



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 03:17 PM UTC

PDB ID : 7PB0 / pdb_00007pb0
Title : Structure of the human heterotetrameric cis-prenyltransferase complex in complex with magnesium, GGsPP and IsPP
Authors : Giladi, M.; Lisnyansky Bar-El, M.; Haitin, Y.
Deposited on : 2021-07-30
Resolution : 2.30 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 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

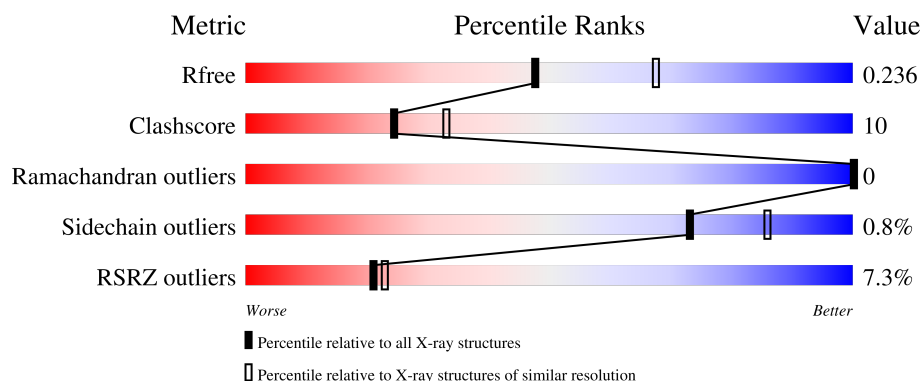
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	340	
2	B	219	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4116 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 Dehydrodolichyl diphosphate synthase complex subunit DHDDS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	321	Total	C	N	O	S	0	0	0
			2466	1569	440	442	15			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	GLY	-	expression tag	UNP Q86SQ9
A	-5	SER	-	expression tag	UNP Q86SQ9
A	-4	GLY	-	expression tag	UNP Q86SQ9
A	-3	SER	-	expression tag	UNP Q86SQ9
A	-2	GLY	-	expression tag	UNP Q86SQ9
A	-1	SER	-	expression tag	UNP Q86SQ9
A	0	GLY	-	expression tag	UNP Q86SQ9

- Molecule 2 is a protein called Dehydrodolichyl diphosphate synthase complex subunit NUS1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	200	Total	C	N	O	S	0	0	0
			1476	941	253	274	8			

There are 16 discrepancies between the modelled and reference sequences:

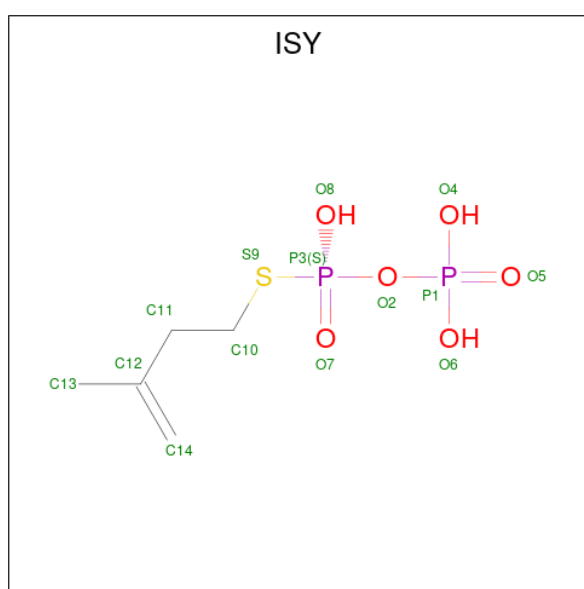
Chain	Residue	Modelled	Actual	Comment	Reference
B	66	GLY	-	expression tag	UNP Q96E22
B	67	SER	-	expression tag	UNP Q96E22
B	68	GLY	-	expression tag	UNP Q96E22
B	69	SER	-	expression tag	UNP Q96E22
B	70	GLY	-	expression tag	UNP Q96E22
B	71	SER	-	expression tag	UNP Q96E22
B	72	GLY	-	expression tag	UNP Q96E22
B	?	-	TYR	deletion	UNP Q96E22
B	?	-	SER	deletion	UNP Q96E22

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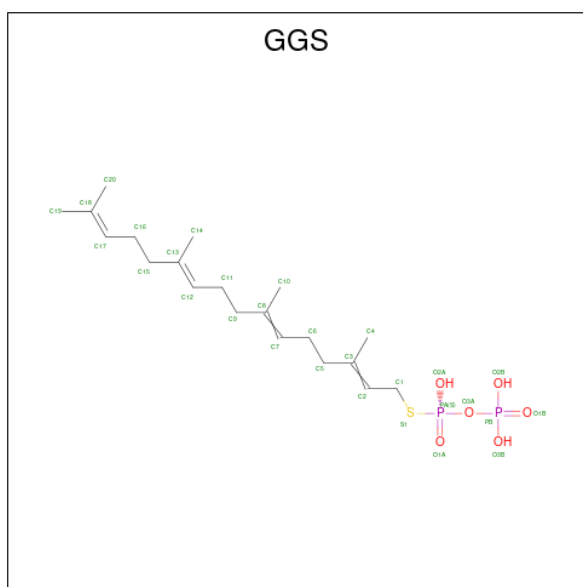
Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	PRO	deletion	UNP Q96E22
B	?	-	GLU	deletion	UNP Q96E22
B	?	-	PHE	deletion	UNP Q96E22
B	?	-	ALA	deletion	UNP Q96E22
B	?	-	ASN	deletion	UNP Q96E22
B	?	-	SER	deletion	UNP Q96E22
B	?	-	ASN	deletion	UNP Q96E22

- Molecule 3 is 3-methylbut-3-enylsulfanyl(phosphonooxy)phosphinic acid (CCD ID: ISY) (formula: $C_5H_{12}O_6P_2S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	O	P	S	0	0
			14	5	6	2	1		

- Molecule 4 is phosphonooxy-[(10E)-3,7,11,15-tetramethylhexadeca-2,6,10,14-tetraenyl] sulfanyl-phosphinic acid (CCD ID: GGS) (formula: $C_{20}H_{36}O_6P_2S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	O	P	S	0	0
			29	20	6	2	1		

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Mg 1 1	0	0

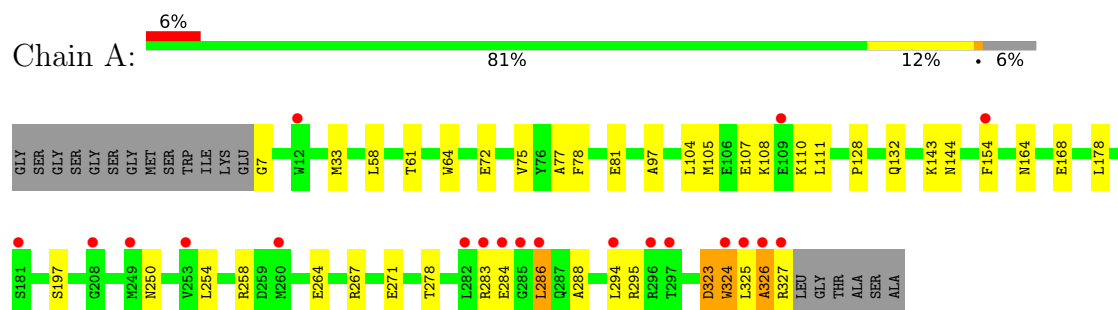
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	86	Total O 86 86	0	0
6	B	44	Total O 44 44	0	0

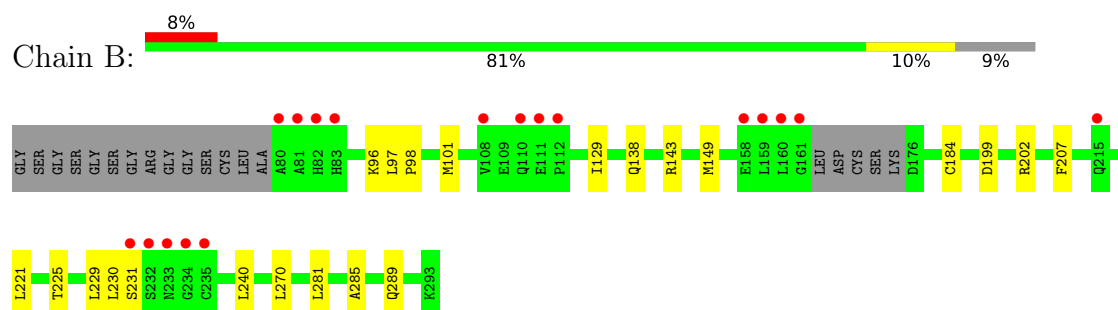
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Dehydrodolichyl diphosphate synthase complex subunit DHDDS



- Molecule 2: Dehydrodolichyl diphosphate synthase complex subunit NUS1



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	185.12Å 185.12Å 113.06Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.20 – 2.30 46.20 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.3 (46.20-2.30) 95.8 (46.20-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.45 (at 2.29Å)	Xtriage
Refinement program	PHENIX (1.14 _ 3260: ???)	Depositor
R, R_{free}	0.191 , 0.237 0.194 , 0.236	Depositor DCC
R_{free} test set	2016 reflections (6.15%)	wwPDB-VP
Wilson B-factor (Å ²)	37.6	Xtriage
Anisotropy	0.309	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 55.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.020 for -2/3*h-1/3*k-4/3*l,-1/3*h-2/3*k+4/3*l,-1/3*h+1/3*k+1/3*l 0.013 for -h,1/3*h-1/3*k-4/3*l,-1/3*h-2/3*k+1/3*l 0.005 for -1/3*h+1/3*k+4/3*l,-k,2/3*h+1/3*k+1/3*l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4116	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.34% 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: ISY, MG, GGS

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	0.19	0/2517	0.45	2/3417 (0.1%)
2	B	0.19	0/1505	0.43	0/2051
All	All	0.19	0/4022	0.44	2/5468 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	326	ALA	N-CA-C	7.29	121.88	112.41
1	A	283	ARG	N-CA-C	-5.25	105.55	111.28

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	2466	0	2322	47	0
2	B	1476	0	1399	22	0
3	A	14	0	9	1	0
4	A	29	0	33	12	0
5	A	1	0	0	0	0
6	A	86	0	0	5	1
6	B	44	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4116	0	3763	77	1

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 10.

All (77) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:324:TRP:CD1	1:A:326:ALA:HB3	1.29	1.64
1:A:324:TRP:CD1	1:A:326:ALA:CB	2.20	1.23
4:A:402:GGG:H17	4:A:402:GGG:H11A	1.28	1.08
2:B:199:ASP:OD2	2:B:230:LEU:O	1.77	1.02
1:A:324:TRP:CG	1:A:326:ALA:HB3	2.01	0.94
2:B:230:LEU:O	2:B:231:SER:HB3	1.68	0.91
4:A:402:GGG:H11A	4:A:402:GGG:C17	2.05	0.85
3:A:401:ISY:O4	6:A:502:HOH:O	1.96	0.84
1:A:258:ARG:NH1	6:A:504:HOH:O	2.10	0.84
1:A:81:GLU:OE2	6:A:501:HOH:O	1.94	0.83
1:A:7:GLY:N	6:A:505:HOH:O	2.12	0.82
1:A:324:TRP:NE1	1:A:326:ALA:HB3	1.97	0.80
1:A:278:THR:OG1	1:A:295:ARG:NH1	2.15	0.79
1:A:323:ASP:O	1:A:325:LEU:CB	2.31	0.78
2:B:202:ARG:HH12	2:B:231:SER:HB2	1.49	0.75
1:A:323:ASP:C	1:A:324:TRP:HE3	1.95	0.74
1:A:324:TRP:NE1	1:A:326:ALA:CB	2.50	0.73
2:B:138:GLN:O	2:B:143:ARG:NH2	2.20	0.73
1:A:7:GLY:O	6:A:503:HOH:O	2.08	0.72
1:A:324:TRP:HD1	1:A:326:ALA:HB3	1.41	0.72
1:A:154:PHE:CE2	4:A:402:GGG:H19	2.26	0.69
2:B:101:MET:HE2	2:B:240:LEU:HD23	1.76	0.68
2:B:202:ARG:NH1	2:B:231:SER:HB2	2.09	0.67
1:A:324:TRP:HA	1:A:325:LEU:CB	2.27	0.64
1:A:326:ALA:N	1:A:327:ARG:HA	2.17	0.60
2:B:225:THR:O	2:B:229:LEU:HD23	2.05	0.56
4:A:402:GGG:H10	4:A:402:GGG:C12	2.35	0.56
2:B:96:LYS:HG3	2:B:285:ALA:HA	1.87	0.56
4:A:402:GGG:C10	4:A:402:GGG:H12	2.36	0.55
1:A:324:TRP:HE3	1:A:324:TRP:N	2.05	0.54
2:B:149:MET:HE1	2:B:184:CYS:HB3	1.90	0.54
1:A:33:MET:O	4:A:402:GGG:H2	2.08	0.54
1:A:77:ALA:O	4:A:402:GGG:H5	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:326:ALA:N	1:A:327:ARG:CA	2.71	0.53
1:A:324:TRP:CG	1:A:326:ALA:CB	2.75	0.53
4:A:402:GGG:C12	4:A:402:GGG:C10	2.85	0.52
4:A:402:GGG:H17	4:A:402:GGG:C11	2.19	0.50
1:A:267:ARG:NH1	1:A:271:GLU:OE2	2.44	0.50
1:A:58:LEU:CD2	4:A:402:GGG:H14B	2.42	0.49
1:A:325:LEU:C	1:A:327:ARG:CB	2.85	0.49
1:A:61:THR:HA	1:A:64:TRP:CE3	2.48	0.48
1:A:323:ASP:C	1:A:324:TRP:CE3	2.84	0.48
2:B:199:ASP:OD2	2:B:231:SER:HB3	2.12	0.48
4:A:402:GGG:C17	4:A:402:GGG:C11	2.85	0.48
2:B:202:ARG:HH12	2:B:231:SER:CB	2.25	0.48
2:B:230:LEU:O	2:B:231:SER:CB	2.48	0.47
1:A:72:GLU:OE2	1:A:197:SER:HB3	2.14	0.47
2:B:96:LYS:NZ	2:B:289:GLN:OE1	2.47	0.47
2:B:97:LEU:HD22	2:B:98:PRO:HD2	1.95	0.47
2:B:270:LEU:HD23	2:B:270:LEU:HA	1.77	0.47
1:A:104:LEU:HD22	1:A:111:LEU:HD11	1.97	0.46
2:B:101:MET:HE1	2:B:281:LEU:HD21	1.97	0.46
1:A:324:TRP:CA	1:A:325:LEU:CB	2.93	0.46
1:A:284:GLU:HB3	1:A:286:LEU:HG	1.97	0.46
1:A:324:TRP:N	1:A:324:TRP:CE3	2.84	0.45
1:A:33:MET:HE2	1:A:75:VAL:HB	1.97	0.45
1:A:108:LYS:O	1:A:110:LYS:N	2.49	0.45
1:A:143:LYS:O	1:A:144:ASN:HB2	2.16	0.45
1:A:286:LEU:N	1:A:286:LEU:HD23	2.31	0.45
2:B:207:PHE:CZ	2:B:221:LEU:HB2	2.51	0.45
1:A:105:MET:C	1:A:107:GLU:H	2.23	0.45
1:A:164:ASN:O	1:A:168:GLU:HG2	2.17	0.45
2:B:101:MET:HE3	2:B:129:ILE:HD13	1.98	0.45
1:A:288:ALA:O	1:A:295:ARG:NH2	2.50	0.44
2:B:199:ASP:CG	2:B:231:SER:HB3	2.42	0.44
1:A:294:LEU:HD23	1:A:294:LEU:H	1.84	0.43
1:A:264:GLU:OE2	1:A:267:ARG:NH2	2.41	0.43
2:B:199:ASP:OD1	2:B:231:SER:HB3	2.18	0.43
1:A:178:LEU:HD12	1:A:178:LEU:HA	1.87	0.43
1:A:254:LEU:HD23	1:A:254:LEU:HA	1.84	0.42
2:B:199:ASP:OD1	2:B:231:SER:CB	2.68	0.42
1:A:326:ALA:N	1:A:327:ARG:CB	2.83	0.42
1:A:97:ALA:HB2	4:A:402:GGG:H19B	2.02	0.41
1:A:78:PHE:HB3	1:A:154:PHE:HD2	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:250:ASN:O	1:A:254:LEU:HB2	2.19	0.41
2:B:199:ASP:OD1	2:B:202:ARG:NH1	2.54	0.41
1:A:128:PRO:O	1:A:132:GLN:HG3	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:570:HOH:O	6:A:570:HOH:O[11_566]	2.16	0.04

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	319/340 (94%)	310 (97%)	9 (3%)	0	100	100
2	B	196/219 (90%)	189 (96%)	7 (4%)	0	100	100
All	All	515/559 (92%)	499 (97%)	16 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	239/295 (81%)	236 (99%)	3 (1%)	61	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	149/188 (79%)	149 (100%)	0	100	100
All	All	388/483 (80%)	385 (99%)	3 (1%)	73	86

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	286	LEU
1	A	323	ASP
1	A	324	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	44	GLN
1	A	195	ASN
1	A	248	GLN
1	A	251	HIS
1	A	255	GLN
1	A	268	GLN
1	A	287	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	GGs	A	402	5	25,28,28	1.31	3 (12%)	30,37,37	1.67	7 (23%)
3	ISY	A	401	5	10,13,13	1.27	2 (20%)	12,19,19	1.15	1 (8%)

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	GGs	A	402	5	-	5/25/31/31	-
3	ISY	A	401	5	-	3/9/13/13	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	402	GGs	C1-S1	-3.62	1.79	1.84
4	A	402	GGs	PA-O2A	-3.54	1.47	1.56
3	A	401	ISY	P3-O7	2.54	1.52	1.46
4	A	402	GGs	PB-O3B	-2.15	1.46	1.54
3	A	401	ISY	P3-O8	-2.02	1.51	1.56

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	402	GGs	C4-C3-C5	4.15	122.42	115.23
4	A	402	GGs	C10-C8-C9	3.09	120.60	115.23
4	A	402	GGs	C6-C7-C8	-2.91	120.96	127.62
4	A	402	GGs	C11-C12-C13	-2.91	120.97	127.62
4	A	402	GGs	C14-C13-C15	2.47	119.52	115.23
4	A	402	GGs	C20-C18-C19	2.40	120.11	114.59
4	A	402	GGs	C16-C17-C18	-2.38	119.70	127.64
3	A	401	ISY	C13-C12-C11	2.30	121.30	114.96

There are no chirality outliers.

All (8) torsion outliers are listed below:

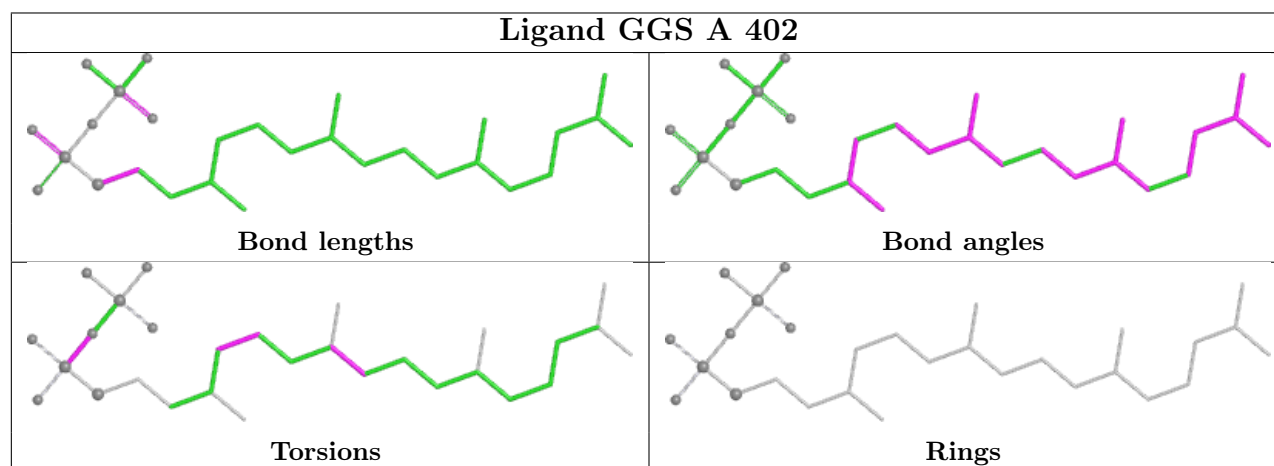
Mol	Chain	Res	Type	Atoms
3	A	401	ISY	C10-C11-C12-C13
3	A	401	ISY	C10-C11-C12-C14
4	A	402	GGs	C10-C8-C9-C11
4	A	402	GGs	C7-C8-C9-C11
4	A	402	GGs	C3-C5-C6-C7
3	A	401	ISY	S9-C10-C11-C12
4	A	402	GGs	PB-O3A-PA-O1A
4	A	402	GGs	PB-O3A-PA-O2A

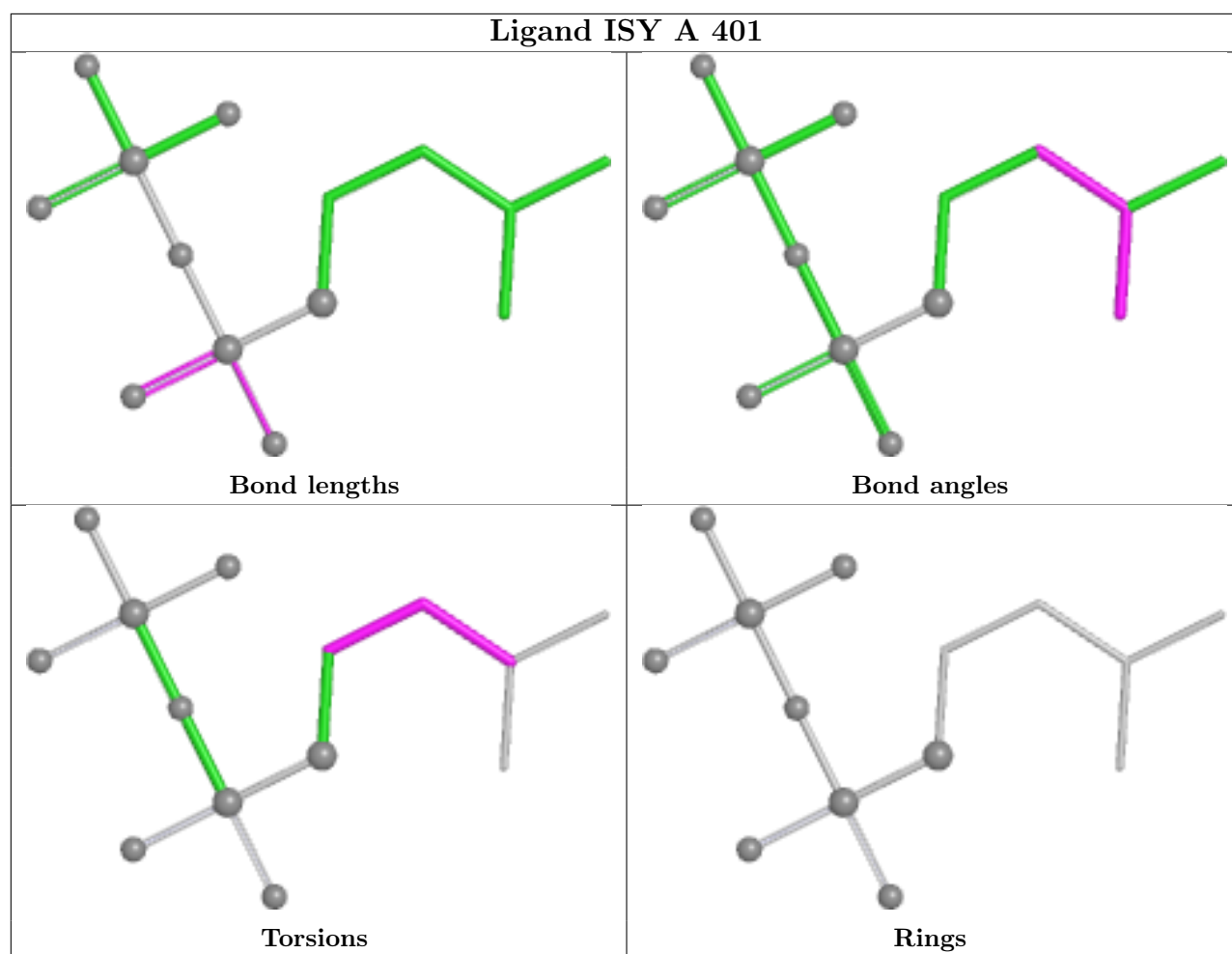
There are no ring outliers.

2 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	402	GGs	12	0
3	A	401	ISY	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	321/340 (94%)	0.25	20 (6%) 26 28	29, 50, 79, 112	0
2	B	200/219 (91%)	0.35	18 (9%) 15 16	32, 47, 88, 112	0
All	All	521/559 (93%)	0.29	38 (7%) 21 23	29, 49, 81, 112	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	232	SER	5.5
1	A	286	LEU	5.3
2	B	82	HIS	4.9
2	B	233	ASN	4.9
2	B	111	GLU	4.8
1	A	12	TRP	4.6
2	B	112	PRO	4.5
1	A	324	TRP	4.1
1	A	327	ARG	4.1
1	A	283	ARG	4.1
2	B	234	GLY	4.0
2	B	108	VAL	3.9
2	B	161	GLY	3.8
1	A	284	GLU	3.8
1	A	325	LEU	3.8
2	B	80	ALA	3.7
2	B	159	LEU	3.4
2	B	81	ALA	3.3
2	B	83	HIS	3.3
2	B	110	GLN	3.2
1	A	285	GLY	3.2
1	A	326	ALA	3.0
1	A	208	GLY	2.9
2	B	160	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
2	B	231	SER	2.8
1	A	109	GLU	2.6
1	A	282	LEU	2.5
2	B	215	GLN	2.5
1	A	154	PHE	2.5
1	A	294	LEU	2.4
1	A	297	THR	2.3
1	A	253	VAL	2.3
1	A	249	MET	2.2
2	B	158	GLU	2.2
1	A	296	ARG	2.0
1	A	260	MET	2.0
1	A	181	SER	2.0
2	B	235	CYS	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

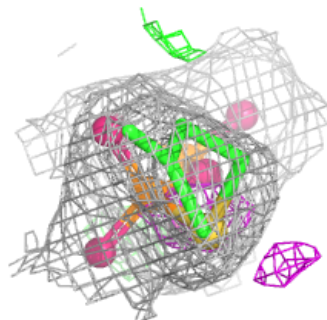
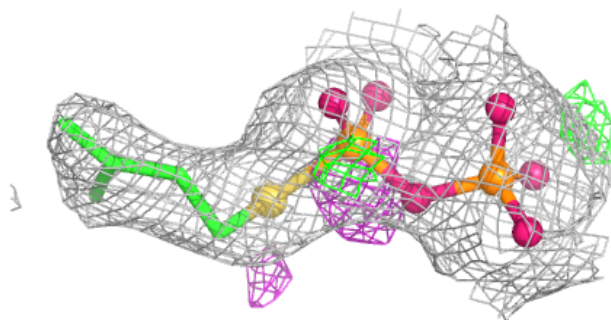
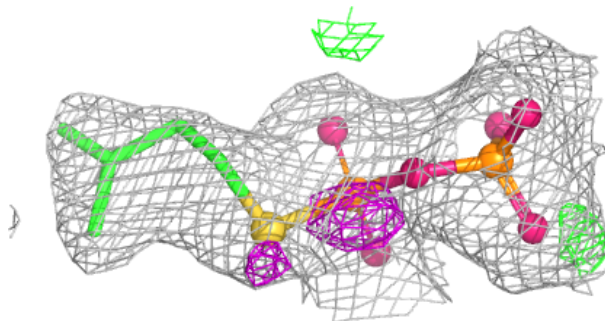
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	ISY	A	401	14/14	0.94	0.11	43,51,68,73	0
4	GGS	A	402	29/29	0.95	0.14	35,58,72,73	0
5	MG	A	403	1/1	0.98	0.04	42,42,42,42	0

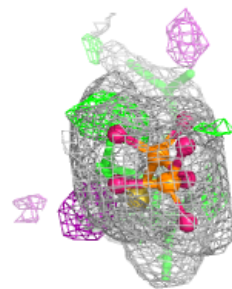
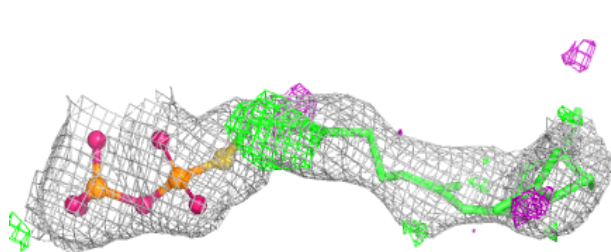
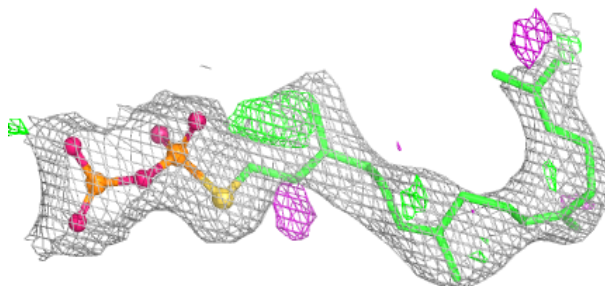
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ISY A 401:

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

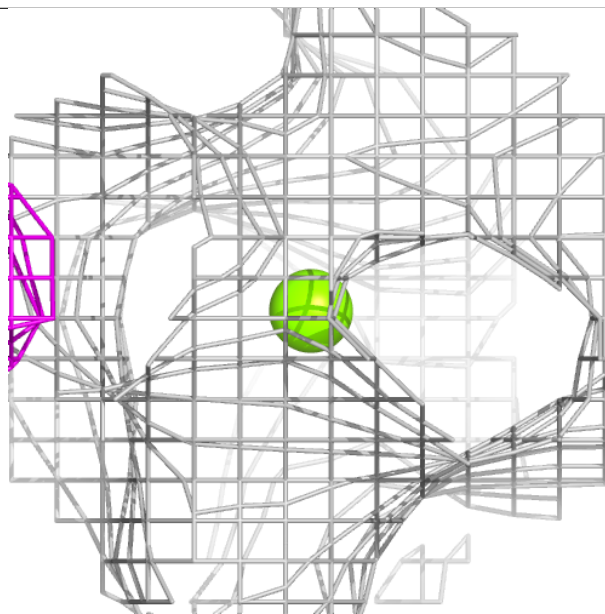
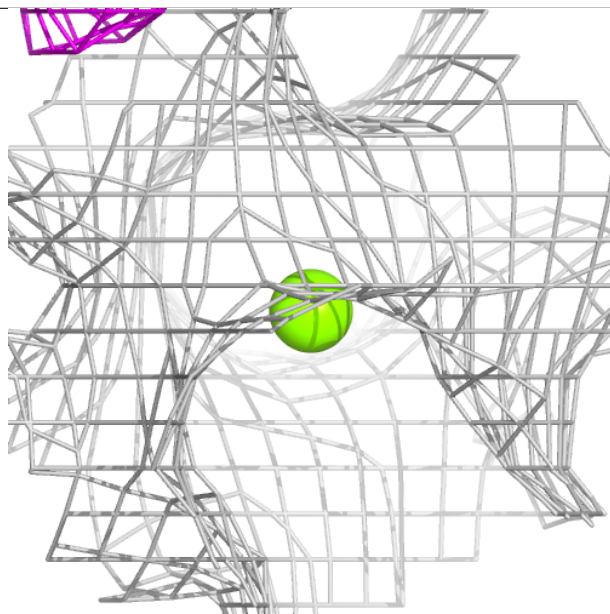
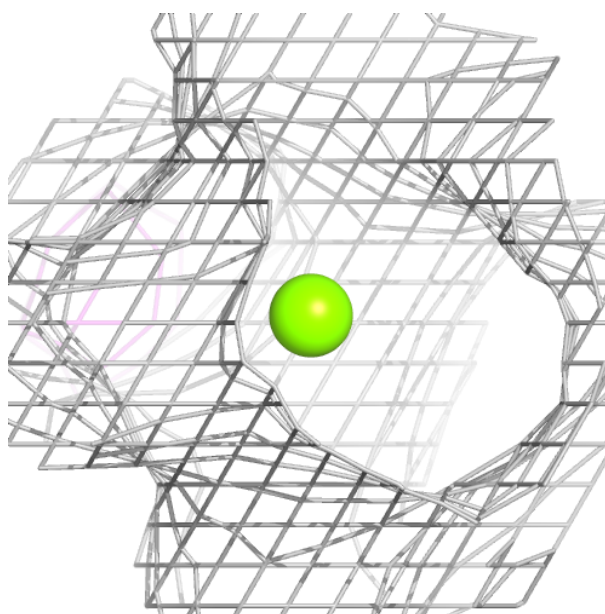
**Electron density around GGS A 402:**

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



Electron density around MG A 403:

$2mF_o-DF_c$ (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.