



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 07:06 AM BST

PDB ID : 6QSK
Title : Crystal structure of a nucleotide sugar transporter with bound nucleotide monophosphate.
Authors : Newstead, S.; Parker, J.L.
Deposited on : 2019-02-21
Resolution : 3.39 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 : 2.13.1
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) : 2.13.1

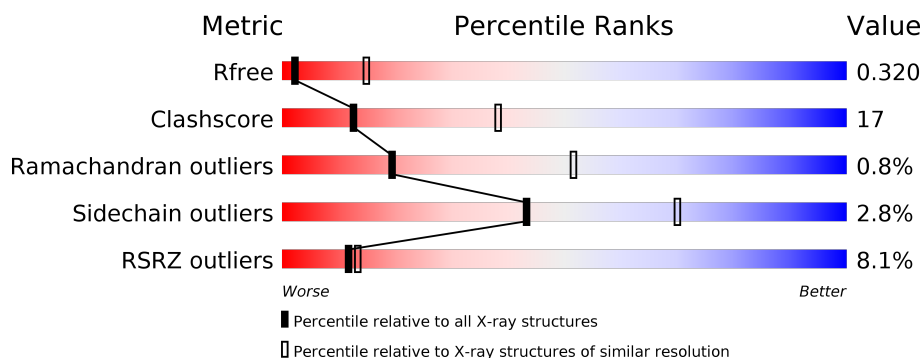
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.39 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	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

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 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	337	<div> <div>4%</div> <div>55%</div> <div>29%</div> <div>•</div> <div>13%</div> </div>
1	B	337	<div> <div>6%</div> <div>59%</div> <div>27%</div> <div>•</div> <div>12%</div> </div>
1	C	337	<div> <div>7%</div> <div>57%</div> <div>29%</div> <div>•</div> <div>13%</div> </div>
1	D	337	<div> <div>6%</div> <div>60%</div> <div>26%</div> <div>•</div> <div>13%</div> </div>
1	E	337	<div> <div>10%</div> <div>61%</div> <div>26%</div> <div>•</div> <div>12%</div> </div>
1	F	337	<div> <div>8%</div> <div>62%</div> <div>24%</div> <div>•</div> <div>13%</div> </div>

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Mol	Chain	Length	Quality of chain
1	G	337	<div><div></div><div>9%</div><div>66%</div><div>20%</div><div>•</div><div>12%</div></div>
1	H	337	<div><div></div><div>7%</div><div>61%</div><div>25%</div><div>•</div><div>13%</div></div>

2 Entry composition

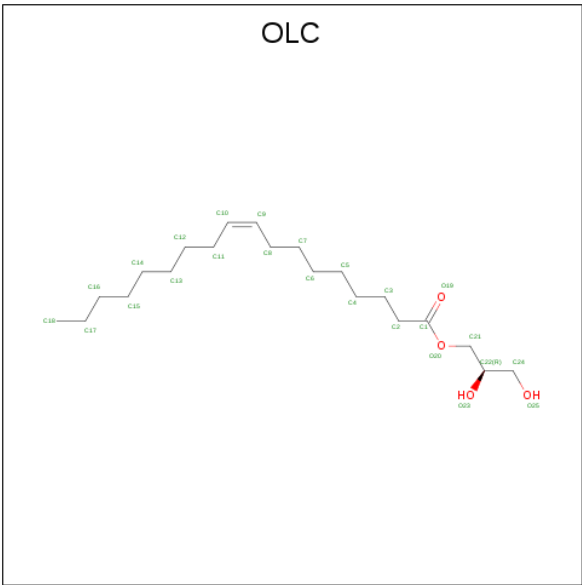
There are 5 unique types of molecules in this entry. The entry contains 18667 atoms, of which 42 are hydrogens and 0 are deuteriums.

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 GDP-mannose transporter 1.

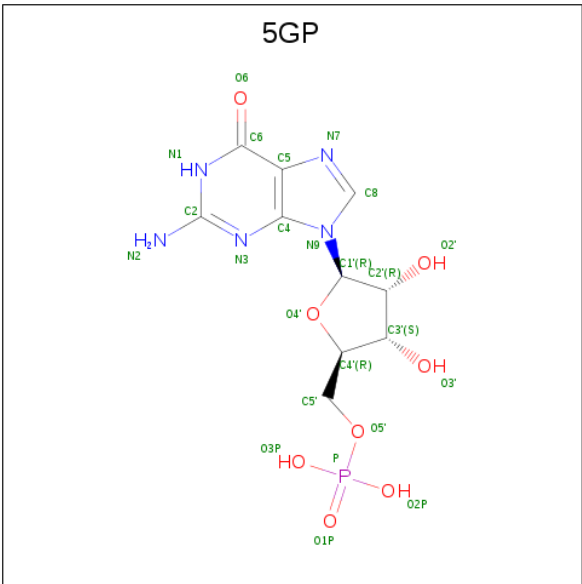
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	292	Total	C	N	O	S	0	0	0
			2291	1516	355	403	17			
1	B	297	Total	C	N	O	S	0	0	0
			2325	1539	360	409	17			
1	C	294	Total	C	N	O	S	0	0	0
			2307	1528	357	405	17			
1	D	294	Total	C	N	O	S	0	0	0
			2307	1528	357	405	17			
1	E	298	Total	C	N	O	S	0	0	0
			2330	1542	361	410	17			
1	F	294	Total	C	N	O	S	0	0	0
			2307	1528	357	405	17			
1	G	296	Total	C	N	O	S	0	0	0
			2318	1534	359	408	17			
1	H	294	Total	C	N	O	S	0	0	0
			2307	1528	357	405	17			

- Molecule 2 is (2R)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (three-letter code: OLC) (formula: C₂₁H₄₀O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			25	21	4		
2	E	1	Total	C	O	0	0
			25	21	4		

- Molecule 3 is GUANOSINE-5'-MONOPHOSPHATE (three-letter code: 5GP) (formula: $C_{10}H_{14}N_5O_8P$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	C	1	Total	C	H	N	O	P	0	0
			38	10	14	5	8	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	D	1	Total	C	H	N	O	P	
			38	10	14	5	8	1	
3	E	1	Total	C	H	N	O	P	
			38	10	14	5	8	1	

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	1	Total	Na		
			1	1	0	0

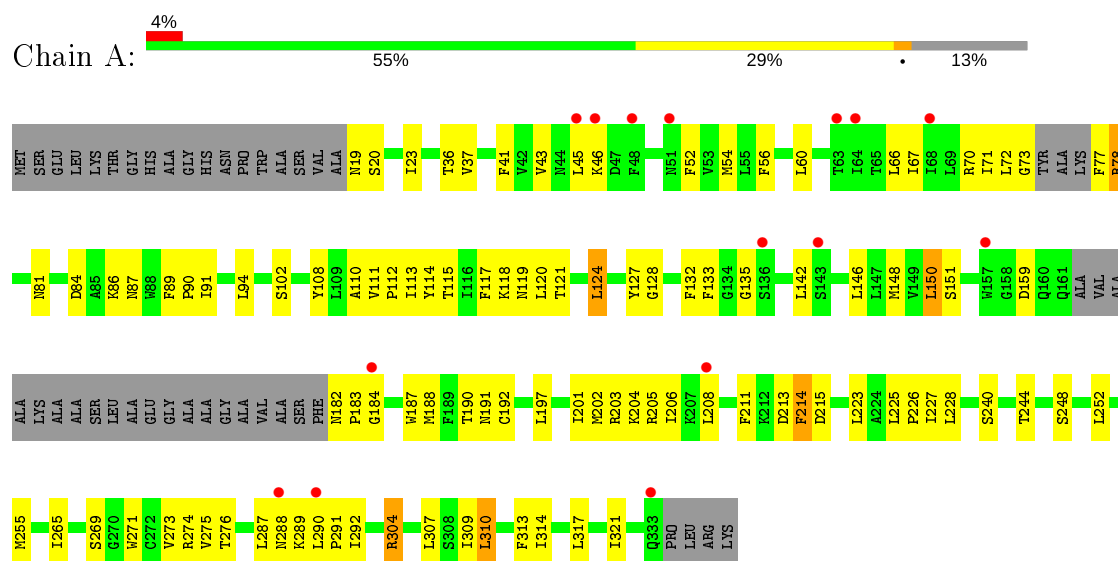
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	5	Total	O		
			5	5	0	0
5	D	2	Total	O		
			2	2	0	0
5	E	1	Total	O		
			1	1	0	0
5	F	1	Total	O		
			1	1	0	0
5	H	1	Total	O		
			1	1	0	0

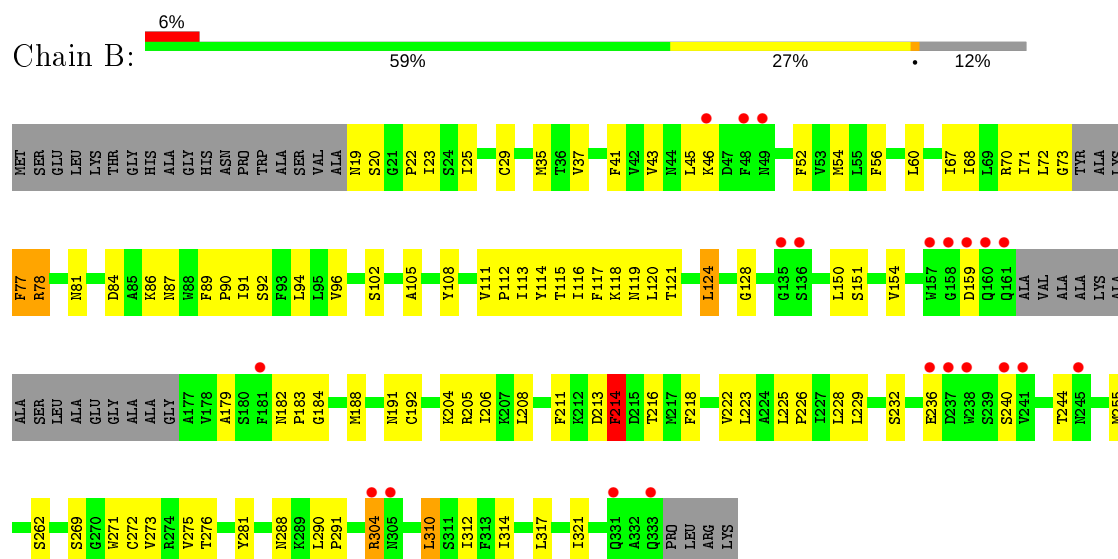
3 Residue-property plots [i](#)

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.

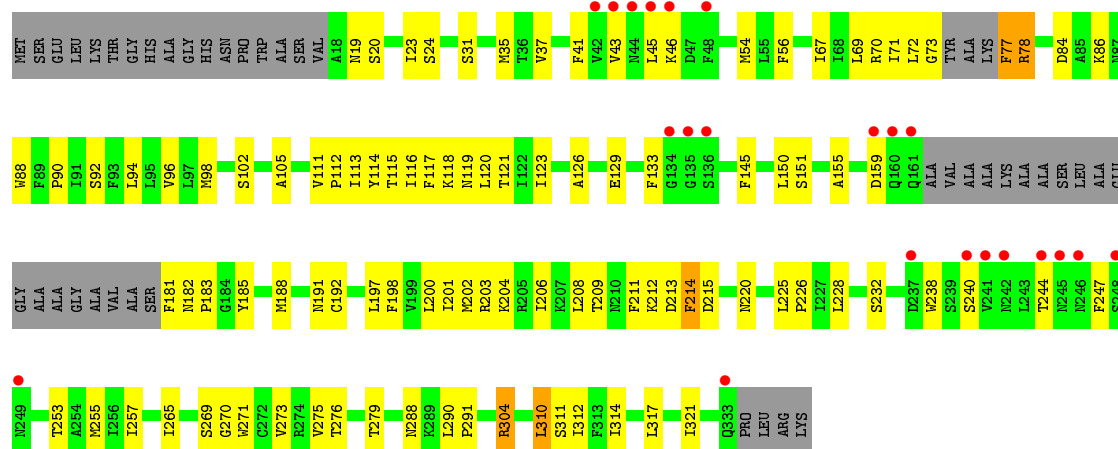
• Molecule 1: GDP-mannose transporter 1



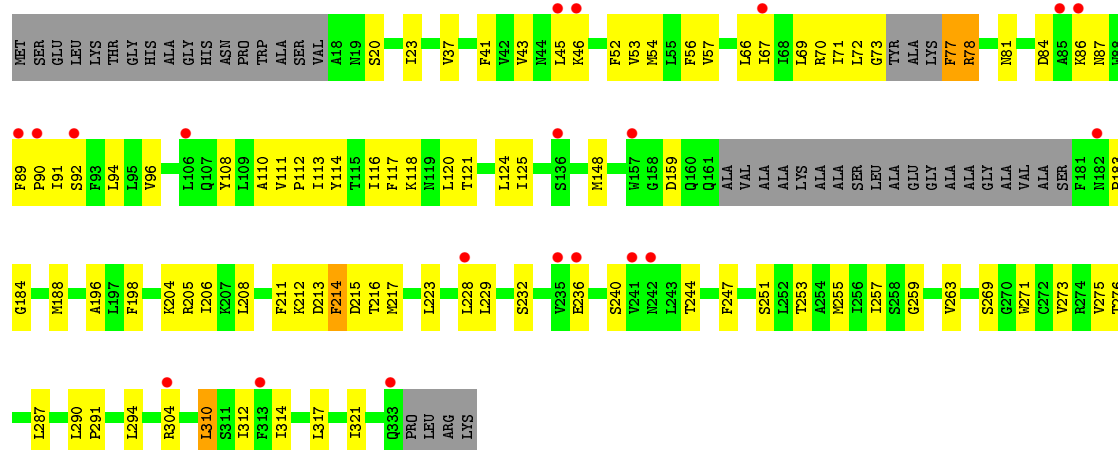
• Molecule 1: GDP-mannose transporter 1



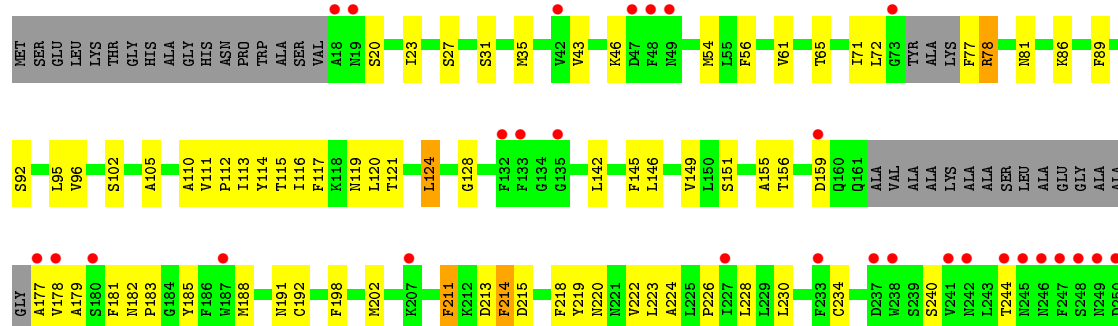
• Molecule 1: GDP-mannose transporter 1



• Molecule 1: GDP-mannose transporter 1

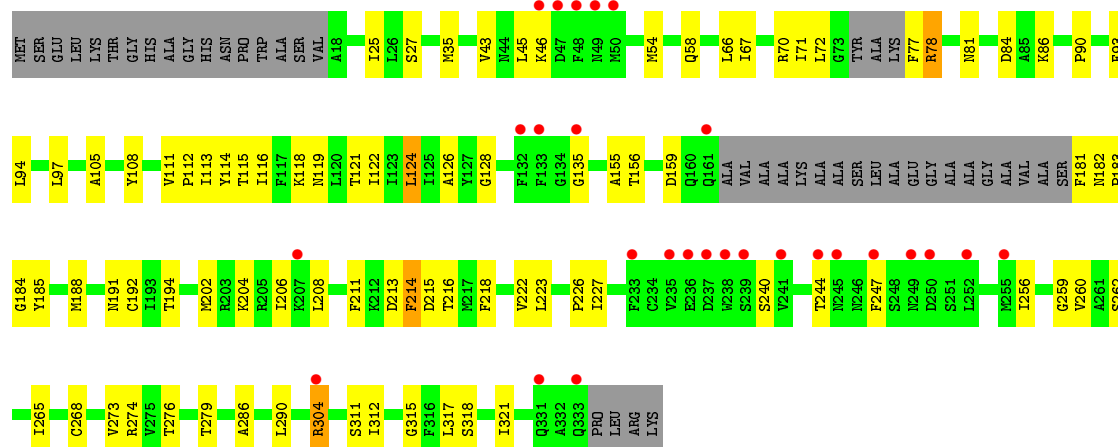


• Molecule 1: GDP-mannose transporter 1

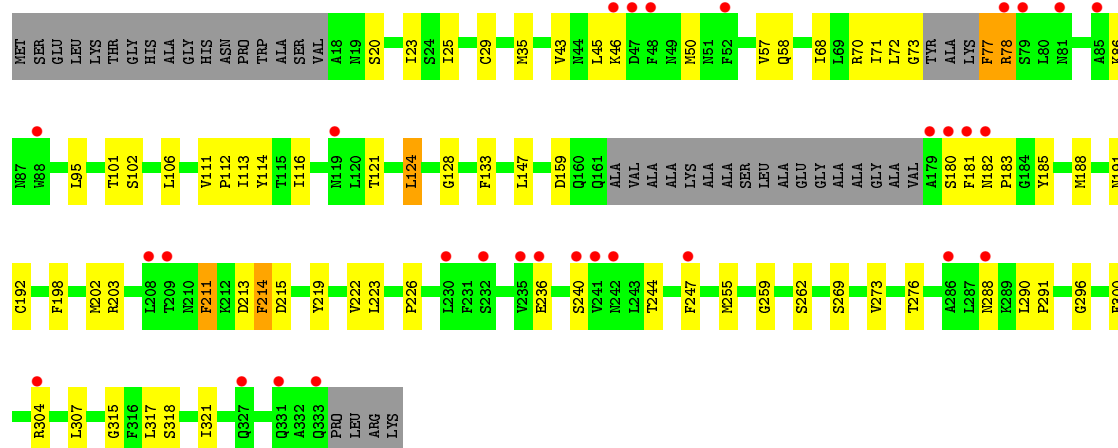




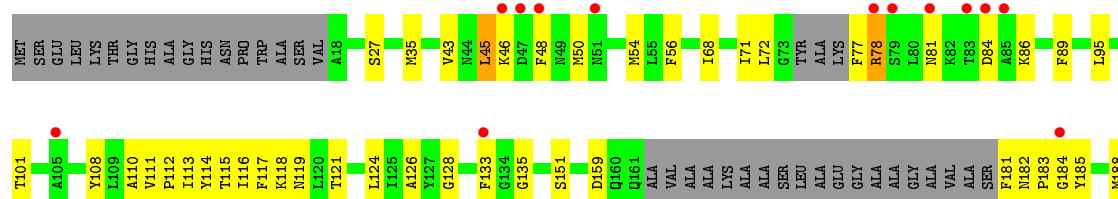
• Molecule 1: GDP-mannose transporter 1

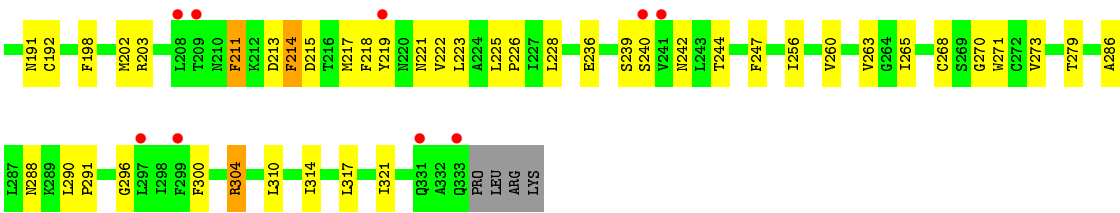


• Molecule 1: GDP-mannose transporter 1



• Molecule 1: GDP-mannose transporter 1





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	45.70 Å 102.72 Å 181.25 Å 89.93° 90.08° 90.19°	Depositor
Resolution (Å)	49.43 – 3.39 49.43 – 3.39	Depositor EDS
% Data completeness (in resolution range)	96.5 (49.43-3.39) 96.1 (49.43-3.39)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.36 (at 3.40 Å)	Xtriage
Refinement program	PHENIX (dev_3360: ???)	Depositor
R, R_{free}	0.253 , 0.320 0.255 , 0.320	Depositor DCC
R_{free} test set	2129 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	92.4	Xtriage
Anisotropy	0.084	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 38.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.349 for h,-k,-l 0.357 for -h,k,-l 0.349 for -h,-k,l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	18667	wwPDB-VP
Average B, all atoms (Å ²)	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.47% 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: 5GP, NA, OLC

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	0.54	0/2340	0.74	0/3174
1	B	0.57	0/2375	0.76	0/3222
1	C	0.56	0/2357	0.72	0/3197
1	D	0.56	0/2357	0.74	0/3197
1	E	0.55	0/2380	0.74	0/3229
1	F	0.57	0/2357	0.73	0/3197
1	G	0.54	0/2368	0.72	0/3212
1	H	0.56	0/2357	0.74	0/3197
All	All	0.56	0/18891	0.74	0/25625

There are no bond length outliers.

There are no bond angle outliers.

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	2291	0	2366	82	0
1	B	2325	0	2399	75	0
1	C	2307	0	2380	88	0
1	D	2307	0	2379	69	0
1	E	2330	0	2404	94	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	2307	0	2380	74	0
1	G	2318	0	2390	71	0
1	H	2307	0	2380	78	0
2	A	25	0	40	2	0
2	E	25	0	40	1	0
3	C	24	14	12	3	0
3	D	24	14	12	0	0
3	E	24	14	12	3	0
4	D	1	0	0	0	0
5	C	5	0	0	1	0
5	D	2	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
5	H	1	0	0	0	0
All	All	18625	42	19194	631	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 17.

All (631) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:114:TYR:CE1	1:E:188:MET:HE1	1.82	1.14
1:E:121:THR:HA	1:E:124:LEU:HD21	1.28	1.14
1:D:232:SER:HA	1:D:236:GLU:OE1	1.45	1.13
1:G:121:THR:HA	1:G:124:LEU:HD21	1.33	1.05
1:B:232:SER:HA	1:B:236:GLU:OE1	1.61	0.99
1:C:105:ALA:CB	1:C:188:MET:HE2	1.92	0.97
1:E:114:TYR:CD1	1:E:188:MET:CE	2.49	0.95
1:E:114:TYR:HE1	1:E:188:MET:HE1	1.27	0.95
1:D:310:LEU:HD22	1:D:314:ILE:HD11	1.48	0.94
1:G:50:MET:HG2	1:G:236:GLU:HG2	1.49	0.94
1:C:114:TYR:CE1	1:C:188:MET:HE1	2.04	0.91
1:F:121:THR:HA	1:F:124:LEU:HD21	1.53	0.91
1:B:310:LEU:HD22	1:B:314:ILE:HD11	1.51	0.90
1:E:114:TYR:HD1	1:E:188:MET:HE3	1.35	0.89
1:H:71:ILE:HG13	1:H:72:LEU:HD22	1.55	0.89
1:E:121:THR:HA	1:E:124:LEU:CD2	2.01	0.89
1:D:232:SER:CA	1:D:236:GLU:OE1	2.22	0.87
1:E:105:ALA:CB	1:E:188:MET:HE2	2.05	0.86
1:C:114:TYR:HD1	1:C:188:MET:CE	1.88	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:70:ARG:NH1	1:C:78:ARG:HH21	1.74	0.86
1:C:114:TYR:CD1	1:C:188:MET:CE	2.59	0.85
1:A:89:PHE:HD1	1:A:223:LEU:HD23	1.39	0.85
1:E:114:TYR:CD1	1:E:188:MET:HE1	2.12	0.84
1:H:71:ILE:O	1:H:72:LEU:HD13	1.77	0.84
1:E:114:TYR:HD1	1:E:188:MET:CE	1.88	0.84
1:C:114:TYR:CD1	1:C:188:MET:HE1	2.13	0.84
1:B:121:THR:HA	1:B:124:LEU:CD2	2.08	0.84
1:G:181:PHE:HB3	1:G:185:TYR:HE2	1.43	0.84
1:A:20:SER:O	1:A:23:ILE:HD12	1.77	0.84
1:C:71:ILE:O	1:C:72:LEU:HD22	1.80	0.82
1:G:121:THR:HA	1:G:124:LEU:CD2	2.09	0.82
1:G:71:ILE:HG13	1:G:72:LEU:HD22	1.61	0.82
1:F:121:THR:HA	1:F:124:LEU:CD2	2.10	0.81
3:C:401:5GP:N3	3:C:401:5GP:H2'	1.95	0.81
1:H:202:MET:CE	1:H:273:VAL:HG21	2.11	0.81
1:D:124:LEU:HD11	1:D:196:ALA:HB2	1.61	0.80
1:A:114:TYR:OH	1:A:118:LYS:HE3	1.82	0.80
1:A:71:ILE:O	1:A:72:LEU:HD22	1.82	0.80
1:C:105:ALA:CB	1:C:188:MET:CE	2.60	0.80
1:C:114:TYR:HD1	1:C:188:MET:HE3	1.46	0.79
1:E:114:TYR:CE1	1:E:188:MET:CE	2.64	0.79
1:C:232:SER:HG	1:C:238:TRP:HZ2	1.32	0.78
2:A:401:OLC:H18A	1:E:310:LEU:HD11	1.65	0.78
1:B:90:PRO:O	1:B:94:LEU:HD23	1.84	0.78
1:C:20:SER:O	1:C:23:ILE:HD12	1.85	0.77
1:E:43:VAL:HG11	1:E:46:LYS:HD3	1.67	0.76
1:E:110:ALA:HB3	1:E:113:ILE:HD13	1.68	0.76
1:E:114:TYR:CD1	1:E:188:MET:HE3	2.16	0.76
1:D:70:ARG:CZ	1:D:78:ARG:HH21	1.99	0.76
1:A:73:GLY:HA3	1:A:77:PHE:CE1	2.20	0.75
1:B:121:THR:HA	1:B:124:LEU:HD21	1.66	0.75
1:D:46:LYS:HE3	1:D:54:MET:SD	2.26	0.75
1:H:202:MET:HE3	1:H:273:VAL:HG21	1.69	0.75
1:H:50:MET:HA	1:H:236:GLU:OE2	1.86	0.75
1:A:310:LEU:HD22	1:A:314:ILE:HD11	1.69	0.74
1:B:20:SER:O	1:B:23:ILE:HD12	1.87	0.74
1:C:105:ALA:HB1	1:C:188:MET:CE	2.18	0.74
1:D:71:ILE:O	1:D:72:LEU:HD22	1.88	0.73
1:D:20:SER:O	1:D:23:ILE:HD12	1.87	0.73
1:E:179:ALA:HA	1:E:182:ASN:OD1	1.89	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:317:LEU:HG	1:G:317:LEU:O	1.87	0.73
1:C:90:PRO:O	1:C:94:LEU:HD23	1.89	0.73
1:F:114:TYR:CD1	1:F:188:MET:HE1	2.23	0.73
1:E:95:LEU:HD12	1:E:198:PHE:CE1	2.23	0.72
1:E:240:SER:HA	1:E:244:THR:OG1	1.88	0.72
1:A:102:SER:HB2	1:A:191:ASN:ND2	2.05	0.71
1:D:70:ARG:NH1	1:D:78:ARG:HH21	1.89	0.71
1:G:181:PHE:HB3	1:G:185:TYR:CE2	2.25	0.71
3:C:401:5GP:O1P	3:C:401:5GP:H4'	1.89	0.71
1:C:269:SER:O	1:C:273:VAL:HG22	1.91	0.71
1:C:117:PHE:O	1:C:121:THR:HG23	1.90	0.70
1:C:105:ALA:HB1	1:C:188:MET:HE2	1.74	0.70
1:E:317:LEU:HG	1:E:317:LEU:O	1.91	0.70
1:F:114:TYR:CE1	1:F:188:MET:HE1	2.27	0.70
1:H:151:SER:HB2	1:H:314:ILE:HG22	1.72	0.70
1:E:105:ALA:CB	1:E:188:MET:CE	2.69	0.69
1:G:124:LEU:H	1:G:124:LEU:HD23	1.57	0.69
1:D:269:SER:O	1:D:273:VAL:HG22	1.92	0.69
1:F:218:PHE:CZ	1:F:222:VAL:HG21	2.26	0.69
1:F:317:LEU:O	1:F:321:ILE:HG12	1.93	0.69
1:F:112:PRO:HB2	1:F:156:THR:OG1	1.92	0.69
1:E:89:PHE:HD1	1:E:223:LEU:HD23	1.56	0.68
1:F:202:MET:CE	1:F:273:VAL:HG21	2.23	0.68
1:F:114:TYR:CD1	1:F:188:MET:CE	2.77	0.68
1:A:89:PHE:CD1	1:A:223:LEU:HD23	2.25	0.68
1:H:50:MET:CA	1:H:236:GLU:OE2	2.42	0.68
1:D:90:PRO:O	1:D:94:LEU:HD23	1.93	0.67
1:A:73:GLY:HA3	1:A:77:PHE:HE1	1.59	0.67
1:E:117:PHE:O	1:E:121:THR:HG23	1.94	0.67
1:D:113:ILE:HA	1:D:116:ILE:HD12	1.77	0.67
1:H:218:PHE:CZ	1:H:222:VAL:HG21	2.29	0.67
1:C:73:GLY:HA3	1:C:77:PHE:CE1	2.30	0.67
1:E:113:ILE:HD12	1:E:113:ILE:H	1.59	0.67
1:C:114:TYR:HE1	1:C:188:MET:HE1	1.55	0.66
1:E:145:PHE:O	1:E:149:VAL:HG23	1.96	0.66
1:C:35:MET:HB2	1:C:265:ILE:HD11	1.77	0.66
1:B:19:ASN:HB2	1:B:271:TRP:CZ2	2.30	0.66
1:F:78:ARG:HA	1:F:215:ASP:OD1	1.96	0.66
1:G:71:ILE:O	1:G:72:LEU:HD13	1.96	0.65
1:H:211:PHE:CD2	1:H:215:ASP:HB2	2.31	0.65
1:A:317:LEU:O	1:A:321:ILE:HG12	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:213:ASP:O	1:F:214:PHE:HB2	1.97	0.65
1:F:240:SER:HA	1:F:244:THR:OG1	1.96	0.65
1:A:182:ASN:N	1:A:183:PRO:HD2	2.11	0.65
1:C:204:LYS:HG3	1:C:208:LEU:HD12	1.79	0.64
1:F:181:PHE:HB3	1:F:185:TYR:HE2	1.63	0.64
1:G:95:LEU:HD12	1:G:198:PHE:CE1	2.33	0.64
1:H:240:SER:HA	1:H:244:THR:OG1	1.97	0.64
1:E:181:PHE:HB3	1:E:185:TYR:HE2	1.61	0.64
1:G:43:VAL:HG11	1:G:46:LYS:HD3	1.79	0.64
1:A:90:PRO:O	1:A:94:LEU:HD23	1.98	0.64
1:E:211:PHE:CD2	1:E:215:ASP:HB2	2.33	0.64
1:B:73:GLY:HA3	1:B:77:PHE:CZ	2.33	0.64
1:H:202:MET:HE1	1:H:273:VAL:HG21	1.79	0.64
1:B:73:GLY:HA3	1:B:77:PHE:CE1	2.33	0.64
1:A:70:ARG:NH1	1:A:78:ARG:HH21	1.96	0.64
1:A:70:ARG:HH11	1:A:78:ARG:HH21	1.44	0.64
1:B:86:LYS:O	1:B:86:LYS:HE3	1.98	0.64
1:G:113:ILE:HA	1:G:116:ILE:HD12	1.79	0.64
1:D:117:PHE:O	1:D:121:THR:HG23	1.98	0.63
1:A:269:SER:O	1:A:273:VAL:HG22	1.99	0.63
1:H:117:PHE:O	1:H:121:THR:HG23	1.99	0.63
1:B:37:VAL:HG13	1:B:41:PHE:CD1	2.33	0.62
1:A:304:ARG:H	1:A:304:ARG:HD3	1.64	0.62
1:C:70:ARG:CZ	1:C:78:ARG:HH21	2.11	0.62
1:E:105:ALA:HB1	1:E:188:MET:CE	2.29	0.62
1:A:70:ARG:CZ	1:A:78:ARG:HE	2.12	0.62
1:B:89:PHE:HD1	1:B:223:LEU:HD23	1.63	0.62
1:C:304:ARG:HE	1:H:300:PHE:HA	1.65	0.62
2:A:401:OLC:O23	1:E:328:LYS:NZ	2.33	0.62
1:H:35:MET:SD	1:H:265:ILE:HG12	2.40	0.62
1:A:108:TYR:CD1	1:A:183:PRO:HG2	2.35	0.62
1:B:232:SER:CA	1:B:236:GLU:OE1	2.44	0.62
1:B:46:LYS:HZ2	1:B:255:MET:HG3	1.63	0.62
1:B:310:LEU:HD22	1:B:314:ILE:CD1	2.28	0.62
1:C:114:TYR:OH	1:C:118:LYS:HE3	2.00	0.62
1:B:117:PHE:HA	1:B:120:LEU:HD12	1.82	0.61
1:E:121:THR:CG2	1:E:192:CYS:SG	2.88	0.61
1:D:310:LEU:HD22	1:D:314:ILE:CD1	2.26	0.61
1:B:70:ARG:NH1	1:B:78:ARG:HH21	1.97	0.61
1:B:114:TYR:HD1	1:B:188:MET:HE3	1.65	0.60
1:E:177:ALA:O	1:E:179:ALA:N	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:50:MET:HG2	1:G:236:GLU:CG	2.27	0.60
1:B:114:TYR:CD1	1:B:188:MET:HE3	2.36	0.60
1:E:35:MET:SD	1:E:265:ILE:HG12	2.40	0.60
1:A:81:ASN:ND2	1:A:84:ASP:OD2	2.34	0.60
1:B:240:SER:HA	1:B:244:THR:OG1	2.01	0.60
1:A:71:ILE:C	1:A:72:LEU:HD22	2.22	0.60
1:A:148:MET:HE3	1:A:287:LEU:HG	1.82	0.60
1:C:126:ALA:HB2	1:C:279:THR:HG21	1.83	0.60
1:E:223:LEU:O	1:E:226:PRO:HD2	2.01	0.60
1:H:89:PHE:HD1	1:H:223:LEU:HD23	1.67	0.60
1:F:71:ILE:O	1:F:72:LEU:HD22	2.03	0.59
1:G:240:SER:HA	1:G:244:THR:OG1	2.02	0.59
1:C:115:THR:HG22	1:C:119:ASN:ND2	2.17	0.59
1:D:114:TYR:OH	1:D:118:LYS:HE3	2.02	0.59
1:E:151:SER:HB2	1:E:314:ILE:HG22	1.83	0.59
1:H:43:VAL:HG11	1:H:46:LYS:HD3	1.83	0.59
1:H:71:ILE:HG13	1:H:72:LEU:CD2	2.31	0.59
1:B:71:ILE:C	1:B:72:LEU:HD22	2.23	0.59
1:C:71:ILE:C	1:C:72:LEU:HD22	2.22	0.59
1:C:304:ARG:H	1:C:304:ARG:HD3	1.68	0.59
1:F:213:ASP:O	1:F:214:PHE:CB	2.50	0.59
1:A:114:TYR:CD1	1:A:188:MET:HE3	2.38	0.58
1:D:317:LEU:O	1:D:321:ILE:HG12	2.03	0.58
1:A:127:TYR:OH	1:A:142:LEU:HD13	2.04	0.58
1:D:124:LEU:CD1	1:D:196:ALA:HB2	2.33	0.58
1:E:202:MET:CE	1:E:273:VAL:HG21	2.32	0.58
1:H:114:TYR:CE1	1:H:188:MET:HE1	2.39	0.58
1:F:181:PHE:HB3	1:F:185:TYR:CE2	2.38	0.58
1:C:105:ALA:HB2	1:C:188:MET:HE2	1.84	0.58
1:E:155:ALA:HB2	1:E:311:SER:CB	2.32	0.58
1:C:121:THR:CG2	1:C:192:CYS:SG	2.92	0.58
1:C:67:ILE:O	1:C:71:ILE:HG12	2.04	0.58
1:F:202:MET:HE1	1:F:273:VAL:HG21	1.85	0.58
1:G:114:TYR:CE1	1:G:188:MET:HE1	2.39	0.58
1:G:211:PHE:CD2	1:G:215:ASP:HB2	2.39	0.58
1:D:71:ILE:C	1:D:72:LEU:HD22	2.24	0.57
1:A:121:THR:HA	1:A:124:LEU:CD2	2.34	0.57
1:A:91:ILE:HD11	1:A:205:ARG:HG3	1.87	0.57
1:G:20:SER:O	1:G:23:ILE:HD12	2.05	0.57
1:G:180:SER:O	1:G:183:PRO:HD2	2.05	0.57
1:E:124:LEU:H	1:E:124:LEU:HD23	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:102:SER:HG	1:G:114:TYR:HH	1.53	0.57
1:D:110:ALA:HB3	1:D:113:ILE:HD12	1.87	0.57
1:D:54:MET:HG3	1:D:255:MET:HG2	1.87	0.57
1:F:35:MET:SD	1:F:265:ILE:HG12	2.44	0.57
1:H:223:LEU:O	1:H:226:PRO:HD2	2.04	0.56
1:A:46:LYS:HE3	1:A:54:MET:SD	2.44	0.56
1:F:202:MET:HE3	1:F:273:VAL:HG21	1.86	0.56
1:A:110:ALA:HB3	1:A:113:ILE:HD12	1.88	0.56
1:E:110:ALA:HB3	1:E:113:ILE:CD1	2.33	0.56
1:G:102:SER:HB2	1:G:191:ASN:HD21	1.69	0.56
1:B:304:ARG:HE	1:G:300:PHE:HA	1.71	0.56
1:C:43:VAL:HG11	1:C:46:LYS:HD3	1.88	0.56
1:F:124:LEU:O	1:F:128:GLY:N	2.39	0.56
1:D:117:PHE:HA	1:D:120:LEU:HD12	1.88	0.56
1:E:119:ASN:HD21	1:E:286:ALA:HB1	1.69	0.56
1:E:112:PRO:HG2	1:E:113:ILE:HD12	1.87	0.56
1:B:46:LYS:NZ	1:B:255:MET:HG3	2.21	0.55
1:E:43:VAL:CG1	1:E:46:LYS:HD3	2.36	0.55
1:C:317:LEU:O	1:C:321:ILE:HG12	2.07	0.55
1:C:105:ALA:HB1	1:C:188:MET:HE3	1.87	0.55
1:C:275:VAL:HG23	1:C:276:THR:HG23	1.88	0.55
1:C:71:ILE:HA	1:F:240:SER:HB3	1.89	0.55
1:H:68:ILE:O	1:H:72:LEU:CD2	2.55	0.55
1:A:111:VAL:N	1:A:112:PRO:HD2	2.22	0.55
1:A:117:PHE:HA	1:A:120:LEU:HD12	1.89	0.55
1:A:87:ASN:HB3	1:A:205:ARG:CZ	2.35	0.55
1:C:111:VAL:N	1:C:112:PRO:HD2	2.21	0.55
1:F:35:MET:CE	1:F:262:SER:HB3	2.37	0.55
1:F:67:ILE:HG13	1:F:78:ARG:HH12	1.71	0.55
1:B:70:ARG:CZ	1:B:78:ARG:HH21	2.20	0.55
1:D:124:LEU:HD12	1:D:125:ILE:N	2.22	0.55
1:E:124:LEU:O	1:E:128:GLY:N	2.40	0.55
1:F:206:ILE:HG12	1:F:216:THR:HG22	1.89	0.55
1:H:27:SER:HB3	1:H:268:CYS:SG	2.46	0.55
1:B:43:VAL:HG11	1:B:46:LYS:HD3	1.88	0.54
1:E:179:ALA:O	1:E:183:PRO:HD3	2.07	0.54
1:F:70:ARG:CZ	1:F:78:ARG:HH21	2.20	0.54
1:H:114:TYR:CD1	1:H:188:MET:HE3	2.41	0.54
1:B:121:THR:HA	1:B:124:LEU:HD23	1.84	0.54
1:D:275:VAL:HG23	1:D:276:THR:HG23	1.89	0.54
1:B:150:LEU:O	1:B:154:VAL:HG23	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:121:THR:HG22	1:C:192:CYS:SG	2.47	0.54
1:A:36:THR:HG21	1:A:292:ILE:HD13	1.90	0.54
1:E:218:PHE:CZ	1:E:222:VAL:HG21	2.42	0.54
1:E:220:ASN:O	1:E:224:ALA:HB2	2.06	0.54
1:E:46:LYS:HE3	1:E:54:MET:SD	2.47	0.54
1:G:202:MET:CE	1:G:273:VAL:HG21	2.38	0.54
1:H:114:TYR:HD1	1:H:188:MET:HE3	1.73	0.54
1:A:43:VAL:HG11	1:A:46:LYS:HD3	1.90	0.54
1:C:118:LYS:HE2	1:C:191:ASN:OD1	2.08	0.54
1:D:111:VAL:N	1:D:112:PRO:HD2	2.22	0.53
1:F:256:ILE:O	1:F:260:VAL:HG23	2.08	0.53
1:D:87:ASN:HB3	1:D:205:ARG:CZ	2.37	0.53
1:E:181:PHE:HB3	1:E:185:TYR:CE2	2.42	0.53
1:D:290:LEU:HB2	1:D:291:PRO:HD3	1.90	0.53
1:E:256:ILE:O	1:E:260:VAL:HG23	2.08	0.53
1:G:111:VAL:N	1:G:112:PRO:HD2	2.24	0.53
1:A:225:LEU:HB2	1:A:226:PRO:HD3	1.91	0.53
1:A:275:VAL:HG23	1:A:276:THR:HG23	1.91	0.53
1:B:114:TYR:CD1	1:B:188:MET:CE	2.92	0.53
1:E:105:ALA:HB1	1:E:188:MET:HG2	1.90	0.53
1:G:57:VAL:HG21	1:G:255:MET:CE	2.38	0.53
1:H:181:PHE:HD2	1:H:185:TYR:HE2	1.56	0.53
1:B:91:ILE:HD11	1:B:205:ARG:HG3	1.91	0.53
1:E:202:MET:HE3	1:E:273:VAL:HG21	1.89	0.53
1:E:218:PHE:CE1	1:E:222:VAL:HG21	2.44	0.53
1:H:111:VAL:N	1:H:112:PRO:HD2	2.24	0.53
1:H:213:ASP:O	1:H:214:PHE:HB2	2.09	0.53
1:B:115:THR:HG22	1:B:119:ASN:ND2	2.24	0.53
1:B:275:VAL:HG23	1:B:276:THR:HG23	1.90	0.53
1:H:95:LEU:HD12	1:H:198:PHE:CE1	2.43	0.53
1:E:317:LEU:O	1:E:321:ILE:HG12	2.08	0.52
1:H:68:ILE:O	1:H:72:LEU:HD23	2.08	0.52
1:F:111:VAL:N	1:F:112:PRO:HD2	2.24	0.52
1:H:48:PHE:HZ	1:H:247:PHE:HB3	1.74	0.52
1:H:239:SER:OG	1:H:242:ASN:HB2	2.08	0.52
1:B:111:VAL:N	1:B:112:PRO:HD2	2.24	0.52
1:H:217:MET:CE	1:H:263:VAL:HG13	2.38	0.52
1:E:102:SER:HB2	1:E:191:ASN:HD21	1.74	0.52
1:H:121:THR:CG2	1:H:192:CYS:SG	2.98	0.52
1:H:256:ILE:O	1:H:260:VAL:HG23	2.09	0.52
1:A:54:MET:HG3	1:A:255:MET:HG2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:37:VAL:HG13	1:D:41:PHE:CD1	2.45	0.52
1:E:112:PRO:HB2	1:E:156:THR:OG1	2.10	0.52
1:G:124:LEU:O	1:G:128:GLY:N	2.42	0.52
1:A:248:SER:O	1:A:252:LEU:HD12	2.09	0.52
1:F:155:ALA:HB2	1:F:311:SER:CB	2.39	0.52
1:G:71:ILE:HG13	1:G:72:LEU:CD2	2.36	0.52
1:G:102:SER:O	1:G:106:LEU:HD12	2.10	0.51
1:E:78:ARG:HA	1:E:215:ASP:OD1	2.09	0.51
1:F:223:LEU:O	1:F:226:PRO:HD2	2.11	0.51
1:F:90:PRO:O	1:F:94:LEU:HD23	2.10	0.51
1:A:19:ASN:HB2	1:A:271:TRP:CZ2	2.45	0.51
1:E:105:ALA:HB3	1:E:188:MET:HE2	1.88	0.51
1:E:89:PHE:CD1	1:E:223:LEU:HD23	2.43	0.51
1:H:78:ARG:HA	1:H:215:ASP:OD1	2.10	0.51
1:C:113:ILE:HA	1:C:116:ILE:HD12	1.91	0.51
1:C:290:LEU:HD22	1:C:312:ILE:HA	1.92	0.51
1:D:56:PHE:CE1	1:D:229:LEU:HD11	2.46	0.51
1:C:94:LEU:HB3	1:C:198:PHE:HB2	1.92	0.51
1:C:213:ASP:OD2	1:C:271:TRP:CD1	2.64	0.51
1:D:204:LYS:HG3	1:D:208:LEU:HD12	1.91	0.51
1:E:111:VAL:N	1:E:112:PRO:HD2	2.25	0.51
1:A:151:SER:HB2	1:A:314:ILE:HG22	1.93	0.51
1:G:25:ILE:HD11	1:G:276:THR:HG21	1.93	0.51
1:A:108:TYR:HB2	1:A:184:GLY:HA3	1.93	0.51
1:A:89:PHE:CZ	1:A:227:ILE:HD11	2.46	0.51
1:G:68:ILE:O	1:G:72:LEU:HD23	2.10	0.51
1:A:202:MET:O	1:A:206:ILE:HG13	2.11	0.51
1:B:204:LYS:HG3	1:B:208:LEU:HD12	1.93	0.51
1:B:71:ILE:O	1:B:72:LEU:HD22	2.11	0.51
1:A:310:LEU:HD22	1:A:314:ILE:CD1	2.40	0.50
1:B:105:ALA:HB1	1:B:188:MET:HG2	1.92	0.50
1:B:67:ILE:HG13	1:B:78:ARG:HH12	1.76	0.50
1:E:61:VAL:O	1:E:65:THR:OG1	2.24	0.50
1:A:213:ASP:O	1:A:214:PHE:HB2	2.11	0.50
1:F:211:PHE:CD2	1:F:215:ASP:HB2	2.46	0.50
1:F:46:LYS:HE3	1:F:54:MET:SD	2.51	0.50
1:H:304:ARG:H	1:H:304:ARG:HD3	1.75	0.50
1:A:117:PHE:O	1:A:121:THR:HG23	2.12	0.50
1:F:113:ILE:HA	1:F:116:ILE:HD12	1.94	0.50
1:A:187:TRP:HA	1:A:190:THR:OG1	2.12	0.50
1:D:148:MET:HE3	1:D:287:LEU:HG	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:114:TYR:HD1	1:F:188:MET:HE3	1.75	0.50
1:H:126:ALA:HA	1:H:279:THR:OG1	2.12	0.50
1:H:217:MET:HE3	1:H:263:VAL:HG13	1.93	0.50
1:C:70:ARG:NH1	1:C:78:ARG:NH2	2.54	0.50
1:F:25:ILE:HD11	1:F:276:THR:HG21	1.94	0.50
1:F:317:LEU:O	1:F:317:LEU:HG	2.10	0.50
1:D:271:TRP:O	1:D:275:VAL:HG22	2.12	0.50
1:F:126:ALA:HB2	1:F:279:THR:HG21	1.94	0.50
1:A:114:TYR:CE2	1:A:118:LYS:HG3	2.47	0.50
1:A:37:VAL:HG13	1:A:41:PHE:CD1	2.47	0.49
1:D:294:LEU:O	1:D:294:LEU:HG	2.11	0.49
1:D:70:ARG:HD2	1:D:78:ARG:NH2	2.26	0.49
1:F:97:LEU:HD23	1:F:194:THR:HG21	1.93	0.49
1:F:27:SER:HB3	1:F:268:CYS:SG	2.52	0.49
1:E:121:THR:HG22	1:E:192:CYS:SG	2.52	0.49
1:D:259:GLY:O	1:D:263:VAL:HG23	2.11	0.49
1:G:147:LEU:HD13	1:G:317:LEU:HD23	1.95	0.49
1:H:222:VAL:O	1:H:226:PRO:HD3	2.12	0.49
1:D:91:ILE:HD11	1:D:205:ARG:HG3	1.93	0.49
1:H:50:MET:HG2	1:H:236:GLU:OE1	2.12	0.49
1:D:73:GLY:HA3	1:D:77:PHE:CE1	2.48	0.49
1:F:114:TYR:CE1	1:F:188:MET:CE	2.96	0.49
1:A:81:ASN:HB2	1:A:84:ASP:HB2	1.95	0.49
1:B:121:THR:CG2	1:B:192:CYS:SG	3.01	0.49
1:C:232:SER:OG	1:C:238:TRP:HZ2	1.94	0.49
1:B:113:ILE:HA	1:B:116:ILE:HD12	1.95	0.49
1:G:35:MET:CE	1:G:262:SER:HB3	2.42	0.49
1:H:50:MET:HG2	1:H:236:GLU:CD	2.32	0.49
1:E:142:LEU:HD11	2:E:402:OLC:H2A	1.95	0.48
1:F:119:ASN:HD21	1:F:286:ALA:HB1	1.76	0.48
1:A:213:ASP:O	1:A:214:PHE:CB	2.60	0.48
1:B:71:ILE:HG13	1:B:72:LEU:CD2	2.43	0.48
1:E:294:LEU:O	1:E:294:LEU:HG	2.13	0.48
1:H:288:ASN:O	1:H:291:PRO:HD2	2.13	0.48
1:A:121:THR:HA	1:A:124:LEU:HD21	1.94	0.48
1:C:155:ALA:HB2	1:C:311:SER:CB	2.42	0.48
1:D:114:TYR:CD1	1:D:188:MET:HE3	2.48	0.48
1:C:225:LEU:HB2	1:C:226:PRO:HD3	1.95	0.48
1:F:35:MET:HE1	1:F:262:SER:HB3	1.95	0.48
1:G:35:MET:HE3	1:G:262:SER:HB3	1.95	0.48
1:E:78:ARG:NH1	1:E:218:PHE:CE1	2.81	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:43:VAL:CG1	1:G:46:LYS:HD3	2.44	0.48
1:C:92:SER:O	1:C:96:VAL:HG23	2.13	0.48
1:E:265:ILE:HD12	1:E:266:SER:N	2.29	0.48
1:H:213:ASP:O	1:H:214:PHE:CB	2.61	0.48
1:A:197:LEU:O	1:A:201:ILE:HD12	2.13	0.48
1:C:54:MET:HG3	1:C:255:MET:HG2	1.96	0.48
1:D:56:PHE:HA	1:D:228:LEU:HD13	1.96	0.48
1:D:92:SER:O	1:D:96:VAL:HG23	2.13	0.48
1:E:27:SER:HB3	1:E:268:CYS:SG	2.54	0.48
1:H:43:VAL:CG1	1:H:46:LYS:HD3	2.44	0.48
1:B:56:PHE:O	1:B:60:LEU:HB2	2.14	0.48
1:D:124:LEU:HD12	1:D:124:LEU:C	2.34	0.48
1:E:304:ARG:HD3	1:E:304:ARG:H	1.79	0.48
1:G:114:TYR:CD1	1:G:188:MET:CE	2.97	0.48
1:C:288:ASN:O	1:C:291:PRO:HD2	2.14	0.48
3:C:401:5GP:C2'	3:C:401:5GP:N3	2.73	0.48
1:C:37:VAL:HG13	1:C:41:PHE:CD1	2.49	0.48
1:E:56:PHE:HA	1:E:228:LEU:HD13	1.96	0.48
1:G:114:TYR:CD1	1:G:188:MET:HE1	2.49	0.48
1:B:108:TYR:HB2	1:B:184:GLY:CA	2.44	0.48
1:C:151:SER:HB2	1:C:314:ILE:HG22	1.95	0.48
1:E:269:SER:OG	3:E:401:5GP:N2	2.46	0.48
1:B:114:TYR:OH	1:B:118:LYS:HE3	2.13	0.47
1:G:147:LEU:CD1	1:G:317:LEU:HD23	2.44	0.47
1:A:66:LEU:HD21	1:A:214:PHE:HD1	1.79	0.47
1:A:289:LYS:HD2	1:A:289:LYS:HA	1.68	0.47
1:C:133:PHE:CZ	1:C:203:ARG:HG3	2.48	0.47
1:C:54:MET:HA	1:C:255:MET:HE2	1.96	0.47
1:E:105:ALA:HB3	1:E:188:MET:CE	2.43	0.47
1:F:121:THR:CG2	1:F:192:CYS:SG	3.02	0.47
1:F:304:ARG:H	1:F:304:ARG:HD3	1.79	0.47
1:F:315:GLY:O	1:F:318:SER:HB3	2.15	0.47
1:A:240:SER:HA	1:A:244:THR:OG1	2.15	0.47
1:C:240:SER:HA	1:C:244:THR:OG1	2.15	0.47
1:D:232:SER:CB	1:D:236:GLU:OE1	2.62	0.47
1:F:43:VAL:HG11	1:F:46:LYS:HD3	1.95	0.47
1:G:57:VAL:HG21	1:G:255:MET:HE2	1.97	0.47
1:D:81:ASN:HB2	1:D:84:ASP:HB2	1.97	0.47
1:F:108:TYR:HB2	1:F:184:GLY:HA3	1.96	0.47
1:G:315:GLY:O	1:G:318:SER:HB3	2.14	0.47
1:H:181:PHE:HD2	1:H:185:TYR:CE2	2.31	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:50:MET:HB3	1:H:236:GLU:OE1	2.14	0.47
1:B:290:LEU:HD22	1:B:312:ILE:HA	1.96	0.47
1:F:240:SER:O	1:F:244:THR:HB	2.14	0.47
1:H:182:ASN:N	1:H:183:PRO:HD2	2.30	0.47
1:H:81:ASN:HB2	1:H:84:ASP:HB2	1.96	0.47
1:B:68:ILE:O	1:B:72:LEU:HD23	2.15	0.47
1:C:213:ASP:O	1:C:214:PHE:CB	2.62	0.47
1:G:213:ASP:O	1:G:214:PHE:CB	2.62	0.47
1:F:118:LYS:HE2	1:F:191:ASN:HD21	1.80	0.47
1:A:67:ILE:O	1:A:71:ILE:HG12	2.15	0.47
1:B:225:LEU:HB2	1:B:226:PRO:HD3	1.96	0.47
1:C:197:LEU:O	1:C:201:ILE:HD12	2.14	0.47
1:A:288:ASN:O	1:A:291:PRO:HD2	2.15	0.46
1:B:179:ALA:HA	1:B:182:ASN:OD1	2.15	0.46
1:D:69:LEU:HB3	1:D:77:PHE:HE2	1.80	0.46
1:G:288:ASN:O	1:G:291:PRO:HD2	2.15	0.46
1:C:56:PHE:HA	1:C:228:LEU:HD13	1.97	0.46
1:F:218:PHE:CE1	1:F:222:VAL:HG21	2.51	0.46
1:A:110:ALA:HB1	1:A:112:PRO:HD2	1.97	0.46
1:B:218:PHE:CE1	1:B:222:VAL:HG21	2.50	0.46
1:D:108:TYR:CD1	1:D:183:PRO:HG2	2.50	0.46
1:G:102:SER:OG	1:G:114:TYR:OH	2.28	0.46
1:A:114:TYR:HD1	1:A:188:MET:HE3	1.80	0.46
1:C:126:ALA:HB2	1:C:279:THR:CG2	2.45	0.46
1:C:72:LEU:HA	1:C:72:LEU:HD13	1.78	0.46
1:G:202:MET:HE3	1:G:273:VAL:HG21	1.97	0.46
1:B:102:SER:HB2	1:B:191:ASN:ND2	2.30	0.46
1:C:105:ALA:HB3	1:C:188:MET:CE	2.45	0.46
1:D:46:LYS:NZ	1:D:255:MET:HG3	2.30	0.46
1:G:211:PHE:CD2	1:G:215:ASP:CB	2.98	0.46
1:H:114:TYR:CE1	1:H:188:MET:CE	2.99	0.46
1:H:46:LYS:HE3	1:H:54:MET:SD	2.56	0.46
1:E:240:SER:O	1:E:244:THR:HB	2.15	0.46
1:B:115:THR:HG22	1:B:119:ASN:HD21	1.81	0.46
1:B:269:SER:O	1:B:273:VAL:HG22	2.15	0.46
1:E:290:LEU:HB2	1:E:291:PRO:HD3	1.97	0.46
1:H:270:GLY:HA2	1:H:273:VAL:HG22	1.98	0.46
1:E:213:ASP:O	1:E:214:PHE:CB	2.63	0.46
1:G:102:SER:HB2	1:G:191:ASN:ND2	2.31	0.46
1:G:247:PHE:CG	1:G:247:PHE:O	2.69	0.46
1:D:69:LEU:O	1:D:77:PHE:CE2	2.69	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:113:ILE:HD12	1:E:113:ILE:N	2.28	0.46
1:E:230:LEU:O	1:E:234:CYS:SG	2.74	0.46
1:F:93:PHE:HA	1:F:227:ILE:HD13	1.98	0.46
1:G:307:LEU:HD22	1:G:307:LEU:N	2.31	0.46
1:A:118:LYS:HE2	1:A:191:ASN:OD1	2.17	0.45
1:C:202:MET:O	1:C:206:ILE:HG13	2.16	0.45
1:A:150:LEU:HD23	1:A:150:LEU:HA	1.64	0.45
1:F:181:PHE:HD2	1:F:185:TYR:CE2	2.34	0.45
1:F:211:PHE:HB3	1:F:216:THR:HG23	1.97	0.45
1:G:213:ASP:O	1:G:214:PHE:HB2	2.16	0.45
1:F:204:LYS:HG3	1:F:208:LEU:HD12	1.98	0.45
1:G:269:SER:O	1:G:273:VAL:HG22	2.16	0.45
1:G:290:LEU:HB2	1:G:291:PRO:HD3	1.98	0.45
1:H:290:LEU:HB2	1:H:291:PRO:HD3	1.98	0.45
1:A:108:TYR:HB2	1:A:184:GLY:CA	2.46	0.45
1:C:213:ASP:O	1:C:214:PHE:HB2	2.16	0.45
1:E:105:ALA:HB1	1:E:188:MET:HE3	1.97	0.45
1:H:114:TYR:OH	1:H:118:LYS:HE3	2.16	0.45
1:H:221:ASN:O	1:H:225:LEU:HG	2.16	0.45
1:A:56:PHE:HA	1:A:228:LEU:HD13	1.98	0.45
1:A:78:ARG:HA	1:A:215:ASP:OD1	2.17	0.45
1:E:202:MET:HE2	1:E:273:VAL:HG21	1.97	0.45
1:H:121:THR:HG22	1:H:192:CYS:SG	2.56	0.45
1:D:81:ASN:ND2	1:D:84:ASP:OD2	2.49	0.45
1:H:181:PHE:CD2	1:H:185:TYR:HE2	2.35	0.45
1:B:56:PHE:CZ	1:B:229:LEU:HD11	2.52	0.45
1:D:124:LEU:CD1	1:D:196:ALA:CB	2.94	0.45
1:D:240:SER:HA	1:D:244:THR:OG1	2.17	0.45
1:D:43:VAL:HG11	1:D:46:LYS:HD3	1.99	0.45
1:D:89:PHE:HD1	1:D:223:LEU:HD23	1.82	0.45
1:H:108:TYR:HB2	1:H:184:GLY:HA3	1.97	0.45
1:C:84:ASP:OD1	1:C:209:THR:HG21	2.16	0.45
1:H:101:THR:HB	1:H:191:ASN:HB2	1.97	0.45
1:H:81:ASN:ND2	1:H:84:ASP:OD2	2.50	0.45
1:A:148:MET:HE1	1:A:287:LEU:CD2	2.47	0.45
1:B:68:ILE:O	1:B:71:ILE:HG13	2.17	0.45
1:C:253:THR:HG22	1:C:257:ILE:HD11	1.99	0.45
1:F:290:LEU:HD22	1:F:312:ILE:HA	1.99	0.45
1:G:296:GLY:HA2	1:G:300:PHE:HD2	1.81	0.45
1:H:211:PHE:CD2	1:H:215:ASP:CB	3.00	0.45
1:B:317:LEU:O	1:B:321:ILE:HG12	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:35:MET:HE3	1:B:262:SER:HB3	1.98	0.44
1:B:71:ILE:HG13	1:B:72:LEU:HD22	1.99	0.44
1:H:56:PHE:HA	1:H:228:LEU:HD13	2.00	0.44
1:F:181:PHE:HD2	1:F:185:TYR:HH	1.65	0.44
1:A:124:LEU:O	1:A:128:GLY:N	2.47	0.44
1:F:182:ASN:N	1:F:183:PRO:HD2	2.32	0.44
1:A:309:ILE:CG2	1:A:313:PHE:HE2	2.31	0.44
1:B:37:VAL:HG13	1:B:41:PHE:HD1	1.81	0.44
1:C:69:LEU:O	1:C:77:PHE:CE2	2.71	0.44
1:E:211:PHE:CD2	1:E:215:ASP:CB	3.00	0.44
1:H:114:TYR:CD1	1:H:188:MET:CE	2.99	0.44
1:H:240:SER:O	1:H:244:THR:HB	2.18	0.44
1:F:213:ASP:OD1	1:F:274:ARG:NE	2.49	0.44
1:F:81:ASN:ND2	1:F:84:ASP:OD2	2.47	0.44
1:C:94:LEU:O	1:C:98:MET:HB2	2.18	0.44
1:E:20:SER:O	1:E:23:ILE:HD12	2.17	0.44
1:E:151:SER:O	1:E:311:SER:HB2	2.17	0.44
1:E:119:ASN:ND2	1:E:286:ALA:HB1	2.33	0.44
1:G:317:LEU:O	1:G:321:ILE:HG12	2.18	0.44
1:B:22:PRO:HA	1:B:25:ILE:HD12	2.00	0.43
1:C:129:GLU:HG2	1:C:200:LEU:HD21	2.00	0.43
1:A:115:THR:HG22	1:A:119:ASN:ND2	2.33	0.43
1:E:213:ASP:O	1:E:214:PHE:HB2	2.17	0.43
1:F:114:TYR:CD1	1:F:188:MET:HE3	2.48	0.43
1:G:211:PHE:CE2	1:G:215:ASP:HB3	2.53	0.43
1:C:123:ILE:HG12	1:C:145:PHE:HB3	2.00	0.43
1:F:108:TYR:HB2	1:F:184:GLY:CA	2.49	0.43
1:H:115:THR:O	1:H:116:ILE:C	2.57	0.43
1:A:56:PHE:O	1:A:60:LEU:HB2	2.19	0.43
1:C:129:GLU:HG2	1:C:200:LEU:CD2	2.48	0.43
1:C:114:TYR:CD1	1:C:188:MET:HE3	2.34	0.43
1:D:247:PHE:CG	1:D:247:PHE:O	2.71	0.43
1:H:181:PHE:C	1:H:183:PRO:HD2	2.39	0.43
1:A:182:ASN:N	1:A:183:PRO:CD	2.77	0.43
1:E:155:ALA:HB2	1:E:311:SER:HB2	2.01	0.43
1:B:124:LEU:O	1:B:128:GLY:N	2.49	0.43
1:C:212:LYS:O	1:C:215:ASP:N	2.47	0.43
1:C:270:GLY:HA2	1:C:273:VAL:CG2	2.48	0.43
1:H:110:ALA:HB3	1:H:113:ILE:HD12	2.00	0.43
1:B:108:TYR:CD1	1:B:183:PRO:HG2	2.53	0.43
1:C:19:ASN:HB2	1:C:271:TRP:CZ2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:MET:HE2	1:A:191:ASN:HB3	2.00	0.43
1:D:213:ASP:O	1:D:214:PHE:CB	2.67	0.43
1:F:244:THR:HA	1:F:247:PHE:HE1	1.84	0.43
1:C:46:LYS:HZ1	1:C:255:MET:HG3	1.84	0.43
1:G:222:VAL:O	1:G:226:PRO:HD3	2.19	0.43
1:A:204:LYS:HG3	1:A:208:LEU:HD12	2.00	0.42
1:B:56:PHE:CE1	1:B:229:LEU:HD11	2.54	0.42
1:B:81:ASN:HB2	1:B:84:ASP:HB2	2.01	0.42
1:C:182:ASN:N	1:C:183:PRO:HD2	2.33	0.42
1:C:31:SER:HB2	5:C:502:HOH:O	2.19	0.42
1:G:114:TYR:HD1	1:G:188:MET:HE3	1.84	0.42
1:A:307:LEU:N	1:A:307:LEU:HD22	2.34	0.42
1:B:213:ASP:O	1:B:214:PHE:CB	2.67	0.42
1:B:46:LYS:HE3	1:B:54:MET:SD	2.59	0.42
1:C:88:TRP:NE1	1:C:220:ASN:OD1	2.51	0.42
1:D:52:PHE:HD1	1:D:228:LEU:HD23	1.83	0.42
1:H:71:ILE:C	1:H:72:LEU:HD22	2.38	0.42
1:B:151:SER:HB2	1:B:314:ILE:HG22	2.01	0.42
1:D:108:TYR:HB2	1:D:184:GLY:CA	2.49	0.42
1:D:67:ILE:HG13	1:D:78:ARG:HH12	1.84	0.42
1:G:113:ILE:HA	1:G:116:ILE:CD1	2.47	0.42
1:A:52:PHE:HD1	1:A:228:LEU:HD23	1.84	0.42
1:A:265:ILE:HG13	1:A:265:ILE:H	1.62	0.42
1:E:92:SER:O	1:E:96:VAL:HG23	2.20	0.42
1:G:240:SER:O	1:G:244:THR:HB	2.18	0.42
1:B:290:LEU:HB2	1:B:291:PRO:HD3	2.00	0.42
1:C:102:SER:HB2	1:C:191:ASN:ND2	2.35	0.42
1:C:46:LYS:HE3	1:C:54:MET:SD	2.59	0.42
1:D:253:THR:HG22	1:D:257:ILE:HD11	2.01	0.42
1:E:31:SER:HB2	1:E:265:ILE:N	2.35	0.42
1:F:105:ALA:HB1	1:F:188:MET:HG2	2.01	0.42
1:G:70:ARG:HD3	1:G:78:ARG:NH1	2.34	0.42
1:A:102:SER:HB2	1:A:191:ASN:HD21	1.79	0.42
1:C:181:PHE:HD2	1:C:185:TYR:HE2	1.66	0.42
1:C:24:SER:HB3	1:C:275:VAL:HG21	2.02	0.42
1:D:118:LYS:O	1:D:121:THR:OG1	2.27	0.42
1:F:58:GLN:HG2	1:F:259:GLY:HA2	2.01	0.42
1:G:182:ASN:N	1:G:183:PRO:HD2	2.35	0.42
1:H:108:TYR:HB2	1:H:184:GLY:CA	2.49	0.42
1:B:52:PHE:HD1	1:B:228:LEU:HD23	1.84	0.42
1:D:290:LEU:HD22	1:D:312:ILE:HA	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:202:MET:HE1	1:G:273:VAL:HG21	2.02	0.42
1:H:119:ASN:HD21	1:H:286:ALA:HB1	1.85	0.42
1:E:269:SER:CB	3:E:401:5GP:N2	2.83	0.42
1:E:95:LEU:HD12	1:E:198:PHE:HE1	1.78	0.42
1:B:87:ASN:HB3	1:B:205:ARG:CZ	2.50	0.42
1:E:117:PHE:HA	1:E:120:LEU:HD12	2.02	0.42
1:E:81:ASN:N	1:E:219:TYR:OH	2.52	0.42
1:H:124:LEU:O	1:H:128:GLY:N	2.44	0.42
1:A:121:THR:CG2	1:A:192:CYS:SG	3.08	0.42
1:B:29:CYS:HA	1:B:288:ASN:HD21	1.84	0.42
1:B:94:LEU:HA	1:B:94:LEU:HD13	1.84	0.42
1:C:247:PHE:CG	1:C:247:PHE:O	2.73	0.42
1:F:181:PHE:CD2	1:F:185:TYR:HE2	2.37	0.42
1:F:211:PHE:CD2	1:F:215:ASP:CB	3.02	0.42
1:A:133:PHE:CZ	1:A:203:ARG:HG3	2.55	0.41
1:D:66:LEU:HD11	1:D:217:MET:SD	2.61	0.41
1:F:126:ALA:HB2	1:F:279:THR:CG2	2.50	0.41
1:H:317:LEU:O	1:H:321:ILE:HG12	2.19	0.41
1:A:72:LEU:HD13	1:A:72:LEU:HA	1.82	0.41
1:G:121:THR:HG22	1:G:192:CYS:SG	2.60	0.41
1:G:57:VAL:HG21	1:G:255:MET:HE1	2.01	0.41
1:H:50:MET:CG	1:H:236:GLU:OE1	2.68	0.41
1:H:27:SER:HG	1:H:271:TRP:HZ3	1.66	0.41
1:E:222:VAL:O	1:E:226:PRO:HD3	2.20	0.41
1:H:296:GLY:HA2	1:H:300:PHE:HD2	1.86	0.41
1:A:274:ARG:NH2	1:A:275:VAL:CG1	2.83	0.41
1:B:92:SER:O	1:B:96:VAL:HG23	2.20	0.41
1:C:253:THR:O	1:C:257:ILE:HD12	2.21	0.41
1:G:101:THR:HB	1:G:191:ASN:HB2	2.01	0.41
1:G:121:THR:CG2	1:G:192:CYS:SG	3.08	0.41
1:B:218:PHE:CZ	1:B:222:VAL:HG21	2.56	0.41
1:B:70:ARG:HD2	1:B:78:ARG:NH2	2.35	0.41
1:D:206:ILE:HG12	1:D:216:THR:HG22	2.03	0.41
1:G:73:GLY:HA3	1:G:77:PHE:CE1	2.56	0.41
1:H:81:ASN:N	1:H:219:TYR:OH	2.53	0.41
1:A:290:LEU:HB2	1:A:291:PRO:HD3	2.02	0.41
1:D:53:VAL:O	1:D:57:VAL:HG23	2.21	0.41
1:G:133:PHE:HZ	1:G:203:ARG:HG3	1.85	0.41
1:H:133:PHE:CZ	1:H:203:ARG:HG3	2.55	0.41
1:F:66:LEU:HB3	1:F:78:ARG:HD3	2.03	0.41
1:A:132:PHE:HB3	1:A:133:PHE:CD2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:269:SER:HB3	3:E:401:5GP:N2	2.35	0.41
1:F:122:ILE:H	1:F:122:ILE:HG13	1.75	0.41
1:G:219:TYR:O	1:G:223:LEU:HB2	2.20	0.41
1:H:223:LEU:C	1:H:226:PRO:HD2	2.42	0.41
1:B:118:LYS:HE2	1:B:191:ASN:OD1	2.21	0.41
1:C:181:PHE:HB3	1:C:185:TYR:HE2	1.86	0.41
1:D:72:LEU:HA	1:D:72:LEU:HD13	1.88	0.41
1:C:181:PHE:C	1:C:183:PRO:HD2	2.41	0.41
1:E:270:GLY:HA2	1:E:273:VAL:HG22	2.02	0.41
1:G:58:GLN:HG2	1:G:259:GLY:HA2	2.03	0.41
1:D:66:LEU:HD21	1:D:214:PHE:HD1	1.86	0.40
1:D:94:LEU:HB3	1:D:198:PHE:HB2	2.02	0.40
1:F:71:ILE:C	1:F:72:LEU:HD22	2.41	0.40
1:G:71:ILE:C	1:G:72:LEU:HD22	2.41	0.40
1:D:212:LYS:O	1:D:215:ASP:N	2.54	0.40
1:D:247:PHE:HA	1:D:251:SER:OG	2.21	0.40
1:D:70:ARG:NH1	1:D:78:ARG:NH2	2.64	0.40
1:E:115:THR:O	1:E:116:ILE:C	2.60	0.40
1:E:71:ILE:O	1:E:72:LEU:HD22	2.21	0.40
1:F:115:THR:O	1:F:116:ILE:C	2.58	0.40
1:F:124:LEU:HD23	1:F:124:LEU:H	1.86	0.40
1:H:68:ILE:O	1:H:72:LEU:HD22	2.21	0.40
1:B:206:ILE:HG12	1:B:216:THR:HG22	2.04	0.40
1:C:115:THR:O	1:C:116:ILE:C	2.59	0.40
1:E:223:LEU:C	1:E:226:PRO:HD2	2.41	0.40
1:F:43:VAL:CG1	1:F:46:LYS:HD3	2.51	0.40
1:G:133:PHE:CZ	1:G:203:ARG:HG3	2.56	0.40
1:H:45:LEU:HD23	1:H:45:LEU:HA	1.80	0.40
1:A:146:LEU:HD23	1:A:146:LEU:HA	1.82	0.40
1:D:206:ILE:HG12	1:D:216:THR:CG2	2.52	0.40
1:E:146:LEU:HD23	1:E:146:LEU:HA	1.89	0.40
1:E:265:ILE:H	1:E:265:ILE:HG13	1.60	0.40
1:G:70:ARG:HG2	1:G:78:ARG:HH12	1.86	0.40
1:B:273:VAL:HG12	1:B:281:TYR:CB	2.51	0.40
1:C:117:PHE:HA	1:C:120:LEU:HD12	2.02	0.40
1:C:310:LEU:HD22	1:C:314:ILE:HD11	2.03	0.40
1:F:265:ILE:HG13	1:F:265:ILE:H	1.73	0.40
1:G:29:CYS:HA	1:G:288:ASN:OD1	2.22	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	286/337 (85%)	275 (96%)	8 (3%)	3 (1%)	15	46
1	B	291/337 (86%)	279 (96%)	10 (3%)	2 (1%)	22	55
1	C	288/337 (86%)	279 (97%)	7 (2%)	2 (1%)	22	55
1	D	288/337 (86%)	277 (96%)	9 (3%)	2 (1%)	22	55
1	E	292/337 (87%)	276 (94%)	14 (5%)	2 (1%)	22	55
1	F	288/337 (86%)	276 (96%)	9 (3%)	3 (1%)	15	46
1	G	290/337 (86%)	280 (97%)	8 (3%)	2 (1%)	22	55
1	H	288/337 (86%)	277 (96%)	8 (3%)	3 (1%)	15	46
All	All	2311/2696 (86%)	2219 (96%)	73 (3%)	19 (1%)	19	51

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	214	PHE
1	B	214	PHE
1	C	214	PHE
1	D	214	PHE
1	E	214	PHE
1	F	214	PHE
1	G	214	PHE
1	H	214	PHE
1	B	45	LEU
1	A	45	LEU
1	C	45	LEU
1	D	45	LEU
1	F	45	LEU
1	G	45	LEU
1	H	45	LEU
1	F	135	GLY
1	H	135	GLY

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Mol	Chain	Res	Type
1	A	135	GLY
1	E	178	VAL

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	262/289 (91%)	254 (97%)	8 (3%)	40	68
1	B	265/289 (92%)	256 (97%)	9 (3%)	37	65
1	C	263/289 (91%)	255 (97%)	8 (3%)	41	68
1	D	263/289 (91%)	256 (97%)	7 (3%)	44	70
1	E	265/289 (92%)	258 (97%)	7 (3%)	46	72
1	F	263/289 (91%)	257 (98%)	6 (2%)	50	74
1	G	264/289 (91%)	257 (97%)	7 (3%)	44	70
1	H	263/289 (91%)	256 (97%)	7 (3%)	44	70
All	All	2108/2312 (91%)	2049 (97%)	59 (3%)	43	70

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	ARG
1	A	86	LYS
1	A	124	LEU
1	A	150	LEU
1	A	159	ASP
1	A	211	PHE
1	A	304	ARG
1	A	310	LEU
1	B	77	PHE
1	B	78	ARG
1	B	124	LEU
1	B	159	ASP
1	B	211	PHE

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Mol	Chain	Res	Type
1	B	214	PHE
1	B	272	CYS
1	B	304	ARG
1	B	310	LEU
1	C	77	PHE
1	C	78	ARG
1	C	86	LYS
1	C	150	LEU
1	C	159	ASP
1	C	211	PHE
1	C	304	ARG
1	C	310	LEU
1	D	77	PHE
1	D	78	ARG
1	D	86	LYS
1	D	159	ASP
1	D	211	PHE
1	D	304	ARG
1	D	310	LEU
1	E	77	PHE
1	E	78	ARG
1	E	86	LYS
1	E	124	LEU
1	E	159	ASP
1	E	211	PHE
1	E	304	ARG
1	F	77	PHE
1	F	78	ARG
1	F	86	LYS
1	F	124	LEU
1	F	159	ASP
1	F	304	ARG
1	G	77	PHE
1	G	78	ARG
1	G	86	LYS
1	G	124	LEU
1	G	159	ASP
1	G	211	PHE
1	G	304	ARG
1	H	77	PHE
1	H	78	ARG
1	H	86	LYS

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Mol	Chain	Res	Type
1	H	159	ASP
1	H	211	PHE
1	H	304	ARG
1	H	310	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	58	GLN
1	B	87	ASN
1	B	119	ASN
1	B	288	ASN
1	C	119	ASN
1	E	119	ASN
1	E	191	ASN
1	G	39	ASN
1	G	58	GLN
1	G	191	ASN

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](#)

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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
3	5GP	C	401	-	22,26,26	1.24	3 (13%)	27,40,40	2.10	4 (14%)
3	5GP	D	401	-	22,26,26	1.19	3 (13%)	27,40,40	2.22	6 (22%)
3	5GP	E	401	-	22,26,26	1.21	3 (13%)	27,40,40	2.38	7 (25%)
2	OLC	E	402	-	24,24,24	0.94	1 (4%)	25,25,25	0.79	0
2	OLC	A	401	-	24,24,24	1.09	2 (8%)	25,25,25	0.83	1 (4%)

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	5GP	C	401	-	-	3/6/26/26	0/3/3/3
3	5GP	D	401	-	-	6/6/26/26	0/3/3/3
3	5GP	E	401	-	-	3/6/26/26	0/3/3/3
2	OLC	E	402	-	-	8/24/24/24	-
2	OLC	A	401	-	-	8/24/24/24	-

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	401	5GP	C6-N1	3.17	1.38	1.33
3	D	401	5GP	C6-N1	3.09	1.38	1.33
2	A	401	OLC	C21-C22	2.93	1.61	1.51
2	E	402	OLC	O20-C1	2.80	1.41	1.33
3	C	401	5GP	P-O1P	-2.79	1.41	1.50
3	E	401	5GP	C6-N1	2.78	1.37	1.33
3	E	401	5GP	P-O1P	-2.51	1.42	1.50
3	C	401	5GP	C8-N7	-2.26	1.30	1.34
2	A	401	OLC	O20-C1	2.19	1.39	1.33
3	D	401	5GP	P-O1P	-2.15	1.43	1.50
3	E	401	5GP	C8-N7	-2.14	1.30	1.34
3	D	401	5GP	P-O3P	-2.03	1.47	1.54

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	401	5GP	C5-C6-N1	-8.43	111.90	123.43
3	C	401	5GP	C5-C6-N1	-7.97	112.53	123.43
3	D	401	5GP	C5-C6-N1	-7.76	112.82	123.43
3	E	401	5GP	C6-N1-C2	5.43	124.55	115.93
3	D	401	5GP	C6-N1-C2	5.33	124.40	115.93
3	C	401	5GP	C6-N1-C2	5.22	124.22	115.93
3	E	401	5GP	P-O5'-C5'	3.76	128.66	118.30
3	E	401	5GP	O5'-P-O1P	3.04	115.00	106.47
3	D	401	5GP	N3-C2-N1	-3.03	123.18	127.22
3	C	401	5GP	N3-C2-N1	-2.87	123.39	127.22
3	D	401	5GP	O5'-P-O1P	2.85	114.48	106.47
3	E	401	5GP	N3-C2-N1	-2.62	123.73	127.22
3	D	401	5GP	C3'-C2'-C1'	-2.29	97.53	100.98
3	E	401	5GP	C2-N3-C4	-2.19	112.86	115.36
3	E	401	5GP	C6-C5-C4	-2.15	118.74	120.80
3	D	401	5GP	C2-N3-C4	-2.14	112.91	115.36
3	C	401	5GP	C2-N3-C4	-2.10	112.95	115.36
2	A	401	OLC	O23-C22-C21	2.07	116.83	109.56

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	401	5GP	C4'-C5'-O5'-P
3	E	401	5GP	C5'-O5'-P-O1P
3	E	401	5GP	C5'-O5'-P-O2P
3	E	401	5GP	C5'-O5'-P-O3P
3	D	401	5GP	C5'-O5'-P-O1P
3	D	401	5GP	C5'-O5'-P-O2P
3	D	401	5GP	C5'-O5'-P-O3P
3	D	401	5GP	O4'-C4'-C5'-O5'
2	A	401	OLC	O20-C21-C22-O23
2	E	402	OLC	O20-C21-C22-O23
2	A	401	OLC	C1-C2-C3-C4
2	E	402	OLC	C2-C3-C4-C5
2	A	401	OLC	C14-C15-C16-C17
2	A	401	OLC	C12-C13-C14-C15
2	E	402	OLC	O20-C21-C22-C24
2	A	401	OLC	C13-C14-C15-C16
2	E	402	OLC	C1-C2-C3-C4
3	D	401	5GP	C3'-C4'-C5'-O5'
2	E	402	OLC	C3-C4-C5-C6
2	A	401	OLC	C6-C7-C8-C9

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Mol	Chain	Res	Type	Atoms
3	D	401	5GP	C4'-C5'-O5'-P
3	C	401	5GP	C5'-O5'-P-O1P
2	E	402	OLC	C6-C7-C8-C9
2	A	401	OLC	C7-C8-C9-C10
2	E	402	OLC	C9-C10-C11-C12
3	C	401	5GP	O4'-C4'-C5'-O5'
2	A	401	OLC	C2-C3-C4-C5
2	E	402	OLC	C12-C13-C14-C15

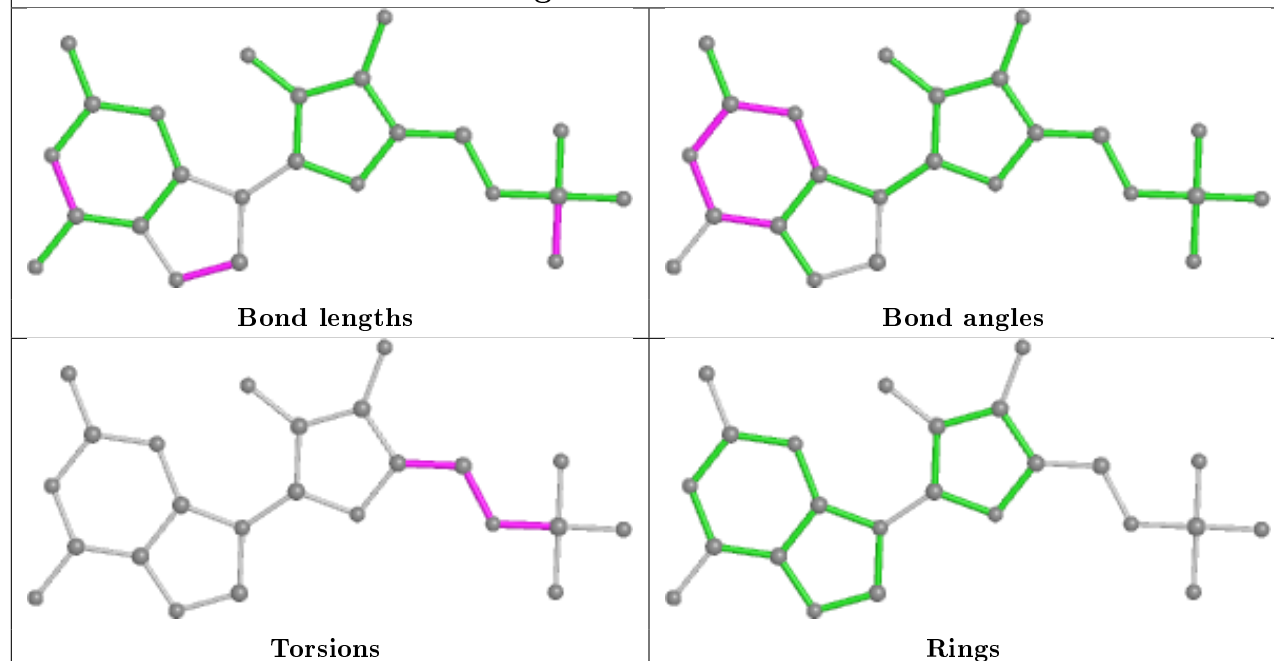
There are no ring outliers.

4 monomers are involved in 9 short contacts:

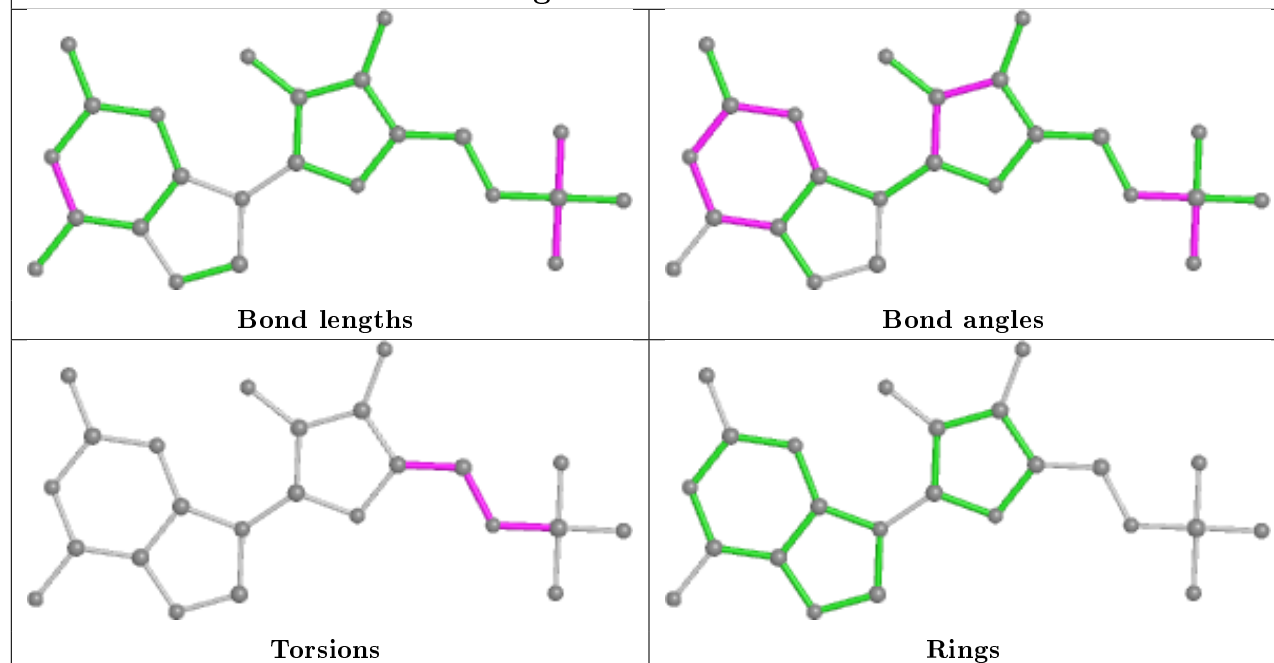
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	401	5GP	3	0
3	E	401	5GP	3	0
2	E	402	OLC	1	0
2	A	401	OLC	2	0

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.

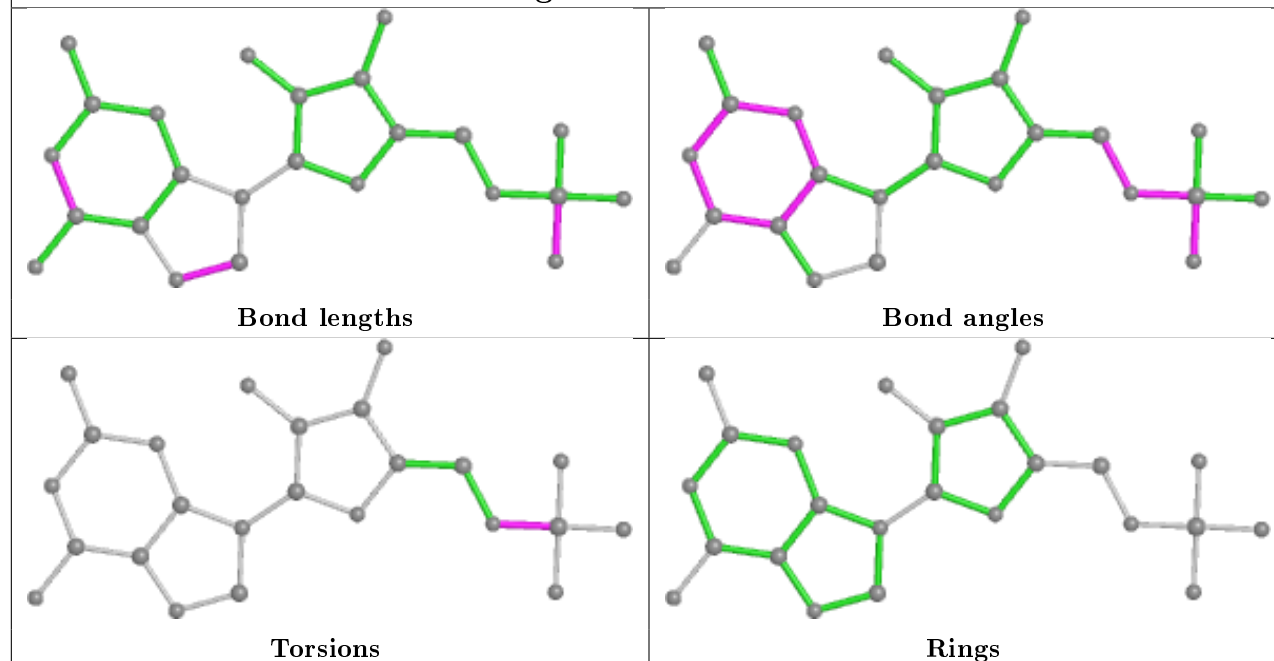
Ligand 5GP C 401



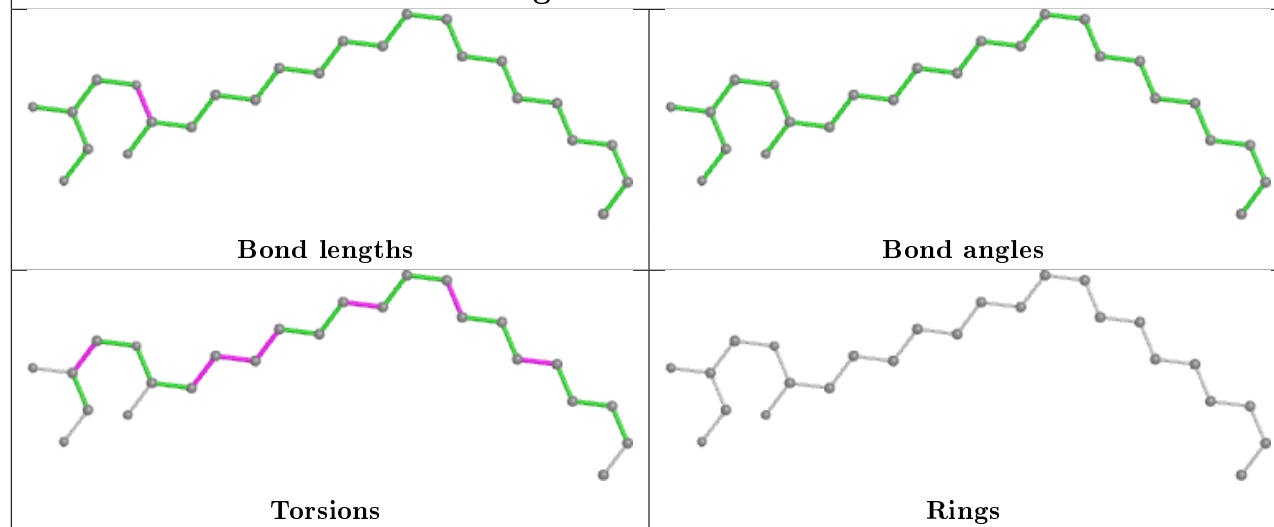
Ligand 5GP D 401

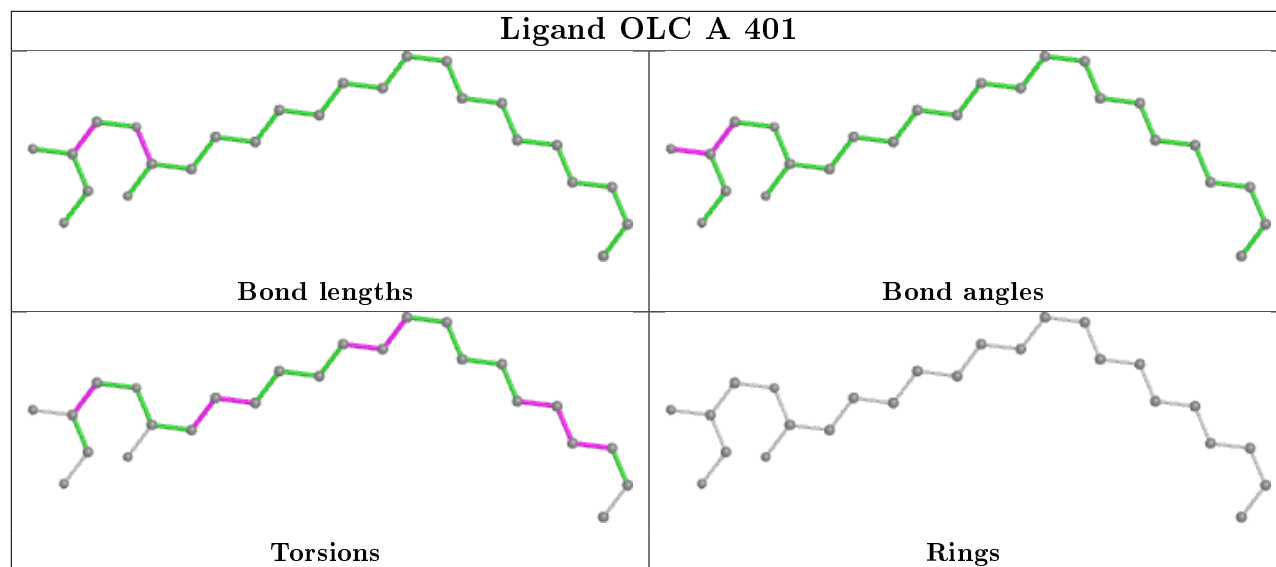


Ligand 5GP E 401



Ligand OLC E 402





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	292/337 (86%)	0.12	15 (5%)	28 28	48, 75, 121, 149	0
1	B	297/337 (88%)	0.26	21 (7%)	16 18	54, 75, 124, 145	0
1	C	294/337 (87%)	0.18	22 (7%)	14 16	45, 76, 118, 140	0
1	D	294/337 (87%)	0.16	20 (6%)	17 19	48, 77, 118, 142	0
1	E	298/337 (88%)	0.39	33 (11%)	5 6	53, 81, 143, 165	0
1	F	294/337 (87%)	0.33	27 (9%)	9 10	44, 79, 142, 167	0
1	G	296/337 (87%)	0.36	30 (10%)	7 8	55, 80, 140, 162	0
1	H	294/337 (87%)	0.22	22 (7%)	14 16	54, 78, 140, 163	0
All	All	2359/2696 (87%)	0.25	190 (8%)	12 13	44, 78, 130, 167	0

All (190) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	236	GLU	9.3
1	E	249	ASN	9.1
1	E	48	PHE	8.2
1	F	47	ASP	8.2
1	G	180	SER	7.3
1	C	135	GLY	7.2
1	C	241	VAL	7.1
1	F	237	ASP	6.8
1	F	48	PHE	6.5
1	E	47	ASP	6.4
1	E	241	VAL	6.3
1	B	241	VAL	6.2
1	D	333	GLN	6.0
1	B	245	ASN	5.7
1	H	48	PHE	5.5
1	B	304	ARG	5.4

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Mol	Chain	Res	Type	RSRZ
1	H	47	ASP	5.4
1	F	238	TRP	5.4
1	B	237	ASP	5.3
1	F	331	GLN	5.3
1	G	331	GLN	5.0
1	E	242	ASN	4.7
1	A	46	LYS	4.7
1	E	247	PHE	4.5
1	E	18	ALA	4.5
1	G	209	THR	4.5
1	C	159	ASP	4.5
1	E	19	ASN	4.4
1	F	46	LYS	4.4
1	F	50	MET	4.3
1	A	333	GLN	4.2
1	H	208	LEU	4.2
1	B	333	GLN	4.1
1	F	241	VAL	4.1
1	C	246	ASN	4.1
1	F	245	ASN	4.1
1	H	81	ASN	4.1
1	E	180	SER	4.1
1	B	136	SER	4.0
1	F	233	PHE	4.0
1	H	85	ALA	3.9
1	C	160	GLN	3.9
1	B	305	ASN	3.8
1	E	42	VAL	3.7
1	C	136	SER	3.7
1	C	44	ASN	3.7
1	E	248	SER	3.7
1	E	245	ASN	3.6
1	G	79	SER	3.6
1	E	244	THR	3.6
1	G	333	GLN	3.6
1	F	133	PHE	3.6
1	F	247	PHE	3.6
1	B	238	TRP	3.6
1	E	49	ASN	3.6
1	E	233	PHE	3.5
1	H	79	SER	3.5
1	B	135	GLY	3.5

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Mol	Chain	Res	Type	RSRZ
1	C	134	GLY	3.5
1	H	51	ASN	3.4
1	E	207	LYS	3.4
1	B	159	ASP	3.4
1	E	251	SER	3.3
1	C	245	ASN	3.3
1	D	46	LYS	3.3
1	G	48	PHE	3.3
1	A	64	ILE	3.3
1	G	241	VAL	3.3
1	E	275	VAL	3.3
1	D	90	PRO	3.2
1	E	132	PHE	3.2
1	H	83	THR	3.2
1	D	236	GLU	3.2
1	B	48	PHE	3.1
1	E	237	ASP	3.1
1	F	249	ASN	3.1
1	D	67	ILE	3.1
1	F	255	MET	3.1
1	B	331	GLN	3.0
1	G	247	PHE	3.0
1	E	246	ASN	3.0
1	F	250	ASP	3.0
1	F	135	GLY	3.0
1	B	158	GLY	3.0
1	C	237	ASP	3.0
1	D	86	LYS	3.0
1	E	227	ILE	3.0
1	A	45	LEU	2.9
1	D	89	PHE	2.9
1	C	249	ASN	2.9
1	E	238	TRP	2.9
1	A	208	LEU	2.9
1	C	45	LEU	2.9
1	H	46	LYS	2.9
1	A	288	ASN	2.9
1	H	331	GLN	2.9
1	B	236	GLU	2.9
1	F	252	LEU	2.8
1	D	313	PHE	2.8
1	D	85	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
1	E	178	VAL	2.8
1	G	85	ALA	2.8
1	C	248	SER	2.8
1	G	46	LYS	2.8
1	C	333	GLN	2.8
1	C	242	ASN	2.8
1	D	242	ASN	2.8
1	G	208	LEU	2.7
1	A	63	THR	2.7
1	E	159	ASP	2.7
1	H	209	THR	2.7
1	F	49	ASN	2.7
1	B	46	LYS	2.7
1	F	333	GLN	2.7
1	G	232	SER	2.7
1	G	288	ASN	2.7
1	B	160	GLN	2.7
1	G	78	ARG	2.6
1	F	239	SER	2.6
1	G	81	ASN	2.6
1	F	235	VAL	2.6
1	G	236	GLU	2.6
1	G	179	ALA	2.6
1	E	177	ALA	2.6
1	G	242	ASN	2.5
1	D	228	LEU	2.5
1	D	157	TRP	2.5
1	A	51	ASN	2.5
1	A	184	GLY	2.5
1	H	297	LEU	2.5
1	C	42	VAL	2.5
1	G	304	ARG	2.5
1	H	78	ARG	2.5
1	H	84	ASP	2.5
1	D	241	VAL	2.4
1	G	181	PHE	2.4
1	G	286	ALA	2.4
1	G	235	VAL	2.4
1	F	304	ARG	2.4
1	F	207	LYS	2.4
1	G	182	ASN	2.4
1	A	290	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	G	327	GLN	2.4
1	H	184	GLY	2.4
1	E	250	ASP	2.3
1	C	244	THR	2.3
1	H	240	SER	2.3
1	A	48	PHE	2.3
1	F	132	PHE	2.3
1	B	161	GLN	2.3
1	A	136	SER	2.3
1	B	181	PHE	2.3
1	D	106	LEU	2.3
1	H	299	PHE	2.3
1	D	235	VAL	2.3
1	E	73	GLY	2.3
1	D	92	SER	2.3
1	H	333	GLN	2.3
1	G	88	TRP	2.3
1	C	43	VAL	2.3
1	A	68	ILE	2.3
1	E	331	GLN	2.3
1	C	161	GLN	2.3
1	A	157	TRP	2.2
1	A	143	SER	2.2
1	E	133	PHE	2.2
1	G	47	ASP	2.2
1	H	133	PHE	2.2
1	H	219	TYR	2.2
1	E	252	LEU	2.2
1	B	157	TRP	2.2
1	E	187	TRP	2.2
1	C	48	PHE	2.2
1	H	105	ALA	2.2
1	C	240	SER	2.1
1	F	161	GLN	2.1
1	D	182	ASN	2.1
1	D	304	ARG	2.1
1	D	45	LEU	2.1
1	H	241	VAL	2.1
1	F	244	THR	2.1
1	B	49	ASN	2.1
1	G	52	PHE	2.1
1	G	240	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	46	LYS	2.1
1	E	135	GLY	2.1
1	G	119	ASN	2.0
1	G	230	LEU	2.0
1	B	240	SER	2.0
1	D	136	SER	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 monosaccharides in this entry.

6.4 Ligands [i](#)

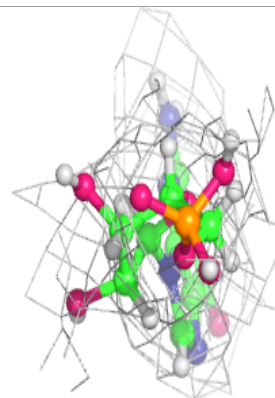
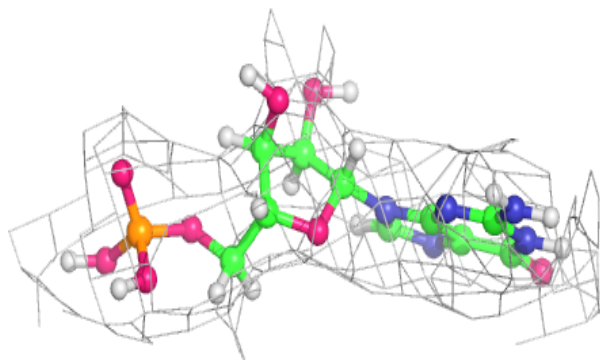
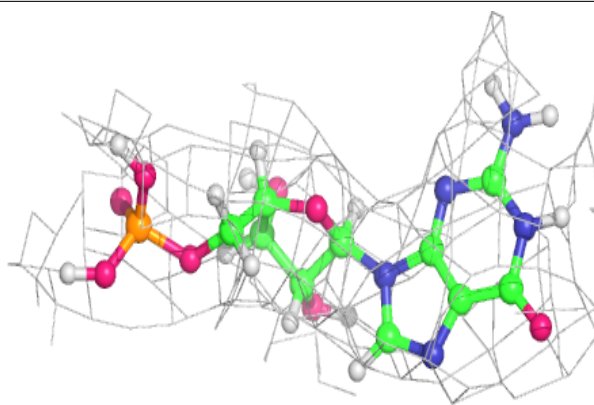
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	5GP	D	401	24/24	0.76	0.22	132,141,172,175	0
3	5GP	E	401	24/24	0.82	0.18	130,135,162,166	0
2	OLC	A	401	25/25	0.84	0.33	49,66,102,104	0
3	5GP	C	401	24/24	0.84	0.15	135,140,171,172	0
4	NA	D	402	1/1	0.89	0.15	77,77,77,77	0
2	OLC	E	402	25/25	0.93	0.34	52,65,77,79	0

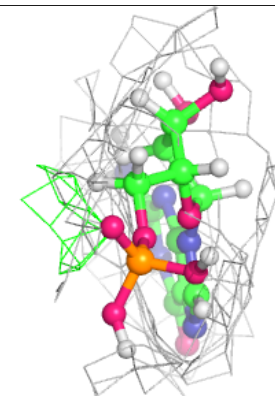
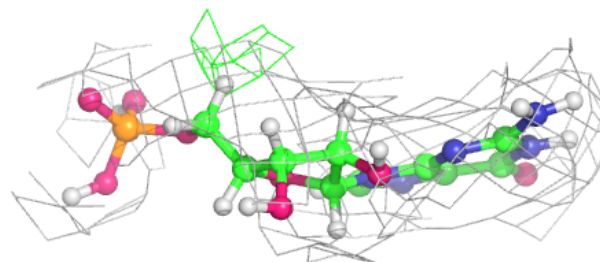
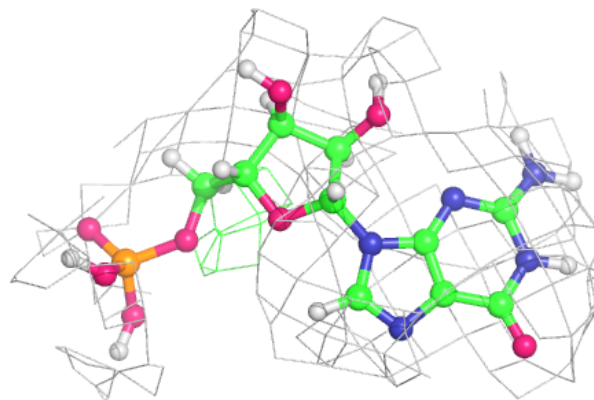
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 5GP D 401:

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

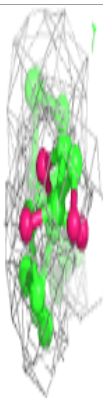
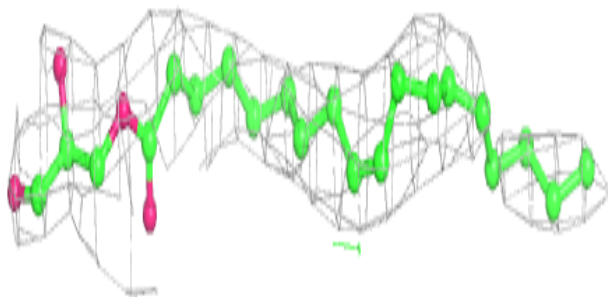
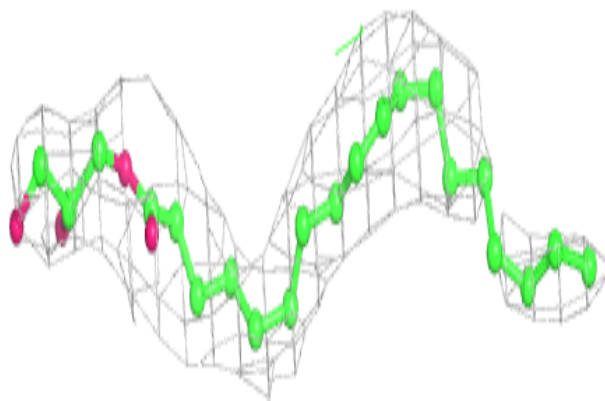
**Electron density around 5GP E 401:**

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

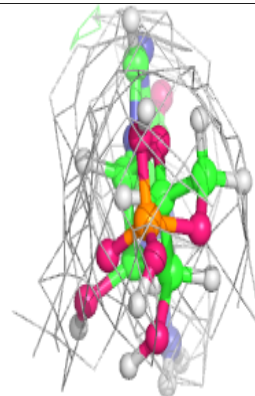
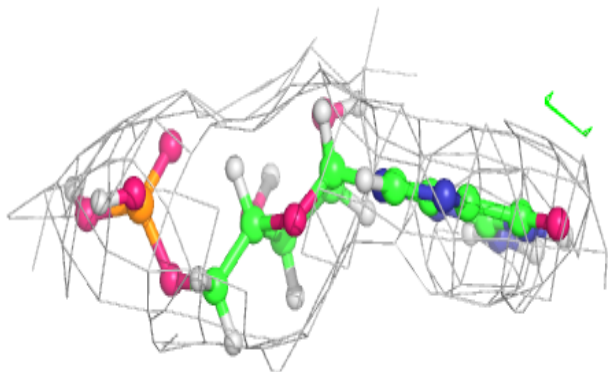
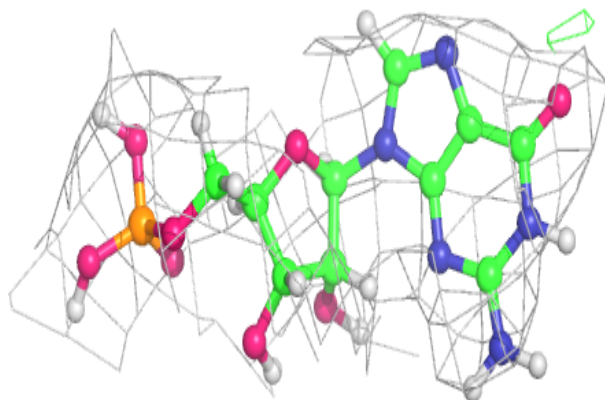


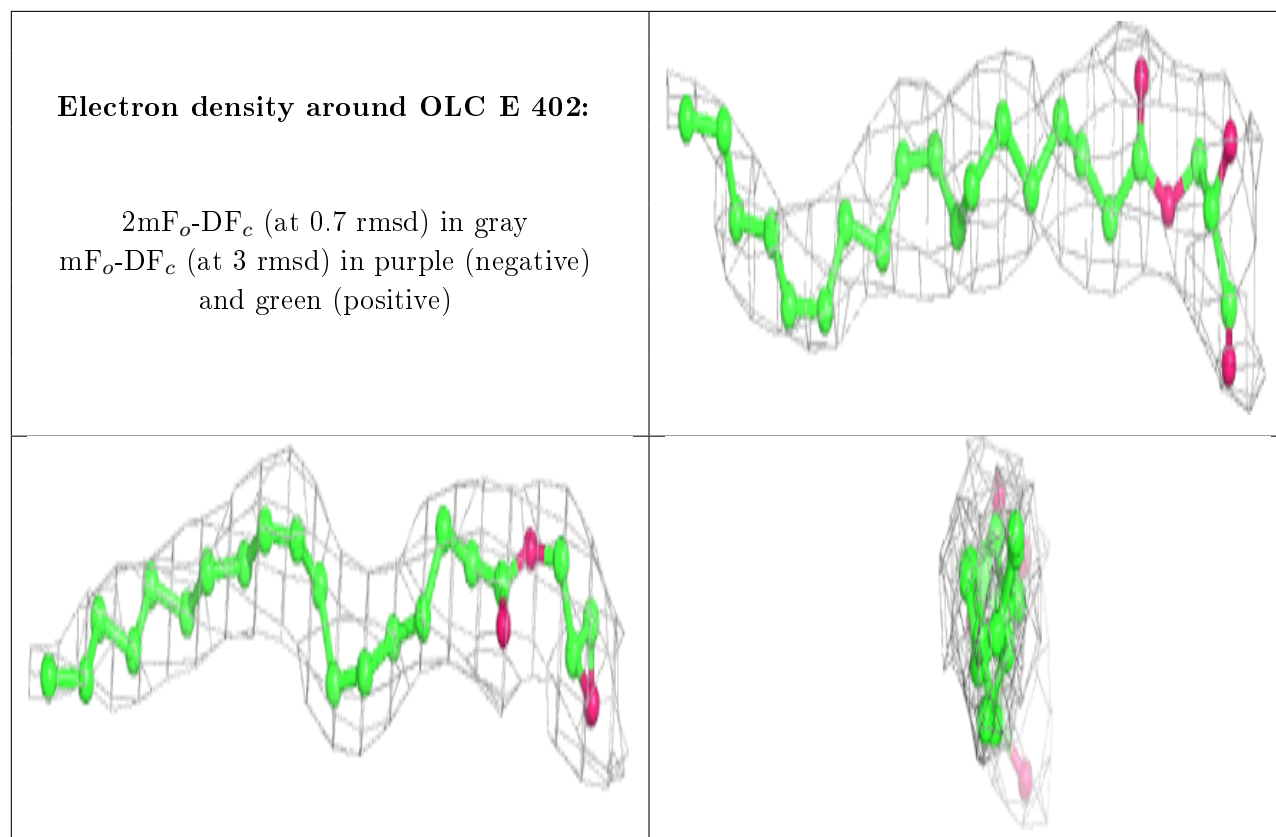
Electron density around OLC A 401:

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

**Electron density around 5GP C 401:**

$2mF_o-DF_c$ (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.