Full wwPDB X-ray Structure Validation Report (i)

Jun 16, 2024 – 07:15 AM EDT

PDB ID	:	4ZXF
Title	:	Crystal Structure of a Soluble Variant of Monoglyceride Lipase from Saccharomyces Cerevisiae in Complex with a Substrate Analog
Authors	:	Aschauer, P.; Lichtenegger, J.; Rengachari, S.; Gruber, K.; Oberer, M.
Deposited on	:	2015-05-20
Resolution	:	2.50 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 (i) 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 (i)) were used in the production of this report:

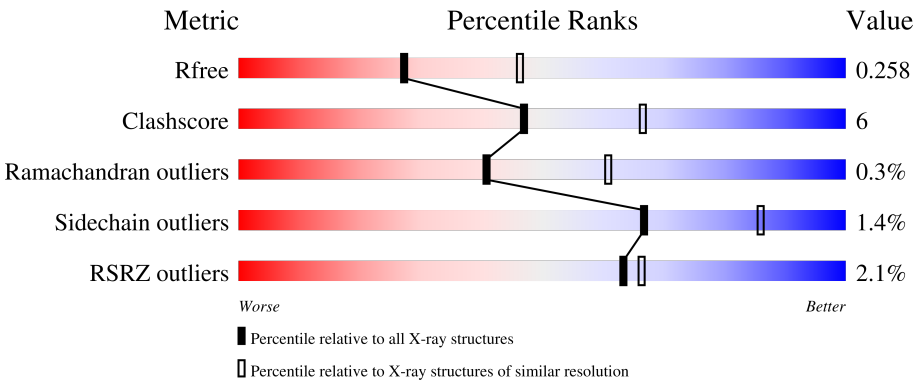
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 <=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	81% 9% 9%
1	B	340	% 77% 12% • 10%
1	C	340	79% 11% 10%
1	D	340	7% 66% 18% • 14%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 9958 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 Monoglyceride lipase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	308	2469	1581	424	451	13	0	0	0
1	B	307	2462	1578	422	448	14	0	0	0
1	C	307	2463	1578	423	448	14	0	0	0
1	D	293	2368	1520	407	429	12	0	1	0

There are 116 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-26	MET	-	initiating methionine	UNP P28321
A	-25	SER	-	expression tag	UNP P28321
A	-24	TYR	-	expression tag	UNP P28321
A	-23	TYR	-	expression tag	UNP P28321
A	-22	HIS	-	expression tag	UNP P28321
A	-21	HIS	-	expression tag	UNP P28321
A	-20	HIS	-	expression tag	UNP P28321
A	-19	HIS	-	expression tag	UNP P28321
A	-18	HIS	-	expression tag	UNP P28321
A	-17	HIS	-	expression tag	UNP P28321
A	-16	ASP	-	expression tag	UNP P28321
A	-15	TYR	-	expression tag	UNP P28321
A	-14	ASP	-	expression tag	UNP P28321
A	-13	ILE	-	expression tag	UNP P28321
A	-12	PRO	-	expression tag	UNP P28321
A	-11	THR	-	expression tag	UNP P28321
A	-10	THR	-	expression tag	UNP P28321
A	-9	GLU	-	expression tag	UNP P28321
A	-8	ASN	-	expression tag	UNP P28321
A	-7	LEU	-	expression tag	UNP P28321
A	-6	TYR	-	expression tag	UNP P28321

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	PHE	-	expression tag	UNP P28321
A	-4	GLN	-	expression tag	UNP P28321
A	-3	GLY	-	expression tag	UNP P28321
A	-2	ALA	-	expression tag	UNP P28321
A	-1	MET	-	expression tag	UNP P28321
A	0	GLY	-	expression tag	UNP P28321
A	175	SER	LEU	engineered mutation	UNP P28321
A	264	ARG	GLN	engineered mutation	UNP P28321
B	-26	MET	-	initiating methionine	UNP P28321
B	-25	SER	-	expression tag	UNP P28321
B	-24	TYR	-	expression tag	UNP P28321
B	-23	TYR	-	expression tag	UNP P28321
B	-22	HIS	-	expression tag	UNP P28321
B	-21	HIS	-	expression tag	UNP P28321
B	-20	HIS	-	expression tag	UNP P28321
B	-19	HIS	-	expression tag	UNP P28321
B	-18	HIS	-	expression tag	UNP P28321
B	-17	HIS	-	expression tag	UNP P28321
B	-16	ASP	-	expression tag	UNP P28321
B	-15	TYR	-	expression tag	UNP P28321
B	-14	ASP	-	expression tag	UNP P28321
B	-13	ILE	-	expression tag	UNP P28321
B	-12	PRO	-	expression tag	UNP P28321
B	-11	THR	-	expression tag	UNP P28321
B	-10	THR	-	expression tag	UNP P28321
B	-9	GLU	-	expression tag	UNP P28321
B	-8	ASN	-	expression tag	UNP P28321
B	-7	LEU	-	expression tag	UNP P28321
B	-6	TYR	-	expression tag	UNP P28321
B	-5	PHE	-	expression tag	UNP P28321
B	-4	GLN	-	expression tag	UNP P28321
B	-3	GLY	-	expression tag	UNP P28321
B	-2	ALA	-	expression tag	UNP P28321
B	-1	MET	-	expression tag	UNP P28321
B	0	GLY	-	expression tag	UNP P28321
B	175	SER	LEU	engineered mutation	UNP P28321
B	264	ARG	GLN	engineered mutation	UNP P28321
C	-26	MET	-	initiating methionine	UNP P28321
C	-25	SER	-	expression tag	UNP P28321
C	-24	TYR	-	expression tag	UNP P28321
C	-23	TYR	-	expression tag	UNP P28321
C	-22	HIS	-	expression tag	UNP P28321

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-21	HIS	-	expression tag	UNP P28321
C	-20	HIS	-	expression tag	UNP P28321
C	-19	HIS	-	expression tag	UNP P28321
C	-18	HIS	-	expression tag	UNP P28321
C	-17	HIS	-	expression tag	UNP P28321
C	-16	ASP	-	expression tag	UNP P28321
C	-15	TYR	-	expression tag	UNP P28321
C	-14	ASP	-	expression tag	UNP P28321
C	-13	ILE	-	expression tag	UNP P28321
C	-12	PRO	-	expression tag	UNP P28321
C	-11	THR	-	expression tag	UNP P28321
C	-10	THR	-	expression tag	UNP P28321
C	-9	GLU	-	expression tag	UNP P28321
C	-8	ASN	-	expression tag	UNP P28321
C	-7	LEU	-	expression tag	UNP P28321
C	-6	TYR	-	expression tag	UNP P28321
C	-5	PHE	-	expression tag	UNP P28321
C	-4	GLN	-	expression tag	UNP P28321
C	-3	GLY	-	expression tag	UNP P28321
C	-2	ALA	-	expression tag	UNP P28321
C	-1	MET	-	expression tag	UNP P28321
C	0	GLY	-	expression tag	UNP P28321
C	175	SER	LEU	engineered mutation	UNP P28321
C	264	ARG	GLN	engineered mutation	UNP P28321
D	-26	MET	-	initiating methionine	UNP P28321
D	-25	SER	-	expression tag	UNP P28321
D	-24	TYR	-	expression tag	UNP P28321
D	-23	TYR	-	expression tag	UNP P28321
D	-22	HIS	-	expression tag	UNP P28321
D	-21	HIS	-	expression tag	UNP P28321
D	-20	HIS	-	expression tag	UNP P28321
D	-19	HIS	-	expression tag	UNP P28321
D	-18	HIS	-	expression tag	UNP P28321
D	-17	HIS	-	expression tag	UNP P28321
D	-16	ASP	-	expression tag	UNP P28321
D	-15	TYR	-	expression tag	UNP P28321
D	-14	ASP	-	expression tag	UNP P28321
D	-13	ILE	-	expression tag	UNP P28321
D	-12	PRO	-	expression tag	UNP P28321
D	-11	THR	-	expression tag	UNP P28321
D	-10	THR	-	expression tag	UNP P28321
D	-9	GLU	-	expression tag	UNP P28321

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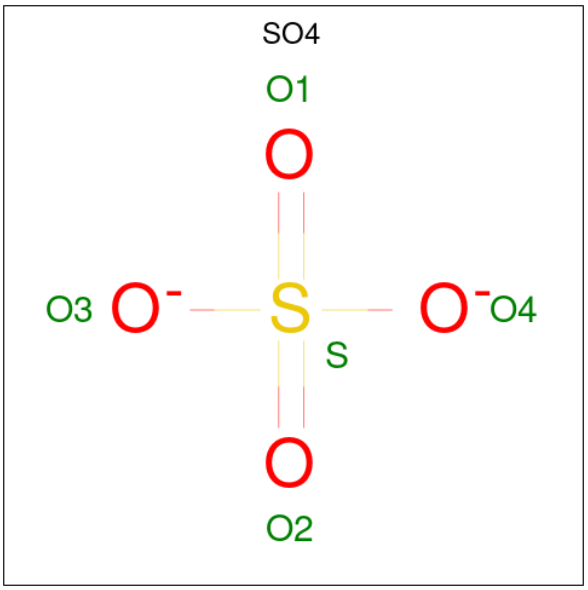
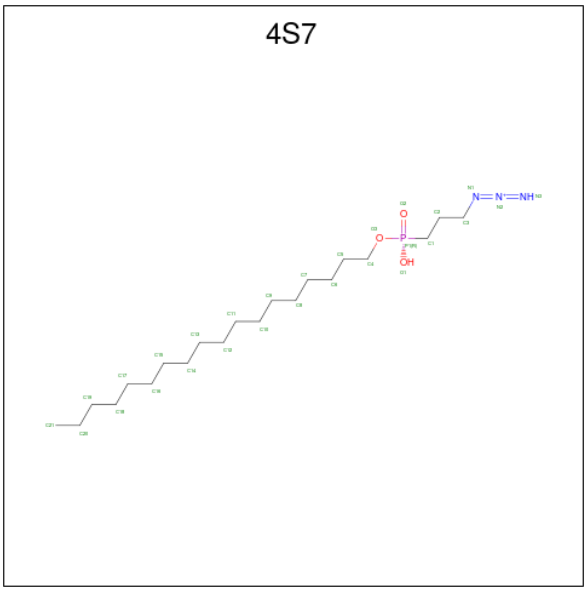
Chain	Residue	Modelled	Actual	Comment	Reference
D	-8	ASN	-	expression tag	UNP P28321
D	-7	LEU	-	expression tag	UNP P28321
D	-6	TYR	-	expression tag	UNP P28321
D	-5	PHE	-	expression tag	UNP P28321
D	-4	GLN	-	expression tag	UNP P28321
D	-3	GLY	-	expression tag	UNP P28321
D	-2	ALA	-	expression tag	UNP P28321
D	-1	MET	-	expression tag	UNP P28321
D	0	GLY	-	expression tag	UNP P28321
D	175	SER	LEU	engineered mutation	UNP P28321
D	264	ARG	GLN	engineered mutation	UNP P28321

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



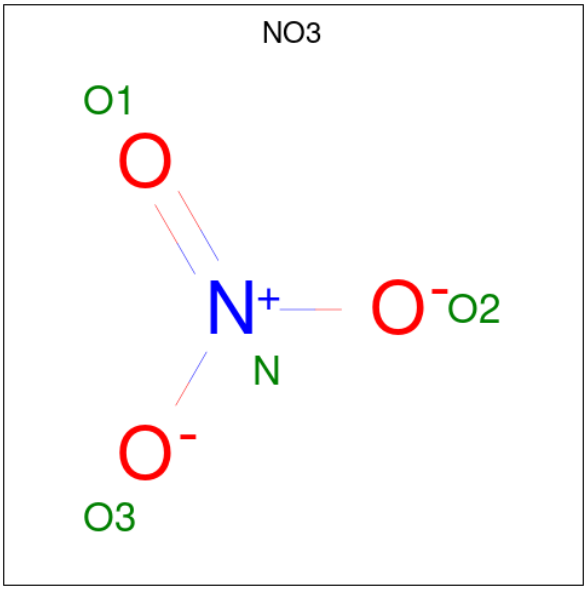
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0
			Total	O	S		
2	B	1	5	4	1	0	0

- Molecule 3 is 1-{3-[(R)-hydroxy(octadecyloxy)phosphoryl]propyl}triaza-1,2-dien-2-ium (three-letter code: 4S7) (formula: $C_{21}H_{45}N_3O_3P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	C	1	27	21	3	2	1	0	0

- Molecule 4 is NITRATE ION (three-letter code: NO3) (formula: NO_3).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	N	O		
4	D	1	4	1	3	0	0
4	D	1	Total	N	O	0	0
			4	1	3		

- Molecule 5 is water.

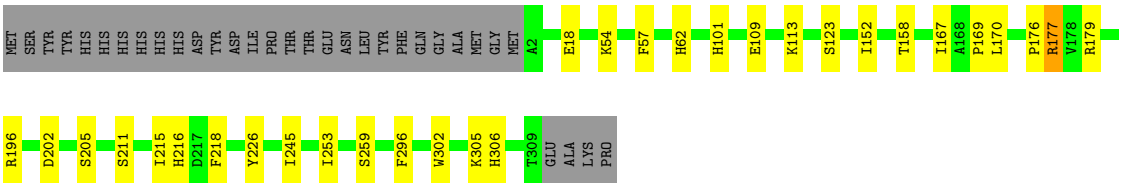
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	54	54	54	0	0
			Total	O		
5	B	45	45	45	0	0
			Total	O		
5	C	28	28	28	0	0
			Total	O		
5	D	24	24	24	0	0

3 Residue-property plots (i)

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.

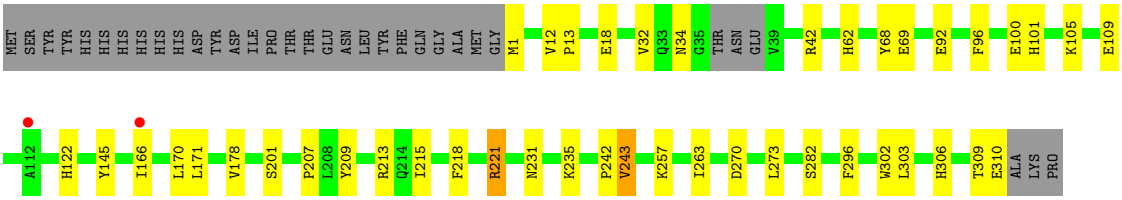
• Molecule 1: Monoglyceride lipase

Chain A:



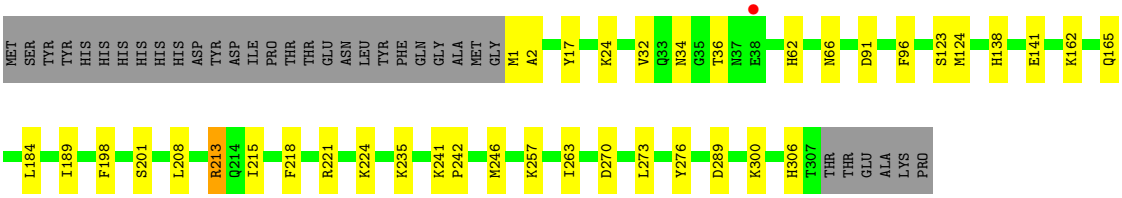
• Molecule 1: Monoglyceride lipase

Chain B:



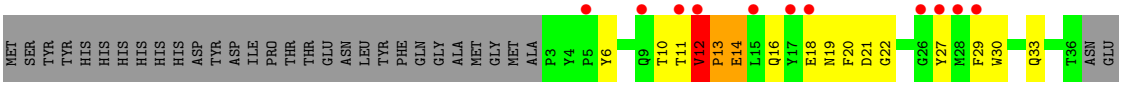
• Molecule 1: Monoglyceride lipase

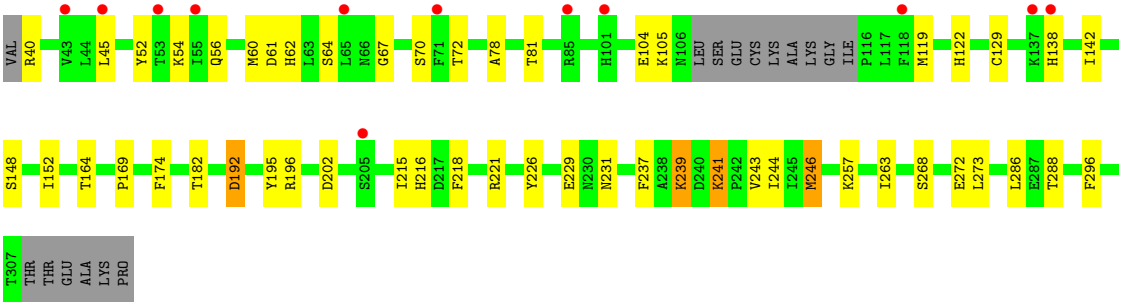
Chain C:



• Molecule 1: Monoglyceride lipase

Chain D:




VAL
R40
V43
L44
L45
Y52
T53
K54
I55
Q56
M60
D61
H62
L63
S64
L65
N66
G67
S70
F71
T72
A78
T81
R85
H101
E104
K105
N106
LEU
SER
GLU
CYS
LYS
ALA
LYS
GLY
ILE
P116
L117
F118
M119
H122
C129
K137
H138
I142
S148
I152
T164
P169
F174
T182
D192
Y195
R196
D202
S205
I215
H216
D217
F218
R221
Y226
E229
N230
N231
F237
A238
K239
D240
K241
P242
V243
I244
I245
M246
K257
I263
S268
E272
L273
L286
E287
T288
F296
T307
THR
THR
GLU
ALA
LYS
PRO

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	76.76Å 107.13Å 165.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	65.48 – 2.50 69.63 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.5 (65.48-2.50) 99.5 (69.63-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.18	Depositor
$< I/\sigma(I) >$ [1]	1.63 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.201 , 0.257 0.208 , 0.258	Depositor DCC
R_{free} test set	2409 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	43.8	Xtriage
Anisotropy	0.003	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 45.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	9958	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: 4S7, NO3, SO4

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	0.23	0/2537	0.42	0/3425
1	B	0.24	0/2529	0.42	0/3411
1	C	0.25	0/2531	0.43	0/3415
1	D	0.30	0/2437	0.51	2/3285 (0.1%)
All	All	0.26	0/10034	0.45	2/13536 (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
1	D	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	12	VAL	C-N-CD	6.61	142.28	128.40
1	D	14	GLU	N-CA-C	-6.49	93.47	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	12	VAL	Peptide

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	2469	0	2413	19	0
1	B	2462	0	2411	27	0
1	C	2463	0	2411	31	0
1	D	2368	0	2309	47	0
2	A	5	0	0	1	0
2	B	5	0	0	0	0
3	C	27	0	0	7	0
4	D	8	0	0	1	0
5	A	54	0	0	0	0
5	B	45	0	0	1	0
5	C	28	0	0	0	0
5	D	24	0	0	1	0
All	All	9958	0	9544	119	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 6.

All (119) 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:D:10:THR:HB	1:D:33:GLN:OE1	1.28	1.31
1:D:10:THR:CB	1:D:33:GLN:OE1	2.19	0.91
1:D:237:PHE:HZ	1:D:243:VAL:HG11	1.44	0.81
1:D:11:THR:OG1	1:D:33:GLN:NE2	2.19	0.76
1:B:92:GLU:OE1	1:B:221:ARG:NH1	2.23	0.71
1:C:184:LEU:HD21	3:C:500:4S7:N3	2.05	0.71
1:C:123:SER:OG	3:C:500:4S7:P1	2.50	0.69
1:D:40:ARG:N	1:D:67:GLY:O	2.28	0.67
1:D:263:ILE:HG13	1:D:273:LEU:HB2	1.76	0.67
1:C:124:MET:HB2	3:C:500:4S7:O2	1.95	0.66
1:C:246:MET:HB2	1:C:276:TYR:HE2	1.60	0.66
1:D:237:PHE:CZ	1:D:243:VAL:HG11	2.30	0.66
1:D:52:TYR:CE2	1:D:54:LYS:HB3	2.32	0.65
1:A:177:ARG:HH11	1:A:177:ARG:HB2	1.62	0.64
1:A:305:LYS:O	1:C:235:LYS:NZ	2.23	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:309:THR:HG22	1:B:310:GLU:H	1.65	0.62
1:D:142:ILE:O	1:D:241:LYS:NZ	2.33	0.61
1:C:124:MET:CB	3:C:500:4S7:O2	2.50	0.60
1:D:6:TYR:OH	1:D:61:ASP:OD2	2.18	0.58
1:D:12:VAL:HB	1:D:13:PRO:HD3	1.85	0.57
1:C:123:SER:CB	3:C:500:4S7:P1	2.92	0.57
1:B:263:ILE:HG13	1:B:273:LEU:HB2	1.86	0.57
1:B:171:LEU:HD13	1:D:164:THR:HG22	1.87	0.56
1:C:32:VAL:HG12	1:C:34:ASN:OD1	2.06	0.55
1:A:167:ILE:HA	1:A:170:LEU:HD12	1.89	0.55
1:C:123:SER:HB3	3:C:500:4S7:P1	2.47	0.55
1:B:270:ASP:OD2	1:B:306:HIS:NE2	2.28	0.55
1:A:196:ARG:NH2	2:A:401:SO4:O4	2.32	0.54
1:A:18:GLU:OE2	1:A:101:HIS:NE2	2.38	0.54
1:D:10:THR:OG1	1:D:61:ASP:OD1	2.19	0.54
1:D:237:PHE:HE2	1:D:268:SER:HB2	1.73	0.54
1:D:27:TYR:CE1	1:D:105:LYS:HE2	2.43	0.54
1:D:52:TYR:HE2	1:D:54:LYS:HB3	1.70	0.54
1:C:138:HIS:ND1	1:C:141:GLU:OE1	2.36	0.53
1:C:208:LEU:HD13	3:C:500:4S7:N3	2.24	0.53
1:B:32:VAL:HG23	1:B:69:GLU:HG3	1.91	0.53
1:B:42:ARG:HH12	1:B:109:GLU:HB2	1.74	0.53
1:B:178:VAL:HG22	1:D:182:THR:HA	1.92	0.52
1:C:34:ASN:OD1	1:C:34:ASN:N	2.42	0.52
1:D:14:GLU:HB2	1:D:29:PHE:H	1.75	0.52
1:C:62:HIS:O	1:C:66:ASN:ND2	2.36	0.51
1:B:32:VAL:HG12	1:B:34:ASN:HB2	1.92	0.51
1:C:257:LYS:HE3	1:D:257:LYS:HZ2	1.75	0.51
1:D:104:GLU:OE1	1:D:138:HIS:NE2	2.43	0.51
1:D:20:PHE:O	1:D:22:GLY:N	2.43	0.51
1:C:162:LYS:NZ	1:C:165:GLN:HG3	2.25	0.51
1:D:237:PHE:HZ	1:D:243:VAL:CG1	2.18	0.51
1:C:1:MET:HB2	1:C:201:SER:HB3	1.93	0.51
1:B:18:GLU:OE1	1:B:105:LYS:HE3	2.10	0.51
1:D:195:TYR:HB3	1:D:286:LEU:HD12	1.93	0.51
1:D:215:ILE:HA	1:D:218:PHE:CE2	2.46	0.50
1:A:169:PRO:HG3	1:A:215:ILE:HG22	1.94	0.50
1:B:62:HIS:HB3	1:B:296:PHE:CZ	2.47	0.49
1:C:66:ASN:HB3	1:C:300:LYS:HE3	1.93	0.49
1:D:237:PHE:CE2	1:D:268:SER:HB2	2.48	0.49
1:A:62:HIS:HB3	1:A:296:PHE:CZ	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:263:ILE:HG13	1:C:273:LEU:HB2	1.94	0.49
1:C:184:LEU:HD22	1:C:189:ILE:HD11	1.94	0.48
1:B:231:ASN:HB2	1:B:235:LYS:HE3	1.95	0.48
1:D:196:ARG:NH2	4:D:402:NO3:O2	2.44	0.47
1:B:166:ILE:O	1:B:170:LEU:HG	2.14	0.47
1:D:13:PRO:HB3	1:D:30:TRP:CE3	2.50	0.47
1:B:257:LYS:NZ	5:B:507:HOH:O	2.47	0.47
1:B:207:PRO:HG2	1:B:209:TYR:CE2	2.49	0.47
1:A:245:ILE:HG21	1:A:259:SER:HB3	1.97	0.46
1:A:202:ASP:HB3	1:A:205:SER:HB2	1.96	0.46
1:A:158:THR:OG1	1:A:253:ILE:HA	2.15	0.46
1:A:302:TRP:O	1:A:306:HIS:ND1	2.47	0.46
1:C:215:ILE:HA	1:C:218:PHE:CE2	2.51	0.46
1:B:242:PRO:HA	1:B:270:ASP:O	2.16	0.46
1:C:91:ASP:HB3	1:C:213:ARG:HG2	1.98	0.45
1:A:54:LYS:HA	1:A:57:PHE:CD1	2.52	0.45
1:A:215:ILE:HA	1:A:218:PHE:CE2	2.51	0.45
1:D:244:ILE:HG23	1:D:246:MET:HE1	1.97	0.45
1:A:177:ARG:HB2	1:A:177:ARG:NH1	2.30	0.45
1:D:56:GLN:O	1:D:60:MET:HG3	2.16	0.45
1:D:62:HIS:HB3	1:D:296:PHE:CE2	2.51	0.45
1:A:179:ARG:HA	1:A:211:SER:HA	1.99	0.45
1:D:192:ASP:HB3	1:D:288:THR:HG22	1.99	0.44
1:D:218:PHE:HA	1:D:221:ARG:HG2	1.99	0.44
1:B:218:PHE:HA	1:B:221:ARG:HG2	1.99	0.44
1:C:162:LYS:HZ1	1:C:165:GLN:HG3	1.82	0.44
1:D:52:TYR:OH	1:D:202:ASP:OD2	2.36	0.44
1:B:18:GLU:OE2	1:B:101:HIS:NE2	2.39	0.44
1:C:2:ALA:HB3	1:C:198:PHE:HA	2.00	0.44
1:D:152:ILE:HG22	1:D:226:TYR:HB2	2.00	0.44
1:A:169:PRO:HB3	1:A:216:HIS:HA	2.00	0.44
1:C:17:TYR:HD2	1:C:24:LYS:HG2	1.83	0.43
1:C:270:ASP:OD2	1:C:306:HIS:NE2	2.33	0.43
1:D:18:GLU:HG2	1:D:19:ASN:H	1.82	0.43
1:A:176:PRO:HD2	1:A:177:ARG:NH2	2.33	0.43
1:D:122:HIS:HA	1:D:148:SER:HB3	2.00	0.43
1:D:239:LYS:HA	1:D:239:LYS:HD2	1.70	0.43
1:D:45:LEU:HB2	1:D:72:THR:HB	1.99	0.43
1:D:12:VAL:CB	1:D:13:PRO:HD3	2.49	0.43
1:A:152:ILE:HG22	1:A:226:TYR:HB2	2.01	0.43
1:C:224:LYS:HB3	1:C:224:LYS:HE2	1.85	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:208:LEU:HD23	1:C:208:LEU:H	1.84	0.42
1:C:257:LYS:HE3	1:D:257:LYS:NZ	2.33	0.42
1:D:30:TRP:CD1	1:D:64:SER:HB2	2.55	0.42
1:B:215:ILE:HA	1:B:218:PHE:CE2	2.54	0.42
1:D:231:ASN:OD1	5:D:501:HOH:O	2.21	0.42
1:B:1:MET:HB2	1:B:201:SER:HB3	2.01	0.42
1:D:169:PRO:HA	1:D:216:HIS:HB2	2.01	0.42
1:C:184:LEU:HG	1:C:208:LEU:HD22	2.02	0.42
1:B:96:PHE:O	1:B:100:GLU:HG2	2.19	0.41
1:D:78:ALA:O	1:D:81:THR:HG22	2.20	0.41
1:B:68:TYR:CZ	1:B:303:LEU:HB3	2.55	0.41
1:B:309:THR:HG22	1:B:310:GLU:N	2.33	0.41
1:D:119:MET:HG2	1:D:129:CYS:SG	2.60	0.41
1:A:109:GLU:O	1:A:113:LYS:HG2	2.20	0.41
1:B:145:TYR:HB2	1:B:243:VAL:HG13	2.03	0.41
1:D:244:ILE:HA	1:D:272:GLU:O	2.21	0.41
1:D:16:GLN:HB2	1:D:27:TYR:CE2	2.56	0.40
1:B:12:VAL:HA	1:B:13:PRO:HD3	1.90	0.40
1:B:122:HIS:CE1	1:B:282:SER:HA	2.56	0.40
1:B:242:PRO:HB2	1:B:302:TRP:CZ2	2.57	0.40
1:C:96:PHE:CE2	1:C:221:ARG:HD2	2.56	0.40
1:C:241:LYS:HA	1:C:242:PRO:HD3	1.90	0.40

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	306/340 (90%)	300 (98%)	6 (2%)	0	100	100
1	B	303/340 (89%)	293 (97%)	10 (3%)	0	100	100
1	C	305/340 (90%)	295 (97%)	10 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	288/340 (85%)	266 (92%)	18 (6%)	4 (1%)	11	20
All	All	1202/1360 (88%)	1154 (96%)	44 (4%)	4 (0%)	41	61

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	13	PRO
1	D	21	ASP
1	D	239	LYS
1	D	12	VAL

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	267/295 (90%)	265 (99%)	2 (1%)	84	94
1	B	266/295 (90%)	263 (99%)	3 (1%)	73	89
1	C	266/295 (90%)	263 (99%)	3 (1%)	73	89
1	D	256/295 (87%)	249 (97%)	7 (3%)	44	71
All	All	1055/1180 (89%)	1040 (99%)	15 (1%)	67	86

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	123	SER
1	A	177	ARG
1	B	213	ARG
1	B	221	ARG
1	B	243	VAL
1	C	36	THR
1	C	213	ARG
1	C	289	ASP
1	D	12	VAL
1	D	70	SER

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Mol	Chain	Res	Type
1	D	174	PHE
1	D	192	ASP
1	D	229	GLU
1	D	241	LYS
1	D	246	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	33	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

5 ligands are modelled in this entry.

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	$\#\|Z\| > 2$
3	4S7	C	500	-	22,26,27	0.46	0	19,26,29	0.88	0
2	SO4	B	401	-	4,4,4	0.15	0	6,6,6	0.04	0
2	SO4	A	401	-	4,4,4	0.14	0	6,6,6	0.05	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	NO3	D	401	-	1,3,3	0.65	0	0,3,3	-	-
4	NO3	D	402	-	1,3,3	0.65	0	0,3,3	-	-

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
3	4S7	C	500	-	-	10/21/25/27	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	500	4S7	C1-C2-C3-N1
3	C	500	4S7	C9-C10-C11-C12
3	C	500	4S7	C10-C11-C12-C13
3	C	500	4S7	C5-C6-C7-C8
3	C	500	4S7	C4-C5-C6-C7
3	C	500	4S7	C7-C8-C9-C10
3	C	500	4S7	C11-C12-C13-C14
3	C	500	4S7	C12-C13-C14-C15
3	C	500	4S7	C18-C19-C20-C21
3	C	500	4S7	C11-C10-C9-C8

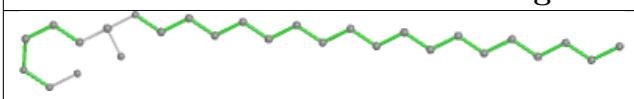
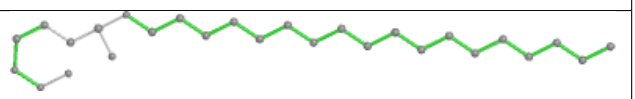
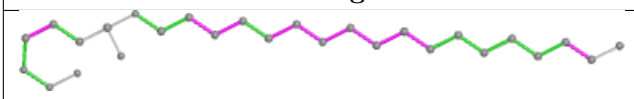
There are no ring outliers.

3 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	500	4S7	7	0
2	A	401	SO4	1	0
4	D	402	NO3	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 then 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.

Ligand 4S7 C 500	
 **Bond lengths**	 **Bond angles**
 **Torsions**	**Rings**

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 (i)

6.1 Protein, DNA and RNA chains (i)

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	308/340 (90%)	-0.26	0	100	100	24, 34, 48, 79	0
1	B	307/340 (90%)	-0.16	2 (0%)	87	89	27, 40, 58, 79	0
1	C	307/340 (90%)	-0.15	1 (0%)	94	94	27, 44, 63, 82	0
1	D	293/340 (86%)	0.44	23 (7%)	13	13	26, 58, 81, 90	0
All	All	1215/1360 (89%)	-0.04	26 (2%)	63	66	24, 41, 72, 90	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	26	GLY	9.4
1	D	43	VAL	4.6
1	D	137	LYS	4.5
1	D	28	MET	3.8
1	D	12	VAL	3.6
1	D	101	HIS	3.3
1	D	118	PHE	3.1
1	C	38	GLU	3.0
1	D	138	HIS	2.8
1	D	65	LEU	2.8
1	D	27	TYR	2.7
1	D	5	PRO	2.6
1	B	166	ILE	2.5
1	D	9	GLN	2.5
1	D	15	LEU	2.5
1	D	53	THR	2.5
1	D	11	THR	2.5
1	D	55	ILE	2.4
1	D	85	ARG	2.4
1	B	112	ALA	2.4
1	D	205	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	29	PHE	2.2
1	D	17	TYR	2.1
1	D	18	GLU	2.1
1	D	45	LEU	2.1
1	D	71	PHE	2.1

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 monosaccharides in this entry.

6.4 Ligands (i)

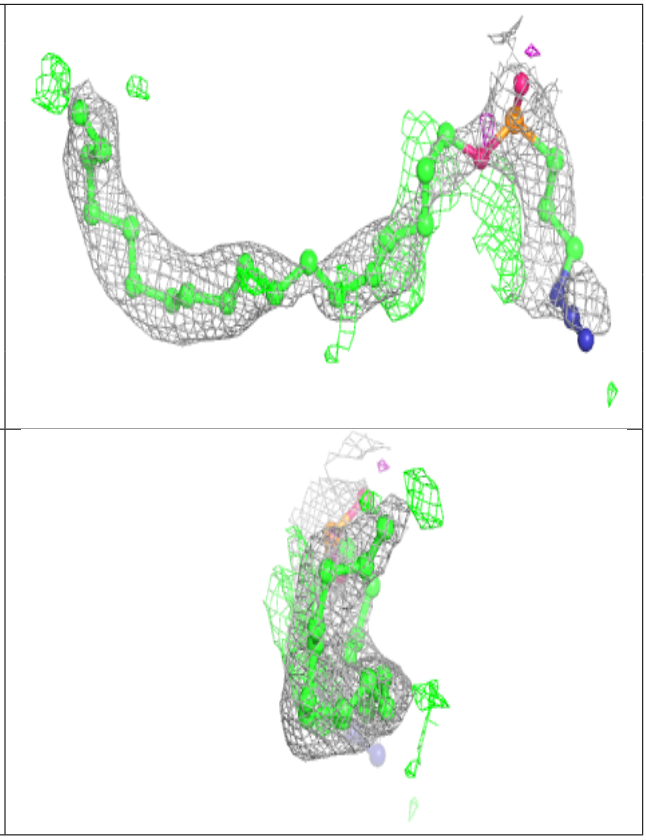
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	4S7	C	500	27/28	0.76	0.27	26,40,56,58	27
4	NO3	D	401	4/4	0.90	0.10	45,46,60,65	0
4	NO3	D	402	4/4	0.90	0.14	68,71,72,73	0
2	SO4	B	401	5/5	0.95	0.11	72,75,80,87	0
2	SO4	A	401	5/5	0.96	0.10	62,63,70,73	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 4S7 C 500:

$2mF_o$-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.