237	GLU	2.2
2	H	359	GLN	2.2
2	F	109	LYS	2.2
1	I	85	SER	2.2
2	B	85	GLU	2.2
2	H	109	LYS	2.2
2	L	314	ASP	2.2
1	G	368	SER	2.2
2	B	109	LYS	2.2
2	F	114	ALA	2.2
2	B	316	HIS	2.2
2	D	39	ARG	2.1
2	H	157	GLU	2.1
2	B	65	ASP	2.1
2	J	127	THR	2.1
2	J	362	LYS	2.1
1	E	329	ASN	2.1
1	A	325	ASN	2.1
2	H	358	HIS	2.1
1	I	327	CYS	2.1
1	K	84	PRO	2.1
2	B	39	ARG	2.1
2	D	127	THR	2.1
2	F	355	ARG	2.1
2	D	361	TRP	2.1
1	C	334	LEU	2.0
1	K	326	GLN	2.0
2	H	312	TRP	2.0
2	J	359	GLN	2.0
2	F	316	HIS	2.0

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Mol	Chain	Res	Type	RSRZ
2	D	356	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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.

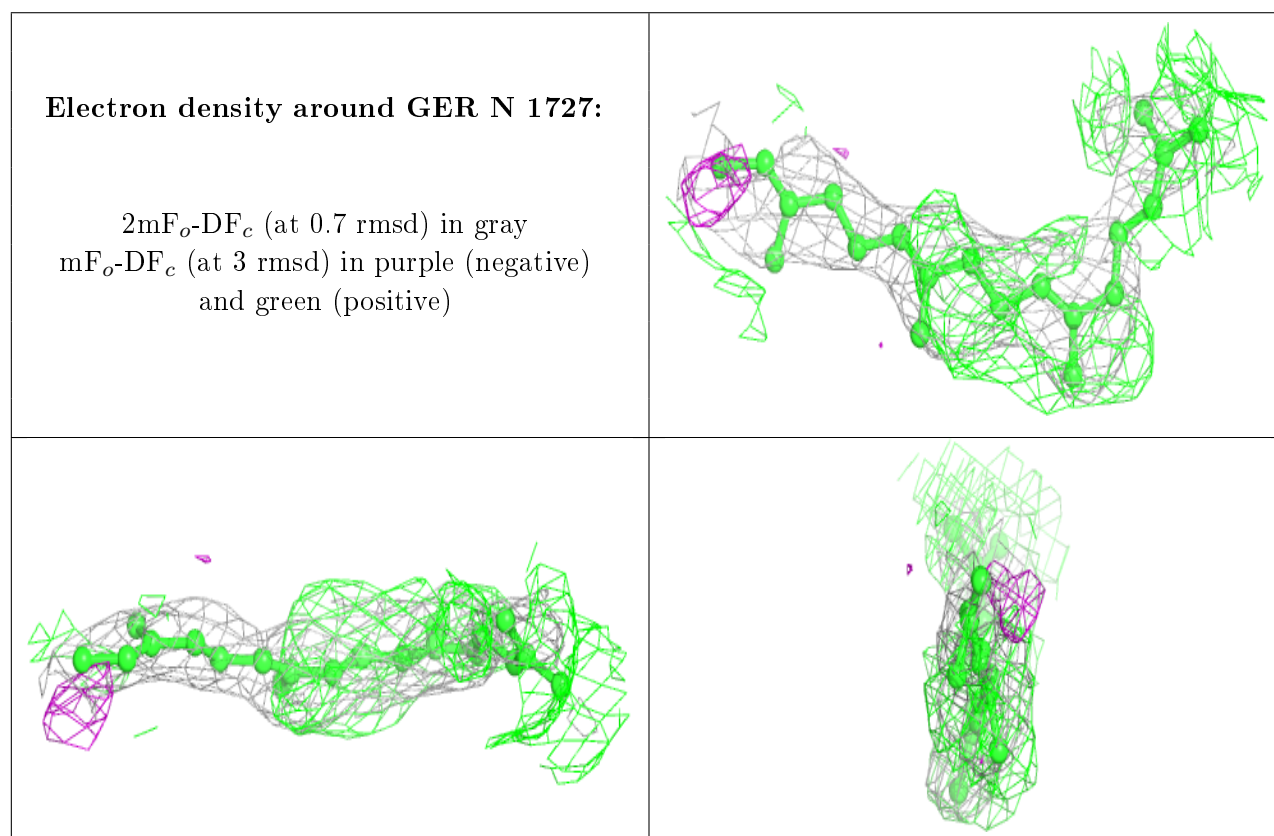
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
7	GER	N	1727	20/20	0.79	0.37	63,70,82,82	20
7	GER	M	1727	20/20	0.82	0.33	67,74,81,82	20
6	GRG	L	1726	29/29	0.95	0.23	37,42,53,58	0
6	GRG	H	1724	29/29	0.95	0.18	52,57,72,73	0
6	GRG	D	1722	29/29	0.95	0.17	42,48,55,57	0
6	GRG	B	1721	29/29	0.96	0.18	48,53,59,60	0
6	GRG	J	1725	29/29	0.96	0.21	38,44,55,58	0
6	GRG	F	1723	29/29	0.96	0.17	47,52,59,59	0
5	CL	G	1711	1/1	0.97	0.19	55,55,55,55	0
5	CL	B	1702	1/1	0.97	0.07	64,64,64,64	0
5	CL	J	1715	1/1	0.97	0.07	58,58,58,58	0
5	CL	C	1705	1/1	0.97	0.25	55,55,55,55	0
5	CL	H	1712	1/1	0.97	0.06	58,58,58,58	0
4	ZN	H	378	1/1	0.98	0.10	54,54,54,54	0
5	CL	D	1706	1/1	0.98	0.07	41,41,41,41	0
5	CL	K	1717	1/1	0.98	0.09	55,55,55,55	0
5	CL	L	1718	1/1	0.99	0.06	43,43,43,43	0
4	ZN	J	378	1/1	0.99	0.10	35,35,35,35	0
5	CL	F	1709	1/1	0.99	0.11	46,46,46,46	0
4	ZN	F	378	1/1	1.00	0.08	40,40,40,40	0
4	ZN	L	378	1/1	1.00	0.09	27,27,27,27	0
4	ZN	D	378	1/1	1.00	0.09	37,37,37,37	0

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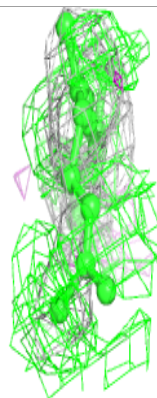
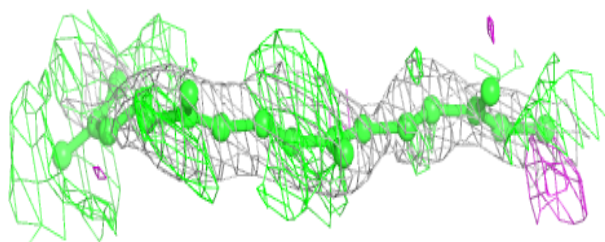
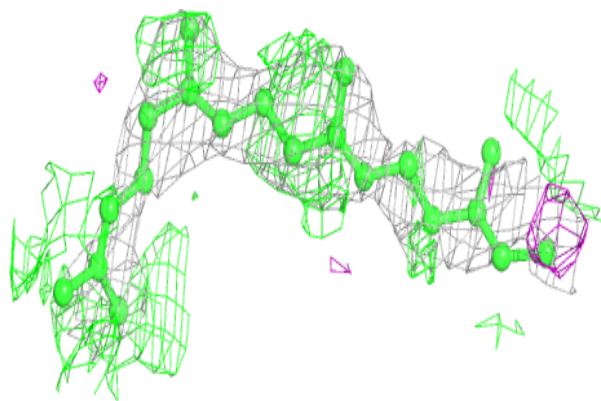
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	ZN	B	378	1/1	1.00	0.10	38,38,38,38	0

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.

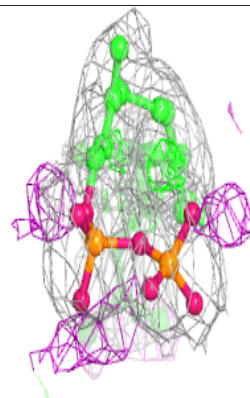
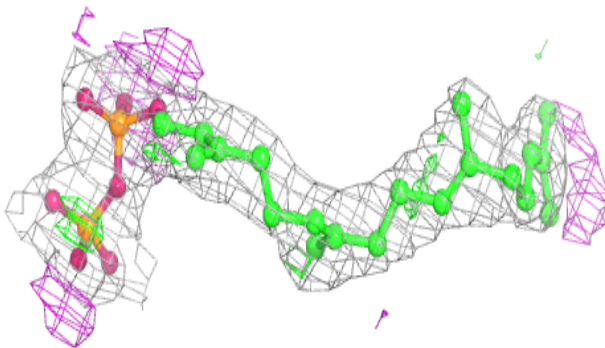
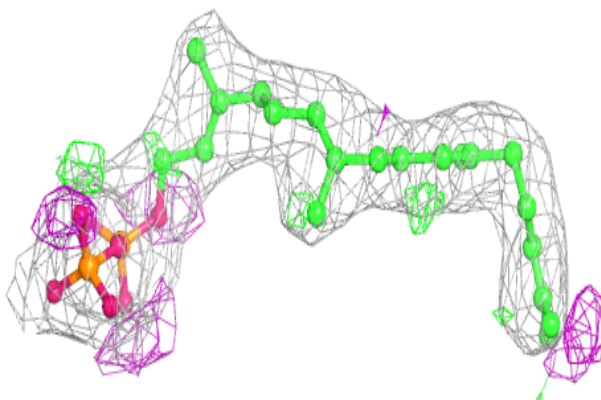


Electron density around GER M 1727:

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

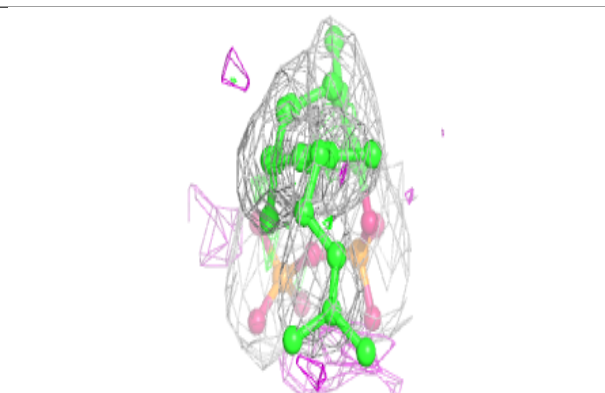
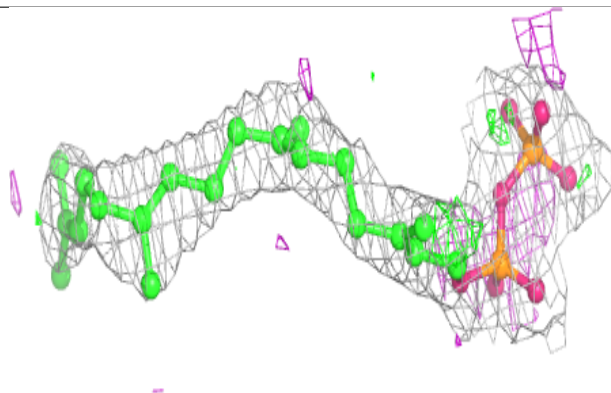
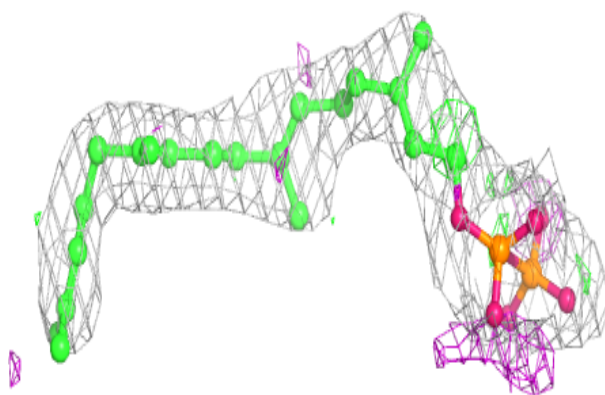
**Electron density around GRG L 1726:**

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

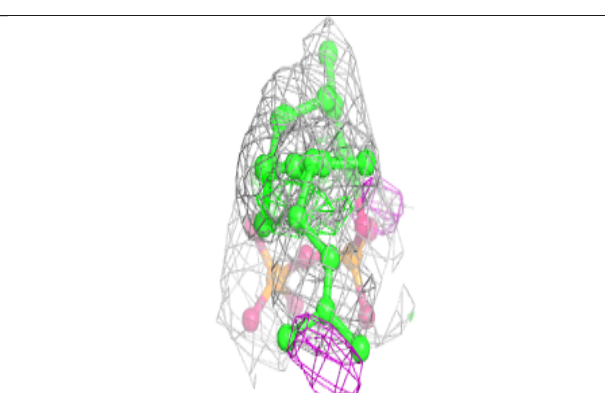
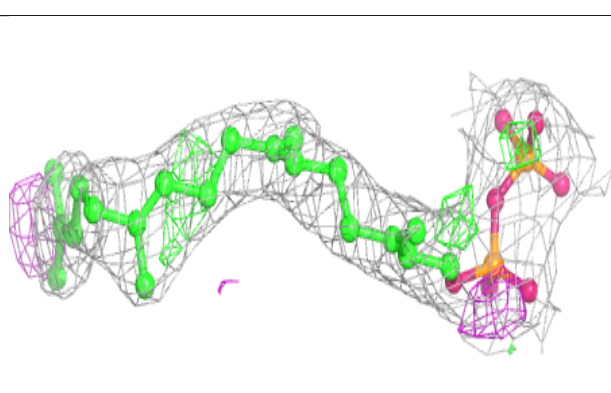
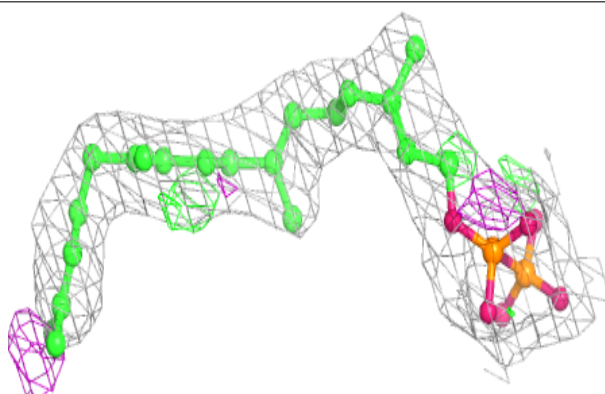


Electron density around GRG H 1724:

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

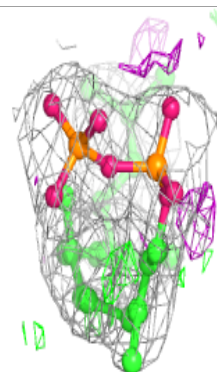
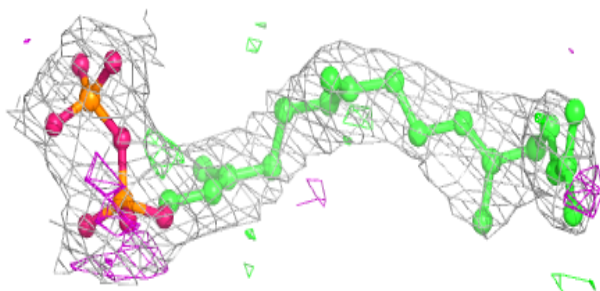
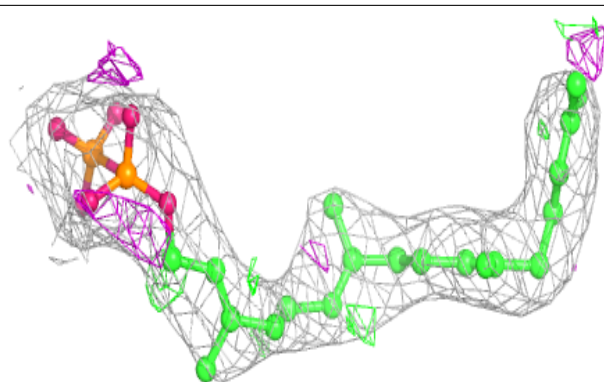
**Electron density around GRG D 1722:**

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

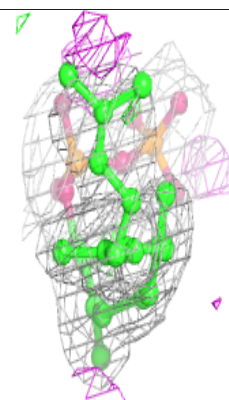
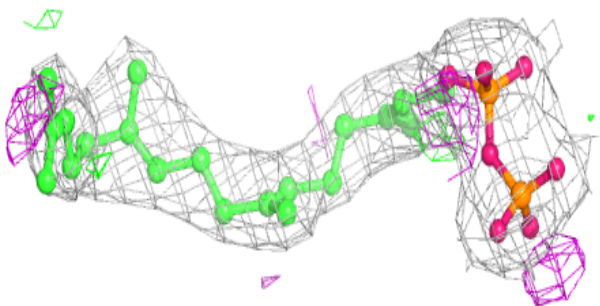
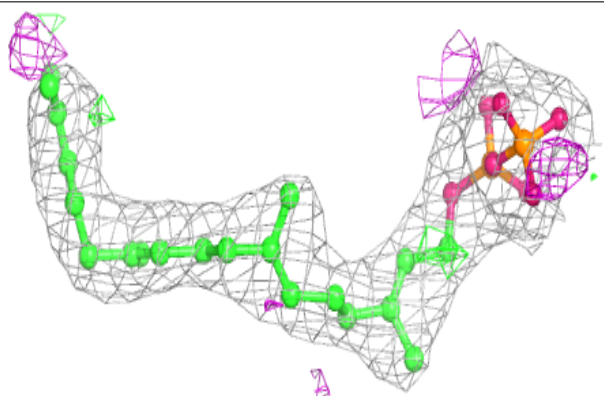


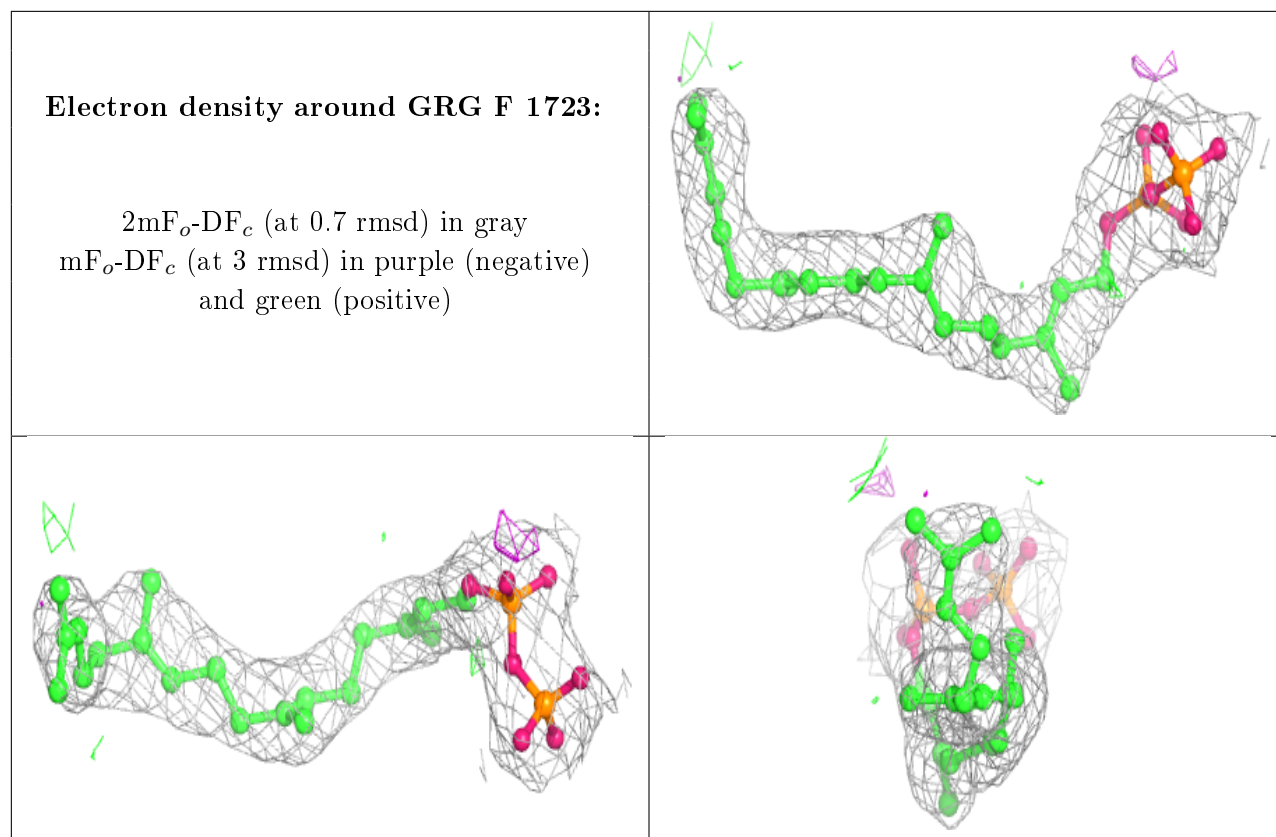
Electron density around GRG B 1721:

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

**Electron density around GRG J 1725:**

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





6.5 Other polymers [i](#)

There are no such residues in this entry.