Full wwPDB X-ray Structure Validation Report ⓘ

Nov 21, 2023 – 05:31 AM JST

PDB ID	:	7ESP
Title	:	Structure and mutation analysis of the hexameric P4 from Pseudomonas aeruginosa phage phiYY
Authors	:	Zhang, C.Y.; Jin, T.C.
Deposited on	:	2021-05-11
Resolution	:	2.43 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:

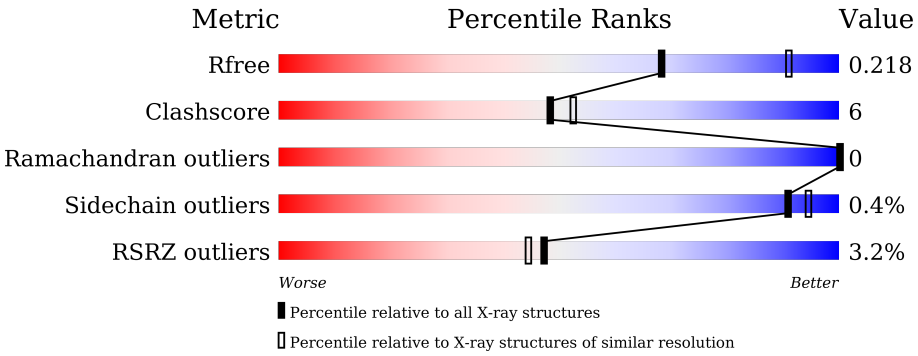
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.43 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	1564 (2.46-2.42)
Clashscore	141614	1631 (2.46-2.42)
Ramachandran outliers	138981	1617 (2.46-2.42)
Sidechain outliers	138945	1617 (2.46-2.42)
RSRZ outliers	127900	1547 (2.46-2.42)

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	350	70% 6% 24%
1	B	350	64% 10% 26%
1	C	350	66% 9% 25%
1	D	350	64% 10% 26%
1	E	350	65% 11% 24%
1	F	350	65% 8% 26%

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Mol	Chain	Length	Quality of chain
1	G	350	3% 63% 11% 25%
1	H	350	2% 62% 11% 26%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	TAR	F	401	-	X	X	-
2	TAR	H	401	-	-	X	-

2 Entry composition (i)

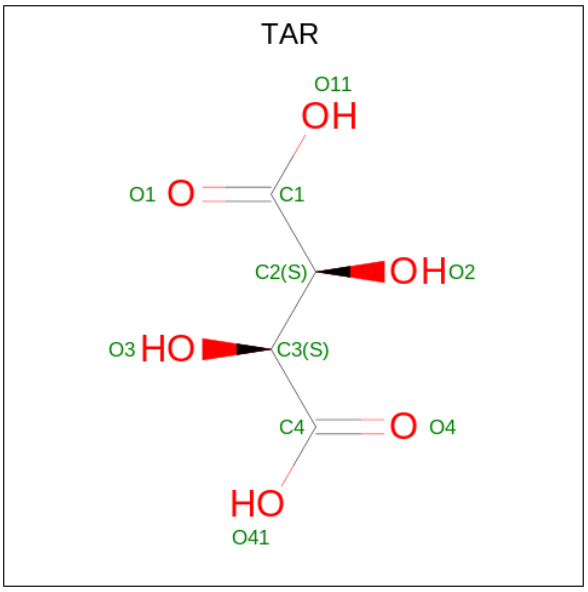
There are 4 unique types of molecules in this entry. The entry contains 15957 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Packaging NTPase.

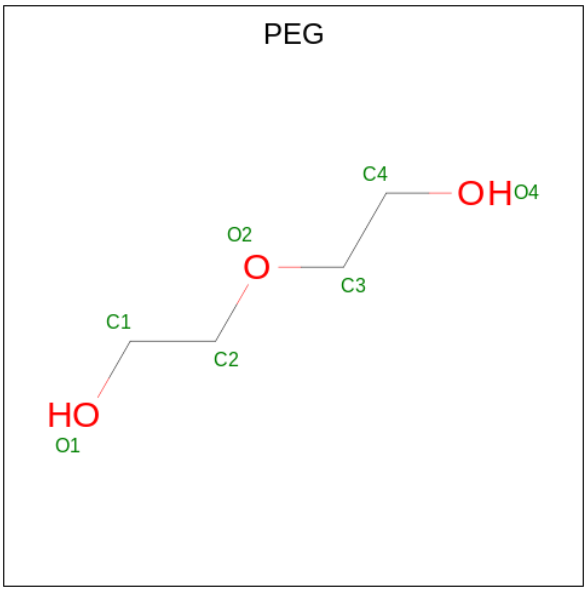
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	265	Total	C	N	O	S	0	0	0
			1968	1244	339	373	12			
1	B	260	Total	C	N	O	S	0	0	0
			1928	1217	332	367	12			
1	C	263	Total	C	N	O	S	0	0	0
			1951	1234	335	370	12			
1	D	259	Total	C	N	O	S	0	1	0
			1932	1222	332	366	12			
1	E	265	Total	C	N	O	S	0	0	0
			1964	1242	338	372	12			
1	F	258	Total	C	N	O	S	0	0	0
			1908	1206	326	364	12			
1	G	263	Total	C	N	O	S	0	0	0
			1949	1233	335	369	12			
1	H	258	Total	C	N	O	S	0	0	0
			1910	1207	327	364	12			

- Molecule 2 is D(-)-TARTARIC ACID (three-letter code: TAR) (formula: $C_4H_6O_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			10	4	6		
2	B	1	Total	C	O	0	0
			10	4	6		
2	C	1	Total	C	O	0	0
			10	4	6		
2	D	1	Total	C	O	0	0
			10	4	6		
2	E	1	Total	C	O	0	0
			10	4	6		
2	F	1	Total	C	O	0	0
			10	4	6		
2	G	1	Total	C	O	0	0
			10	4	6		
2	H	1	Total	C	O	0	0
			10	4	6		

- Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 7 4 3	0	0
3	D	1	Total C O 7 4 3	0	0
3	F	1	Total C O 7 4 3	0	0
3	H	1	Total C O 7 4 3	0	0

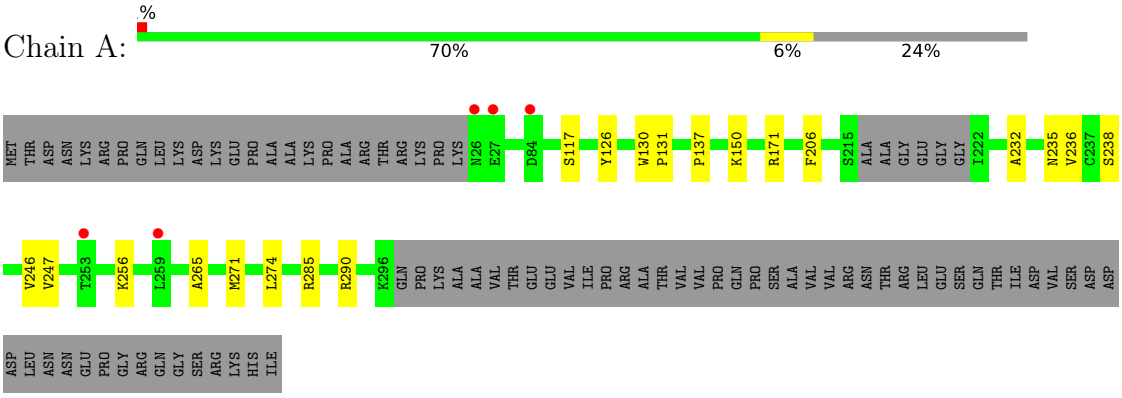
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	58	Total O 58 58	0	0
4	B	40	Total O 40 40	0	0
4	C	34	Total O 34 34	0	0
4	D	42	Total O 42 42	0	0
4	E	56	Total O 56 56	0	0
4	F	49	Total O 49 49	0	0
4	G	24	Total O 24 24	0	0
4	H	36	Total O 36 36	0	0

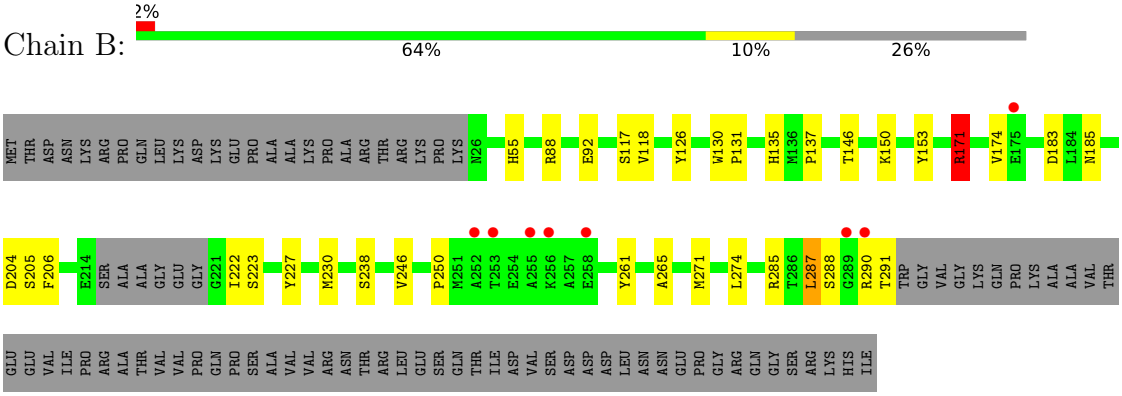
3 Residue-property plots (i)

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.

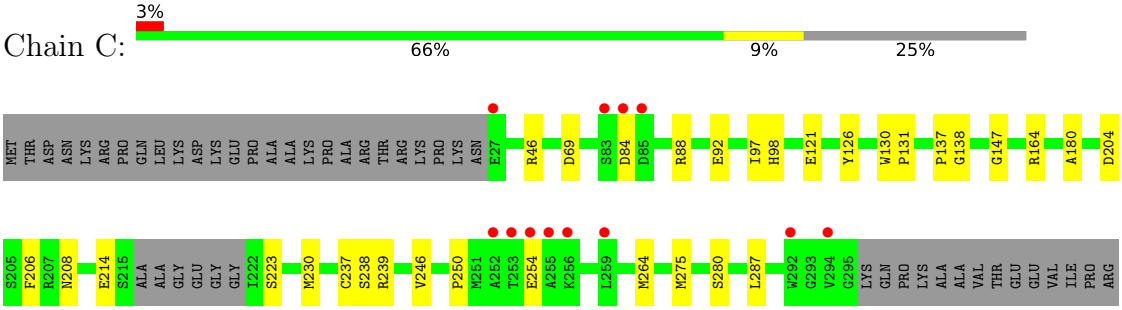
• Molecule 1: Packaging NTPase



• Molecule 1: Packaging NTPase

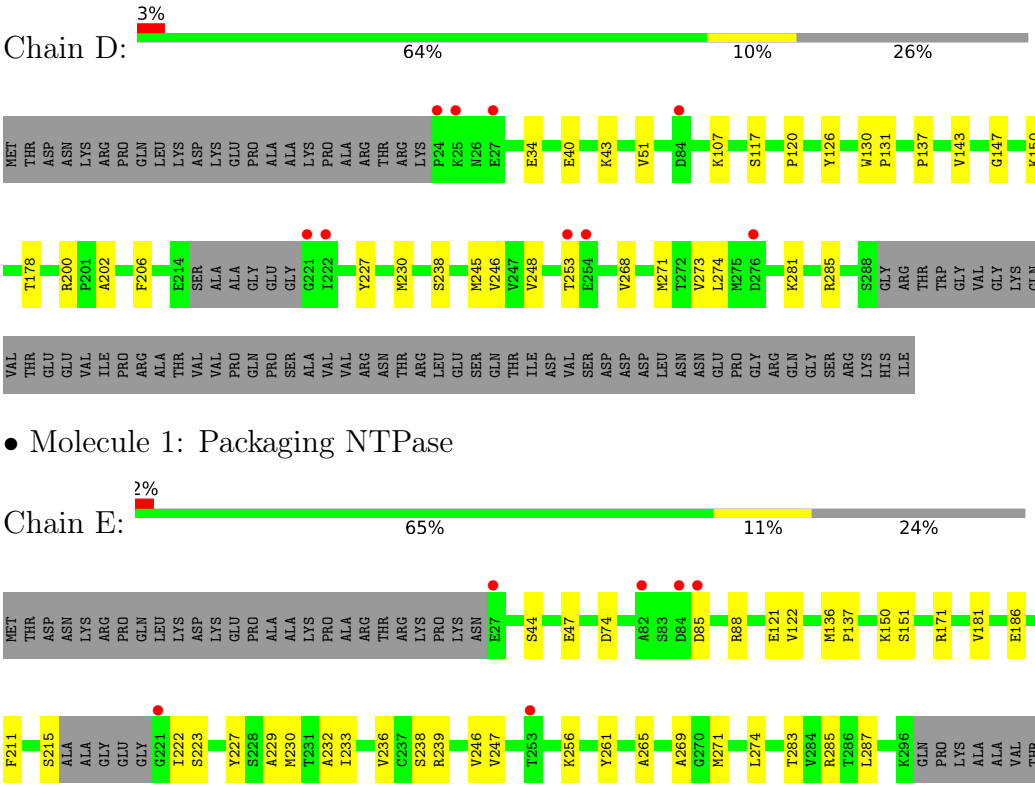


• Molecule 1: Packaging NTPase



• Molecule 1: Packaging NTPase

Chain D:

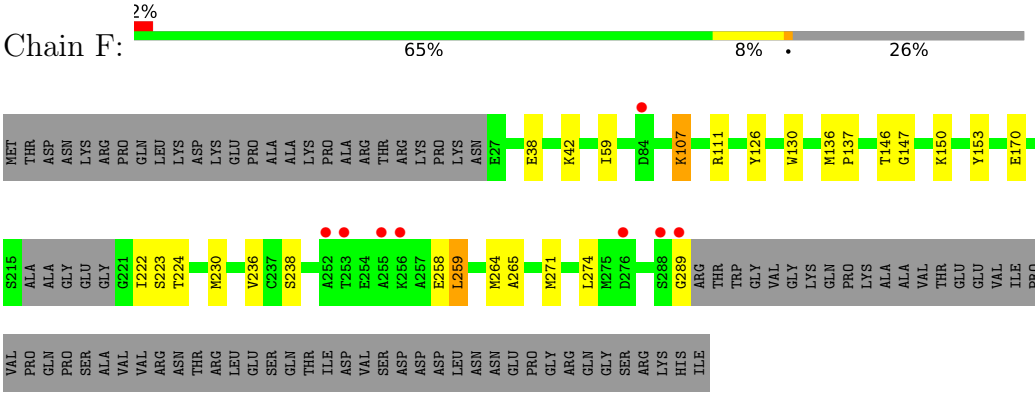


• Molecule 1: Packaging NTPase

Chain E:

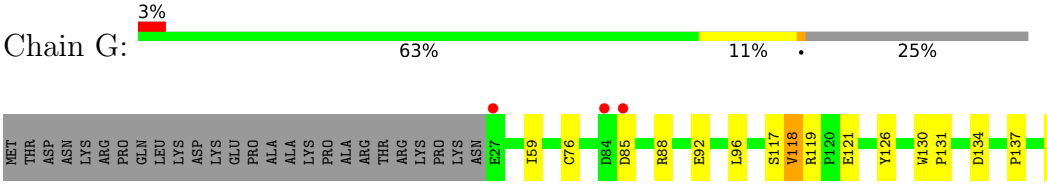
• Molecule 1: Packaging NTPase

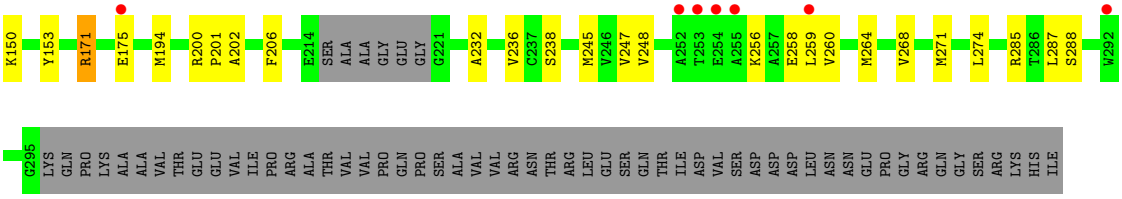
Chain F:



• Molecule 1: Packaging NTPase

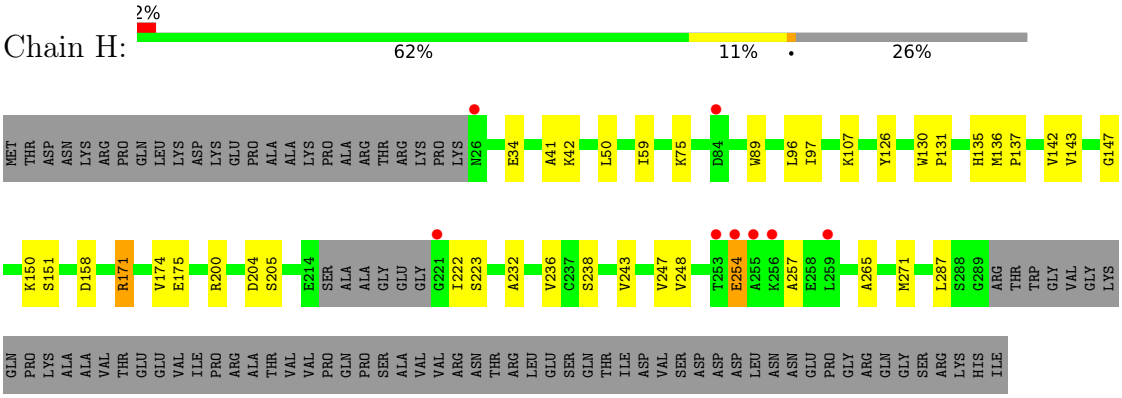
Chain G:





- Molecule 1: Packaging NTPase

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α, β, γ	240.13Å 240.13Å 152.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.97 – 2.43 40.97 – 2.43	Depositor EDS
% Data completeness (in resolution range)	97.8 (40.97-2.43) 97.8 (40.97-2.43)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.19 (at 2.42Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.178 , 0.217 0.178 , 0.218	Depositor DCC
R_{free} test set	2004 reflections (1.65%)	wwPDB-VP
Wilson B-factor (Å^2)	56.6	Xtriage
Anisotropy	0.118	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 44.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.012 for -1/3*h+1/3*k+4/3*l,-k,2/3*h+1/3*k+1/3*l 0.009 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 0.011 for -h,1/3*h-1/3*k-4/3*l,-1/3*h-2/3*k+1/3*l 0.064 for -1/3*h-2/3*k+4/3*l,-2/3*h-1/3*k-4/3*l,1/3*h-1/3*k-1/3*l 0.043 for -h,2/3*h+1/3*k+4/3*l,1/3*h+2/3*k-1/3*l 0.024 for 1/3*h+2/3*k-4/3*l,-k,-2/3*h-1/3*k-1/3*l 0.017 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	15957	wwPDB-VP
Average B, all atoms (Å^2)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TAR, PEG

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	0.48	0/2004	0.67	0/2730
1	B	0.53	0/1962	0.68	2/2673 (0.1%)
1	C	0.47	0/1987	0.62	1/2708 (0.0%)
1	D	0.52	0/1968	0.69	1/2681 (0.0%)
1	E	0.45	0/2000	0.65	0/2724
1	F	0.55	1/1942 (0.1%)	0.65	0/2646
1	G	0.50	0/1985	0.68	3/2705 (0.1%)
1	H	0.46	1/1944 (0.1%)	0.68	2/2649 (0.1%)
All	All	0.49	2/15792 (0.0%)	0.66	9/21516 (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	B	0	1
1	G	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	171	ARG	CZ-NH1	5.20	1.39	1.33
1	F	111	ARG	CZ-NH2	-5.08	1.26	1.33

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	G	171	ARG	NE-CZ-NH1	-9.99	115.31	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	171	ARG	CD-NE-CZ	7.66	134.32	123.60
1	B	171	ARG	NE-CZ-NH2	-7.47	116.56	120.30
1	C	254	GLU	CA-CB-CG	6.92	128.62	113.40
1	H	171	ARG	NE-CZ-NH2	-6.18	117.21	120.30
1	G	171	ARG	CD-NE-CZ	5.52	131.33	123.60
1	D	253	THR	C-N-CA	-5.34	108.36	121.70
1	H	254	GLU	CA-CB-CG	5.32	125.11	113.40
1	G	118	VAL	C-N-CA	-5.09	108.97	121.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	171	ARG	Sidechain
1	G	171	ARG	Sidechain

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	1968	0	1978	15	0
1	B	1928	0	1938	27	0
1	C	1951	0	1959	19	0
1	D	1932	0	1942	23	0
1	E	1964	0	1975	24	0
1	F	1908	0	1917	23	0
1	G	1949	0	1957	27	1
1	H	1910	0	1918	37	1
2	A	10	0	4	1	0
2	B	10	0	4	1	0
2	C	10	0	4	1	0
2	D	10	0	4	1	0
2	E	10	0	4	1	0
2	F	10	0	4	4	0
2	G	10	0	4	0	0
2	H	10	0	4	6	0
3	B	7	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	7	0	10	0	0
3	F	7	0	10	0	0
3	H	7	0	10	0	0
4	A	58	0	0	0	0
4	B	40	0	0	1	0
4	C	34	0	0	0	0
4	D	42	0	0	2	0
4	E	56	0	0	0	0
4	F	49	0	0	0	0
4	G	24	0	0	0	0
4	H	36	0	0	0	0
All	All	15957	0	15656	187	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 6.

All (187) 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:H:147:GLY:H	2:H:401:TAR:H2	1.29	0.97
1:E:137:PRO:HB2	1:E:238:SER:HA	1.59	0.84
1:D:143:VAL:HG21	1:D:271:MET:HE2	1.67	0.77
1:C:121:GLU:HG2	1:C:239:ARG:HG2	1.65	0.76
1:F:147:GLY:H	2:F:401:TAR:H3	1.54	0.72
1:G:150:LYS:HD3	1:G:247:VAL:HG13	1.72	0.72
1:E:181:VAL:HB	1:E:186:GLU:HG3	1.71	0.71
2:H:401:TAR:O2	2:H:401:TAR:O4	2.03	0.70
1:E:150:LYS:HD2	1:E:247:VAL:HG13	1.76	0.68
1:G:143:VAL:HG21	1:G:271:MET:HE2	1.75	0.67
1:B:171:ARG:O	1:B:174:VAL:HG12	1.95	0.67
1:H:137:PRO:HB2	1:H:238:SER:HA	1.76	0.66
1:G:130:TRP:CE2	1:G:200:ARG:HD3	2.31	0.65
1:H:142:VAL:HG12	1:H:150:LYS:HG2	1.78	0.65
1:G:256:LYS:HA	1:G:256:LYS:HE2	1.79	0.64
1:C:137:PRO:HB2	1:C:238:SER:HA	1.80	0.64
1:B:291:THR:O	1:B:291:THR:OG1	2.12	0.63
1:D:273:VAL:CG1	1:D:281:LYS:HB3	2.29	0.63
1:H:222:ILE:HG13	1:H:223:SER:H	1.62	0.63
1:B:171:ARG:O	1:B:174:VAL:CG1	2.48	0.62
1:D:273:VAL:HG12	1:D:281:LYS:HB3	1.82	0.61
1:C:214:GLU:HA	1:C:223:SER:HB2	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:LYS:NZ	2:A:401:TAR:O2	2.28	0.61
1:H:151:SER:HB3	2:H:401:TAR:O41	2.00	0.61
1:E:85:ASP:HB3	1:E:88:ARG:HB3	1.82	0.61
1:H:89:TRP:HZ3	1:H:97:ILE:HD11	1.67	0.60
1:D:137:PRO:HB2	1:D:238:SER:HA	1.84	0.59
1:F:259:LEU:O	1:F:259:LEU:HD22	2.02	0.59
1:B:131:PRO:HD2	1:B:135:HIS:CD2	2.36	0.59
1:E:136:MET:HE3	1:E:137:PRO:HD2	1.84	0.59
1:B:250:PRO:HG3	1:B:261:TYR:HE1	1.68	0.59
1:D:268:VAL:O	1:D:285:ARG:NH1	2.35	0.58
1:D:130:TRP:CE2	1:D:200:ARG:HD3	2.38	0.58
1:G:268:VAL:O	1:G:285:ARG:NH2	2.35	0.58
1:G:153:TYR:HB2	1:G:274:LEU:HD11	1.85	0.58
1:F:136:MET:HE3	1:F:137:PRO:HD2	1.86	0.58
1:B:88:ARG:O	1:B:92:GLU:HG3	2.05	0.56
1:G:194:MET:HE2	1:G:201:PRO:HB3	1.87	0.56
1:H:34:GLU:OE1	1:H:107:LYS:HD2	2.05	0.56
1:D:172:PHE:CE2	1:D:178:THR:HG22	2.40	0.55
1:F:59:ILE:HG12	1:F:236:VAL:HG21	1.88	0.55
1:H:143:VAL:HG12	1:H:248:VAL:HG13	1.89	0.55
1:H:147:GLY:N	2:H:401:TAR:H2	2.12	0.55
1:H:150:LYS:N	2:H:401:TAR:O4	2.38	0.55
1:H:222:ILE:HG13	1:H:223:SER:N	2.22	0.55
1:B:227:TYR:HA	1:B:230:MET:HE2	1.90	0.54
1:C:164:ARG:NH1	1:C:204:ASP:OD2	2.41	0.54
1:B:171:ARG:HD2	1:C:287:LEU:O	2.08	0.54
1:A:290:ARG:NH2	1:F:170:GLU:OE1	2.42	0.53
1:D:126:TYR:CE2	1:D:137:PRO:HD3	2.44	0.53
2:F:401:TAR:O11	2:F:401:TAR:O3	2.22	0.53
1:G:85:ASP:HB3	1:G:88:ARG:HB3	1.92	0.52
1:A:265:ALA:HB2	1:A:271:MET:HE2	1.92	0.52
1:F:230:MET:HE1	1:F:264:MET:HG2	1.91	0.52
1:F:153:TYR:HB2	1:F:274:LEU:HD21	1.92	0.52
1:H:205:SER:HB3	1:H:247:VAL:HG23	1.93	0.51
1:B:265:ALA:HB2	1:B:271:MET:HE2	1.92	0.50
1:A:206:PHE:CD2	1:A:246:VAL:HG11	2.46	0.50
1:B:126:TYR:CE1	1:B:137:PRO:HD3	2.46	0.50
1:D:40:GLU:HA	1:D:43:LYS:HE2	1.94	0.50
1:D:150:LYS:HA	1:D:274:LEU:HD12	1.94	0.50
1:B:222:ILE:HG13	1:B:223:SER:H	1.76	0.50
1:A:150:LYS:HD2	1:A:247:VAL:HG13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:151:SER:H	2:E:401:TAR:H2	1.77	0.49
1:D:172:PHE:CE2	1:D:178:THR:CG2	2.95	0.49
1:E:215:SER:HB3	1:E:223:SER:OG	2.13	0.49
1:H:204:ASP:HA	1:H:247:VAL:HG22	1.95	0.49
1:G:119:ARG:NE	1:G:121:GLU:OE2	2.38	0.49
1:C:130:TRP:CD1	1:C:131:PRO:HA	2.47	0.49
1:C:275:MET:HG3	1:C:280:SER:HB2	1.95	0.49
1:F:137:PRO:HB2	1:F:238:SER:HA	1.95	0.48
1:B:137:PRO:HB2	1:B:238:SER:HA	1.94	0.48
1:E:261:TYR:O	1:E:271:MET:HE1	2.13	0.48
1:B:285:ARG:HA	1:B:290:ARG:HA	1.94	0.48
1:H:131:PRO:HD2	1:H:135:HIS:CD2	2.49	0.48
1:A:290:ARG:HH21	1:F:170:GLU:CD	2.17	0.48
1:C:126:TYR:CE2	1:C:137:PRO:HD3	2.48	0.48
1:E:227:TYR:HA	1:E:230:MET:HE2	1.96	0.48
1:A:232:ALA:O	1:A:236:VAL:HG23	2.14	0.47
1:C:84:ASP:OD1	1:C:84:ASP:N	2.44	0.47
1:F:107:LYS:HD3	1:F:107:LYS:HA	1.50	0.47
1:F:150:LYS:HA	1:F:274:LEU:HD22	1.94	0.47
1:D:147:GLY:H	2:D:401:TAR:H3	1.79	0.47
1:D:206:PHE:HB2	1:D:248:VAL:HG22	1.97	0.47
1:G:59:ILE:HG12	1:G:236:VAL:HG21	1.95	0.47
1:F:38:GLU:O	1:F:42:LYS:HG3	2.14	0.47
1:H:174:VAL:HG13	1:H:175:GLU:HG3	1.97	0.47
1:B:55:HIS:HB3	4:B:504:HOH:O	2.13	0.47
1:E:44:SER:OG	1:E:47:GLU:HG3	2.13	0.47
1:G:143:VAL:CG2	1:G:271:MET:HE2	2.44	0.47
1:G:232:ALA:O	1:G:236:VAL:HG23	2.15	0.47
1:B:146:THR:HA	2:B:401:TAR:O41	2.15	0.47
1:B:174:VAL:O	1:B:174:VAL:HG22	2.15	0.47
1:D:227:TYR:HA	1:D:230:MET:HE2	1.97	0.46
1:H:130:TRP:CG	1:H:131:PRO:HA	2.49	0.46
1:D:34:GLU:OE2	1:D:107:LYS:HD3	2.15	0.46
1:H:150:LYS:HE2	2:H:401:TAR:O2	2.15	0.46
1:B:183:ASP:OD2	1:B:185:ASN:HB2	2.15	0.46
1:C:138:GLY:HA2	1:C:237:CYS:HB2	1.97	0.46
1:H:254:GLU:OE1	1:H:257:ALA:HB3	2.16	0.46
1:E:229:ALA:O	1:E:233:ILE:HG13	2.16	0.46
1:A:126:TYR:CE2	1:A:137:PRO:HD3	2.50	0.46
1:G:150:LYS:HD3	1:G:247:VAL:CG1	2.44	0.45
1:D:206:PHE:CD2	1:D:246:VAL:HG11	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:222:ILE:HG13	1:F:223:SER:N	2.30	0.45
1:F:259:LEU:HD23	1:F:259:LEU:HA	1.80	0.45
2:F:401:TAR:O4	2:F:401:TAR:O2	2.32	0.45
1:H:222:ILE:CG1	1:H:223:SER:H	2.29	0.45
1:B:55:HIS:CD2	1:B:55:HIS:H	2.34	0.45
1:E:206:PHE:CD2	1:E:246:VAL:HG11	2.51	0.45
1:C:208:ASN:ND2	1:D:117:SER:HB2	2.32	0.45
1:G:134:ASP:HB3	1:G:287:LEU:HB2	1.99	0.45
1:D:171:ARG:HG3	1:E:287:LEU:O	2.17	0.45
1:E:269:ALA:O	1:E:285:ARG:HD2	2.17	0.45
1:E:122:VAL:HG22	1:E:137:PRO:HG2	1.99	0.45
1:C:46:ARG:NH2	1:C:69:ASP:OD2	2.44	0.45
1:H:130:TRP:CD1	1:H:131:PRO:HA	2.52	0.45
1:A:117:SER:HB2	1:F:208:ASN:HD21	1.82	0.44
1:C:230:MET:HE1	1:C:264:MET:HG2	1.99	0.44
1:H:158:ASP:HB3	1:H:200:ARG:NH1	2.32	0.44
1:H:131:PRO:HD3	1:H:243:VAL:HG11	1.98	0.44
1:C:180:ALA:HB1	1:D:120:PRO:HD2	2.00	0.44
1:H:126:TYR:CE2	1:H:137:PRO:HD3	2.52	0.44
1:G:206:PHE:HB2	1:G:248:VAL:HG22	1.98	0.44
1:H:89:TRP:CZ3	1:H:97:ILE:HD11	2.50	0.44
1:H:265:ALA:HB2	1:H:271:MET:CE	2.46	0.44
1:G:130:TRP:CD1	1:G:131:PRO:HA	2.53	0.44
1:G:85:ASP:HB3	1:G:88:ARG:CB	2.47	0.44
1:B:153:TYR:HB2	1:B:274:LEU:HD11	2.00	0.43
1:B:171:ARG:O	1:B:171:ARG:HG3	2.17	0.43
1:H:171:ARG:O	1:H:174:VAL:HG12	2.17	0.43
1:H:265:ALA:HB2	1:H:271:MET:HE2	1.98	0.43
1:E:222:ILE:HG13	1:E:223:SER:H	1.82	0.43
1:A:290:ARG:NH2	1:F:170:GLU:CD	2.71	0.43
1:C:88:ARG:O	1:C:92:GLU:HG3	2.18	0.43
1:F:130:TRP:CE2	1:F:200:ARG:HD3	2.53	0.43
1:G:126:TYR:CE2	1:G:137:PRO:HD3	2.53	0.43
1:F:265:ALA:HB2	1:F:271:MET:CE	2.48	0.43
1:H:158:ASP:HB3	1:H:200:ARG:HH11	1.83	0.43
1:F:146:THR:HA	2:F:401:TAR:H3	2.01	0.43
1:C:250:PRO:HG3	1:C:264:MET:HE1	2.00	0.43
1:D:130:TRP:CD1	1:D:131:PRO:HA	2.53	0.43
1:E:74:ASP:OD1	1:E:196:ARG:NH2	2.52	0.43
1:E:256:LYS:HA	1:E:256:LYS:HE2	2.00	0.43
1:G:260:VAL:O	1:G:264:MET:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:ASN:HA	1:A:238:SER:HB3	2.01	0.42
1:E:232:ALA:O	1:E:236:VAL:HG23	2.19	0.42
1:G:76:CYS:SG	1:G:96:LEU:HD13	2.59	0.42
1:G:117:SER:OG	1:G:118:VAL:N	2.52	0.42
1:B:117:SER:OG	1:B:118:VAL:N	2.51	0.42
1:H:42:LYS:HB3	1:H:42:LYS:HE2	1.71	0.42
1:E:211:PHE:CD1	1:F:224:THR:HB	2.55	0.42
1:G:137:PRO:HB2	1:G:238:SER:HA	2.02	0.42
1:E:150:LYS:HA	1:E:274:LEU:HD12	2.00	0.42
1:F:126:TYR:CE2	1:F:137:PRO:HD3	2.54	0.42
1:B:150:LYS:HE2	1:B:150:LYS:HB2	1.72	0.42
1:C:97:ILE:HG13	1:C:98:HIS:N	2.35	0.42
1:G:92:GLU:N	1:G:92:GLU:OE1	2.53	0.42
1:D:51:VAL:HG13	4:D:537:HOH:O	2.20	0.41
1:E:265:ALA:HB1	1:E:283:THR:HG21	2.02	0.41
1:G:258:GLU:HG3	1:G:259:LEU:N	2.35	0.41
1:H:287:LEU:HD23	1:H:287:LEU:HA	1.69	0.41
1:B:150:LYS:HA	1:B:274:LEU:HD12	2.01	0.41
1:B:287:LEU:HD13	1:B:287:LEU:HA	1.73	0.41
1:A:274:LEU:HA	1:A:274:LEU:HD23	1.81	0.41
1:D:202:ALA:HA	1:D:245:MET:O	2.21	0.41
1:H:130:TRP:CD2	1:H:200:ARG:HD2	2.55	0.41
1:A:256:LYS:HA	1:A:256:LYS:HE2	2.02	0.41
1:H:75:LYS:HE3	1:H:96:LEU:HD21	2.02	0.41
1:A:130:TRP:CD1	1:A:131:PRO:HA	2.55	0.41
1:B:206:PHE:CD2	1:B:246:VAL:HG11	2.56	0.41
1:C:147:GLY:HA2	2:C:401:TAR:H3	2.02	0.41
1:G:202:ALA:HA	1:G:245:MET:O	2.21	0.41
1:G:287:LEU:HA	1:G:287:LEU:HD23	1.87	0.41
1:H:232:ALA:O	1:H:236:VAL:HG23	2.21	0.41
1:C:206:PHE:CD2	1:C:246:VAL:HG11	2.56	0.41
1:D:170:GLU:HG3	4:D:501:HOH:O	2.20	0.41
1:E:121:GLU:HG2	1:E:239:ARG:HG2	2.01	0.41
1:H:59:ILE:HG12	1:H:236:VAL:HG21	2.03	0.41
1:A:285:ARG:HD3	1:F:170:GLU:HG2	2.02	0.40
1:B:130:TRP:CD1	1:B:131:PRO:HA	2.56	0.40
1:B:204:ASP:OD1	1:B:205:SER:HB3	2.22	0.40
1:E:171:ARG:HD3	1:F:289:GLY:HA3	2.03	0.40
1:H:41:ALA:HB1	1:H:50:LEU:HD12	2.03	0.40
1:H:136:MET:HE3	1:H:137:PRO:HD2	2.04	0.40
1:G:143:VAL:HG21	1:G:271:MET:CE	2.48	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:205:SER:CB	1:H:247:VAL:HG23	2.52	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)
1:G:288:SER:CA	1:H:171:ARG:NH2[2_655]	2.05	0.15

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	261/350 (75%)	252 (97%)	9 (3%)	0	100	100
1	B	256/350 (73%)	248 (97%)	8 (3%)	0	100	100
1	C	259/350 (74%)	249 (96%)	10 (4%)	0	100	100
1	D	256/350 (73%)	246 (96%)	10 (4%)	0	100	100
1	E	261/350 (75%)	252 (97%)	9 (3%)	0	100	100
1	F	254/350 (73%)	247 (97%)	7 (3%)	0	100	100
1	G	259/350 (74%)	248 (96%)	11 (4%)	0	100	100
1	H	254/350 (73%)	244 (96%)	10 (4%)	0	100	100
All	All	2060/2800 (74%)	1986 (96%)	74 (4%)	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	207/278 (74%)	206 (100%)	1 (0%)	88 93
1	B	203/278 (73%)	201 (99%)	2 (1%)	76 84
1	C	205/278 (74%)	205 (100%)	0	100 100
1	D	204/278 (73%)	204 (100%)	0	100 100
1	E	206/278 (74%)	206 (100%)	0	100 100
1	F	201/278 (72%)	198 (98%)	3 (2%)	65 76
1	G	204/278 (73%)	203 (100%)	1 (0%)	88 93
1	H	201/278 (72%)	201 (100%)	0	100 100
All	All	1631/2224 (73%)	1624 (100%)	7 (0%)	91 94

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	171	ARG
1	B	287	LEU
1	B	288	SER
1	F	107	LYS
1	F	258	GLU
1	F	259	LEU
1	G	175	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

12 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	$\#\|Z\| > 2$
2	TAR	D	401	-	9,9,9	1.00	0	12,12,12	1.97	4 (33%)
2	TAR	A	401	-	9,9,9	1.33	1 (11%)	12,12,12	1.76	4 (33%)
2	TAR	B	401	-	9,9,9	1.26	0	12,12,12	1.69	2 (16%)
2	TAR	G	401	-	9,9,9	1.13	0	12,12,12	1.41	3 (25%)
3	PEG	B	402	-	6,6,6	0.50	0	5,5,5	0.55	0
3	PEG	F	402	-	6,6,6	0.47	0	5,5,5	0.32	0
2	TAR	F	401	-	9,9,9	1.12	0	12,12,12	1.86	5 (41%)
2	TAR	H	401	-	9,9,9	1.01	0	12,12,12	1.68	2 (16%)
3	PEG	D	402	-	6,6,6	0.49	0	5,5,5	0.45	0
2	TAR	C	401	-	9,9,9	1.06	0	12,12,12	1.65	2 (16%)
2	TAR	E	401	-	9,9,9	1.15	0	12,12,12	2.02	4 (33%)
3	PEG	H	402	-	6,6,6	0.48	0	5,5,5	0.39	0

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
2	TAR	D	401	-	-	8/12/12/12	-
2	TAR	A	401	-	-	8/12/12/12	-
2	TAR	B	401	-	-	4/12/12/12	-
2	TAR	G	401	-	-	10/12/12/12	-
3	PEG	B	402	-	-	2/4/4/4	-
3	PEG	F	402	-	-	3/4/4/4	-
2	TAR	F	401	-	-	12/12/12/12	-
2	TAR	H	401	-	-	10/12/12/12	-
3	PEG	D	402	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	TAR	C	401	-	-	6/12/12/12	-
2	TAR	E	401	-	-	4/12/12/12	-
3	PEG	H	402	-	-	2/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	TAR	C3-C4	2.28	1.55	1.52

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	401	TAR	O2-C2-C3	-3.57	103.14	110.23
2	D	401	TAR	O41-C4-C3	3.53	122.82	113.27
2	A	401	TAR	O2-C2-C1	-3.48	103.38	110.66
2	B	401	TAR	O2-C2-C1	-3.41	103.51	110.66
2	F	401	TAR	O41-C4-C3	3.23	122.01	113.27
2	E	401	TAR	C2-C3-C4	-3.19	102.74	109.87
2	C	401	TAR	O11-C1-C2	3.13	121.72	113.27
2	F	401	TAR	O11-C1-C2	2.98	121.34	113.27
2	C	401	TAR	O41-C4-C3	2.96	121.28	113.27
2	G	401	TAR	O41-C4-C3	2.81	120.88	113.27
2	H	401	TAR	O41-C4-C3	2.77	120.77	113.27
2	D	401	TAR	O11-C1-C2	2.72	120.61	113.27
2	E	401	TAR	O11-C1-C2	2.65	120.44	113.27
2	H	401	TAR	O11-C1-C2	2.63	120.39	113.27
2	D	401	TAR	O3-C3-C2	-2.54	105.19	110.23
2	E	401	TAR	O41-C4-C3	2.52	120.08	113.27
2	A	401	TAR	O41-C4-O4	-2.50	118.41	124.09
2	F	401	TAR	O2-C2-C1	-2.49	105.45	110.66
2	F	401	TAR	O41-C4-O4	-2.45	118.52	124.09
2	A	401	TAR	O41-C4-C3	2.36	119.65	113.27
2	D	401	TAR	C3-C2-C1	-2.32	104.70	109.87
2	A	401	TAR	C2-C3-C4	2.28	114.97	109.87
2	G	401	TAR	O41-C4-O4	-2.26	118.95	124.09
2	F	401	TAR	O11-C1-O1	-2.19	119.11	124.09
2	G	401	TAR	O11-C1-C2	2.18	119.17	113.27
2	B	401	TAR	O41-C4-C3	2.17	119.13	113.27

There are no chirality outliers.

All (69) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	401	TAR	O1-C1-C2-C3
2	D	401	TAR	O11-C1-C2-C3
2	F	401	TAR	C2-C3-C4-O41
2	H	401	TAR	C1-C2-C3-C4
2	H	401	TAR	O2-C2-C3-O3
2	F	401	TAR	C1-C2-C3-C4
2	B	401	TAR	O1-C1-C2-O2
2	D	401	TAR	O1-C1-C2-O2
2	D	401	TAR	O11-C1-C2-O2
2	E	401	TAR	O1-C1-C2-O2
2	E	401	TAR	O11-C1-C2-O2
2	F	401	TAR	O1-C1-C2-O2
2	F	401	TAR	O11-C1-C2-O2
2	H	401	TAR	O1-C1-C2-O2
2	H	401	TAR	O11-C1-C2-O2
2	A	401	TAR	C2-C3-C4-O4
2	A	401	TAR	C2-C3-C4-O41
2	F	401	TAR	O1-C1-C2-C3
2	F	401	TAR	O11-C1-C2-C3
2	F	401	TAR	C2-C3-C4-O4
2	F	401	TAR	C1-C2-C3-O3
2	F	401	TAR	O2-C2-C3-C4
2	H	401	TAR	C1-C2-C3-O3
2	F	401	TAR	O2-C2-C3-O3
2	A	401	TAR	O3-C3-C4-O4
2	A	401	TAR	O3-C3-C4-O41
2	B	401	TAR	O11-C1-C2-O2
2	B	401	TAR	O3-C3-C4-O4
2	B	401	TAR	O3-C3-C4-O41
2	G	401	TAR	O1-C1-C2-O2
2	G	401	TAR	O11-C1-C2-O2
2	H	401	TAR	O2-C2-C3-C4
2	F	401	TAR	O3-C3-C4-O4
2	F	401	TAR	O3-C3-C4-O41
2	C	401	TAR	C2-C3-C4-O41
2	H	401	TAR	O11-C1-C2-C3
3	H	402	PEG	O2-C3-C4-O4
2	C	401	TAR	C2-C3-C4-O4
2	H	401	TAR	O1-C1-C2-C3
3	H	402	PEG	O1-C1-C2-O2
2	G	401	TAR	C2-C3-C4-O4
2	C	401	TAR	O1-C1-C2-C3
2	G	401	TAR	C2-C3-C4-O41

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Mol	Chain	Res	Type	Atoms
2	G	401	TAR	O2-C2-C3-C4
2	G	401	TAR	O2-C2-C3-O3
2	C	401	TAR	O11-C1-C2-C3
3	B	402	PEG	O1-C1-C2-O2
3	F	402	PEG	O2-C3-C4-O4
2	D	401	TAR	C2-C3-C4-O4
2	G	401	TAR	C1-C2-C3-O3
2	D	401	TAR	C2-C3-C4-O41
2	A	401	TAR	O11-C1-C2-C3
3	F	402	PEG	C1-C2-O2-C3
2	A	401	TAR	O1-C1-C2-C3
2	E	401	TAR	C2-C3-C4-O4
3	F	402	PEG	C4-C3-O2-C2
2	E	401	TAR	C2-C3-C4-O41
2	G	401	TAR	O3-C3-C4-O4
2	C	401	TAR	O3-C3-C4-O41
2	C	401	TAR	O3-C3-C4-O4
3	B	402	PEG	C4-C3-O2-C2
2	G	401	TAR	C1-C2-C3-C4
2	H	401	TAR	C2-C3-C4-O4
2	A	401	TAR	O1-C1-C2-O2
2	G	401	TAR	O3-C3-C4-O41
2	H	401	TAR	C2-C3-C4-O41
2	D	401	TAR	O3-C3-C4-O4
2	A	401	TAR	O11-C1-C2-O2
2	D	401	TAR	O3-C3-C4-O41

There are no ring outliers.

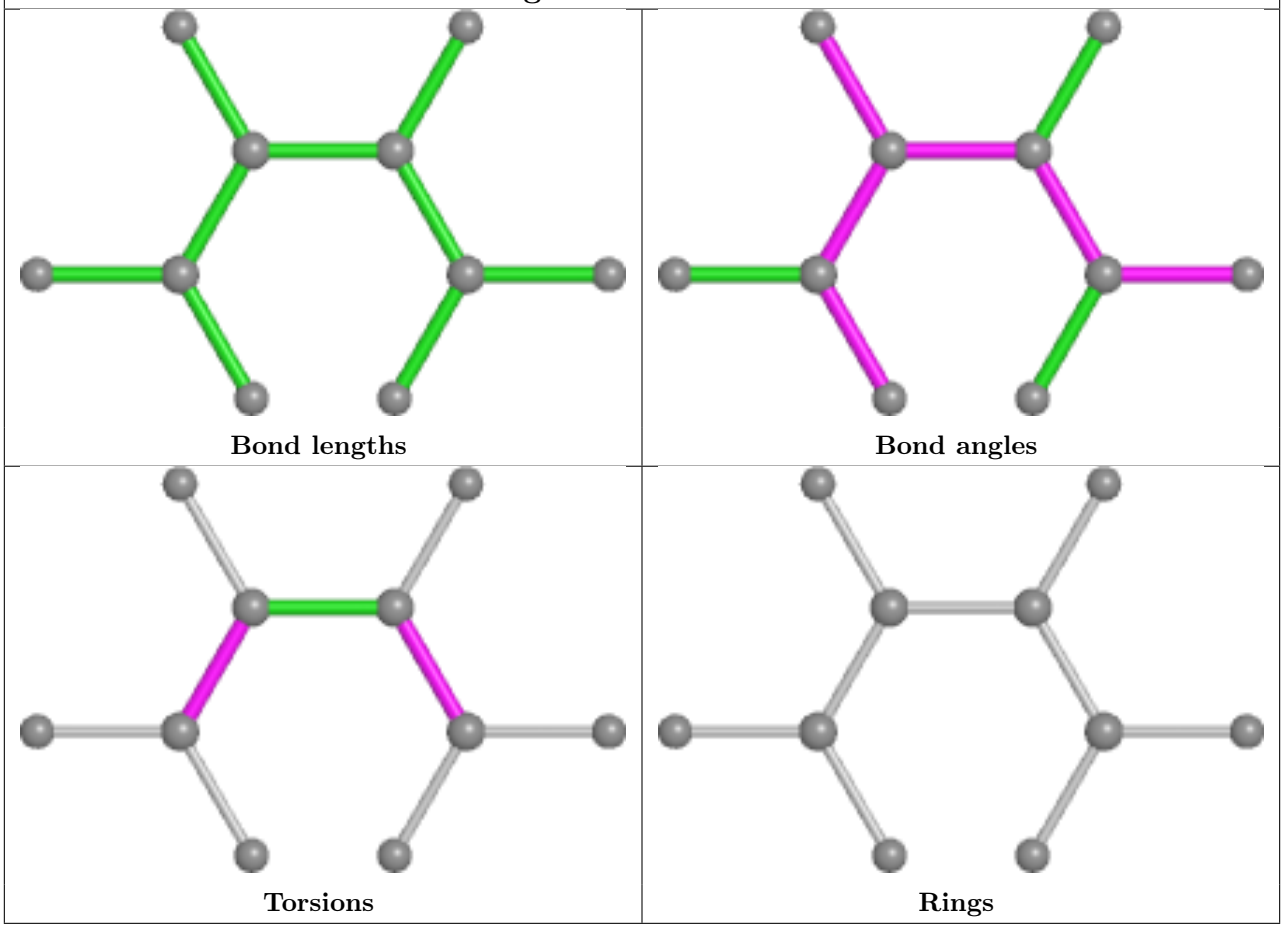
7 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	401	TAR	1	0
2	A	401	TAR	1	0
2	B	401	TAR	1	0
2	F	401	TAR	4	0
2	H	401	TAR	6	0
2	C	401	TAR	1	0
2	E	401	TAR	1	0

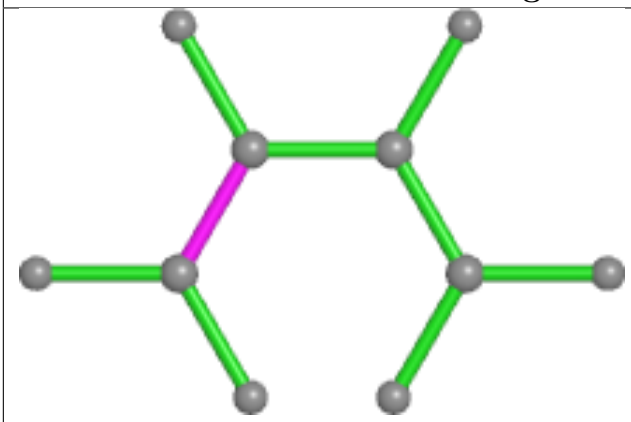
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

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.

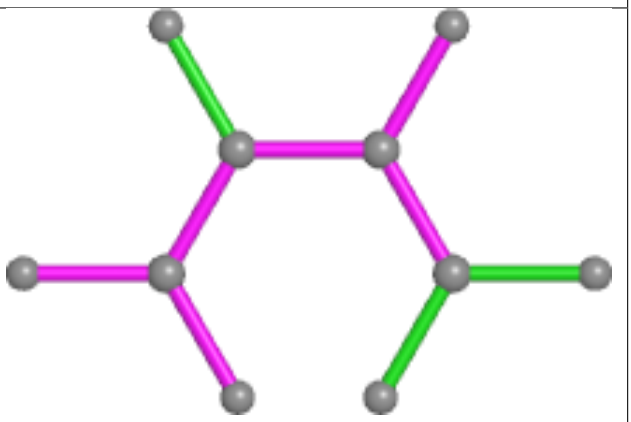
Ligand TAR D 401



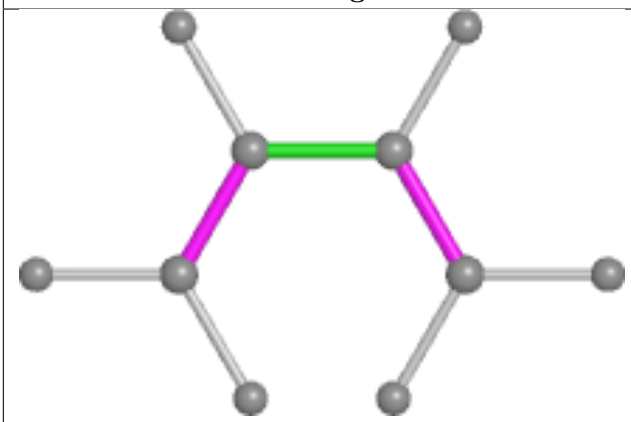
Ligand TAR A 401



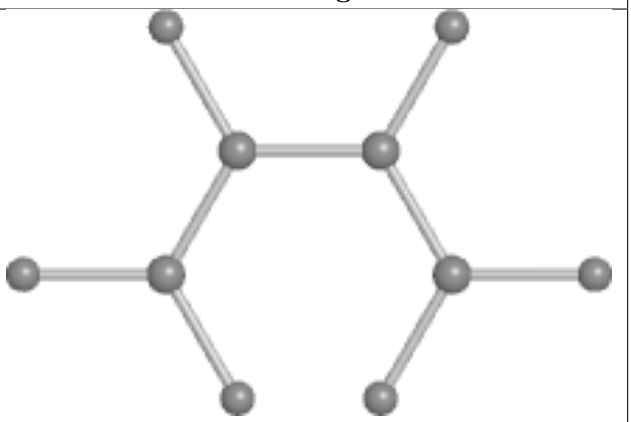
Bond lengths



Bond angles

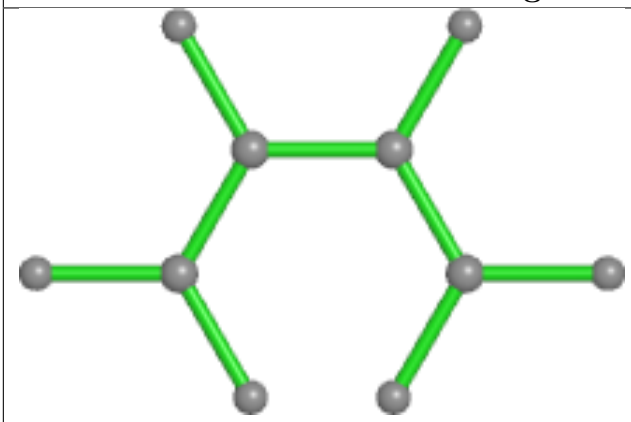


Torsions

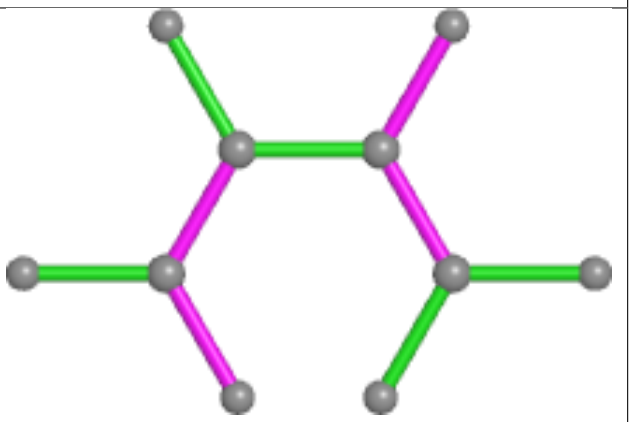


Rings

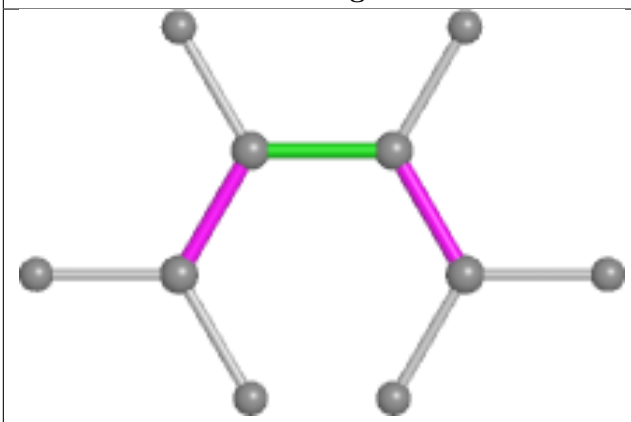
Ligand TAR B 401



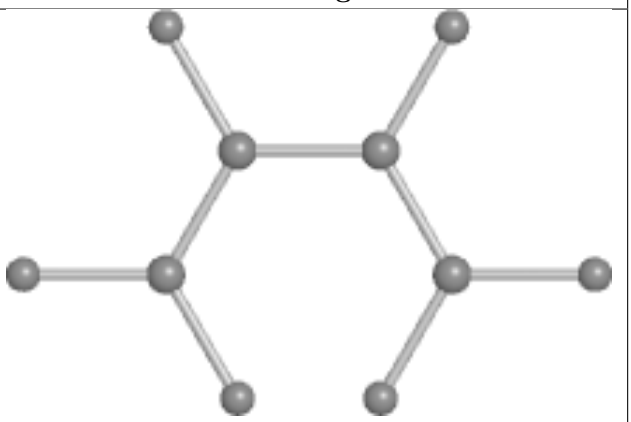
Bond lengths



Bond angles

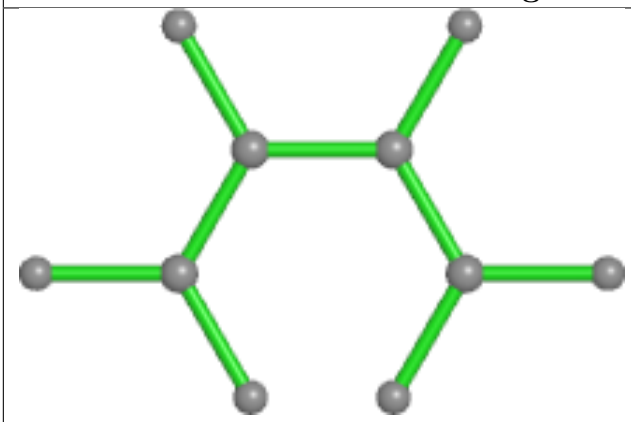


Torsions

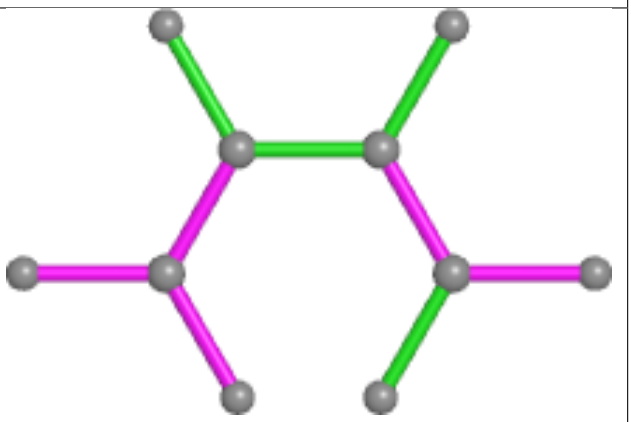


Rings

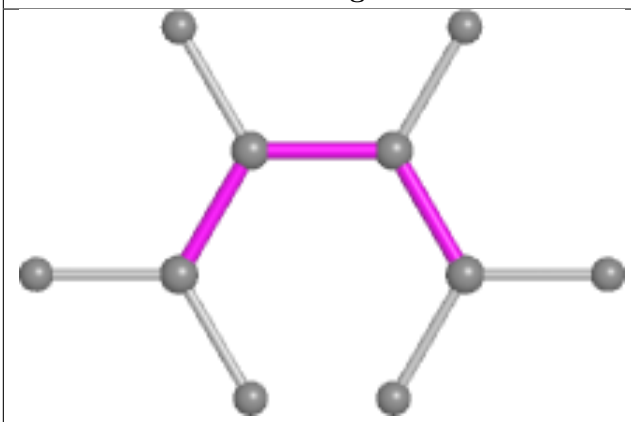
Ligand TAR G 401



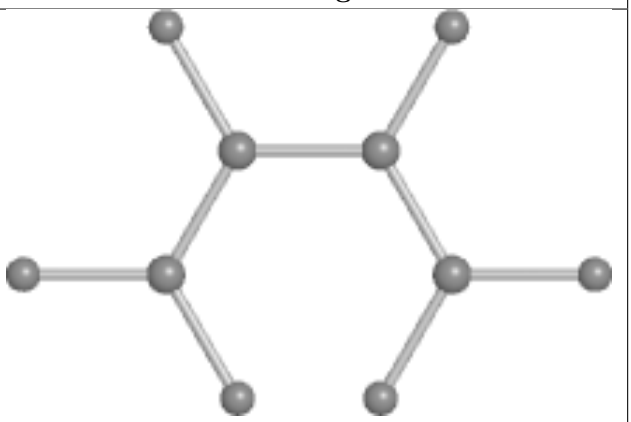
Bond lengths



Bond angles

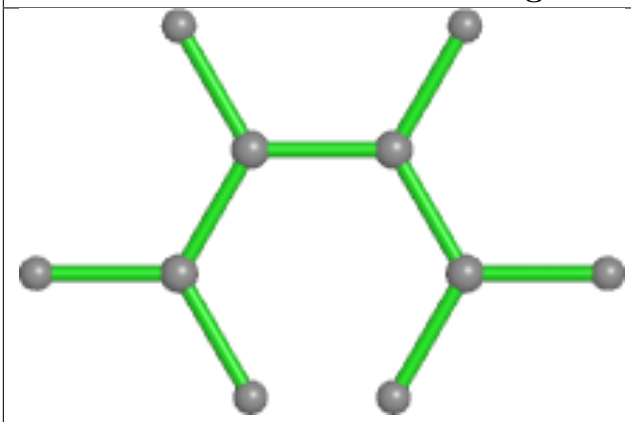


Torsions

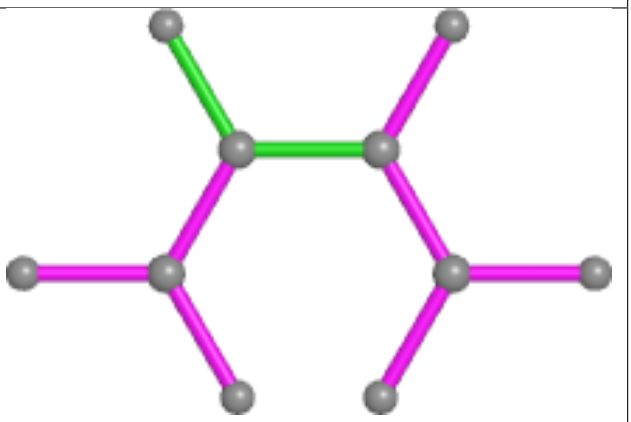


Rings

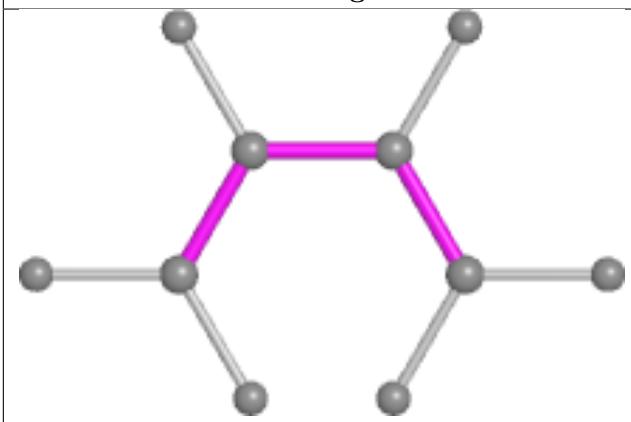
Ligand TAR F 401



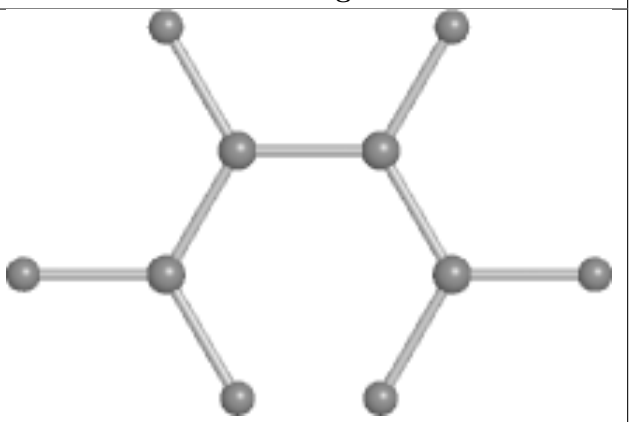
Bond lengths



Bond angles

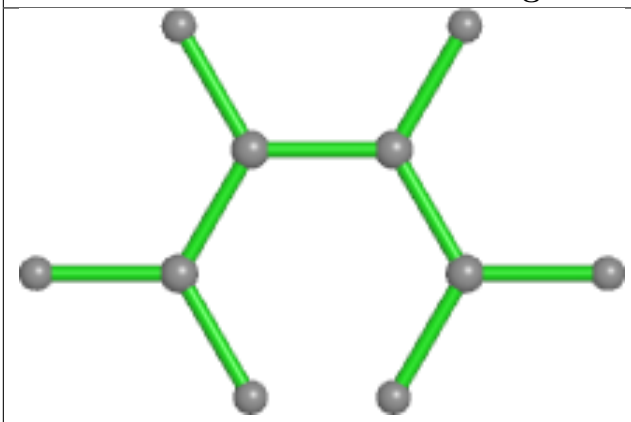


Torsions

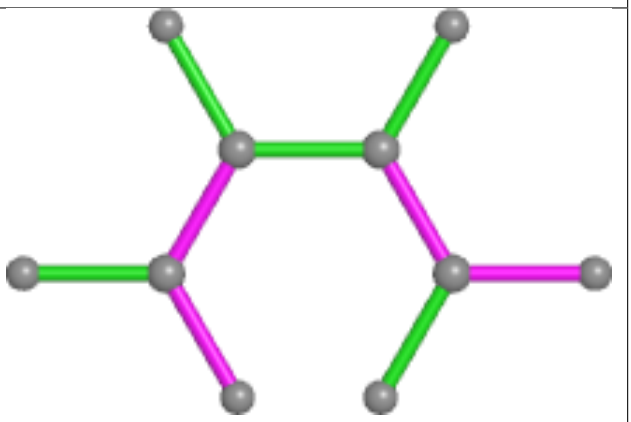


Rings

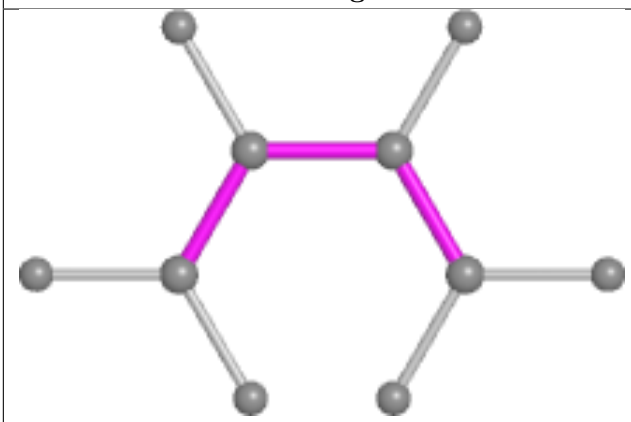
Ligand TAR H 401



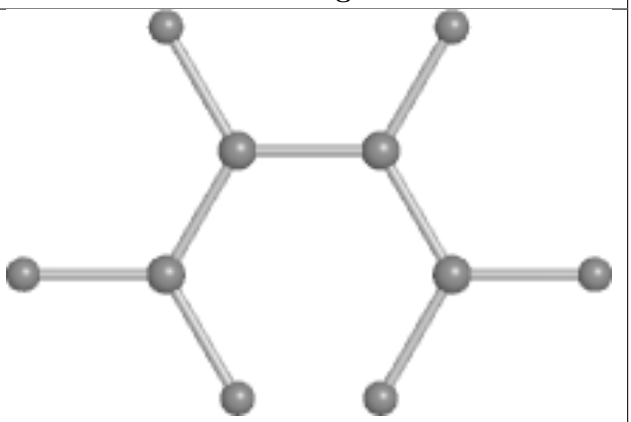
Bond lengths



Bond angles

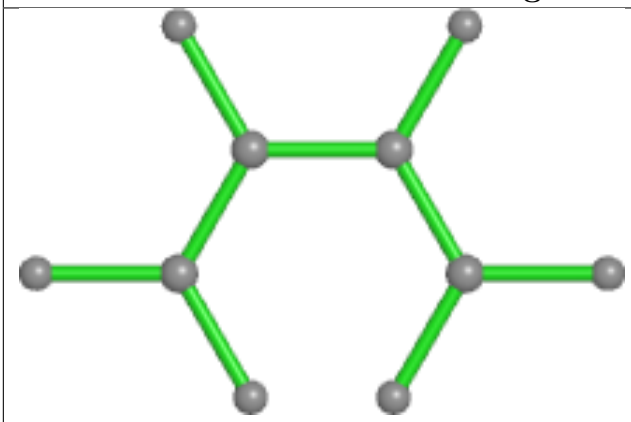


Torsions

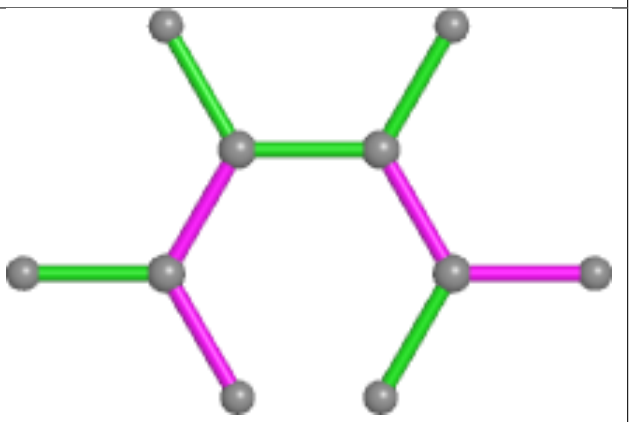


Rings

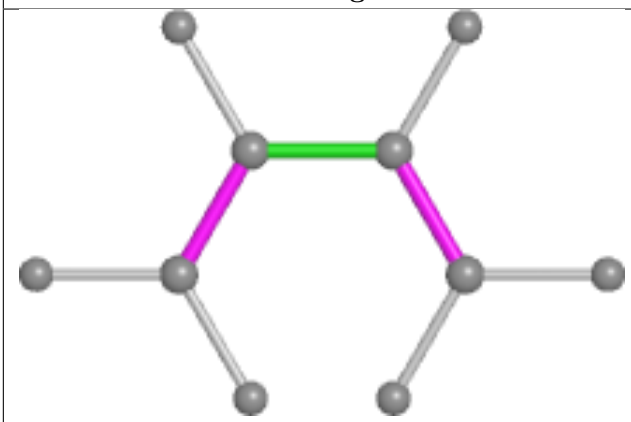
Ligand TAR C 401



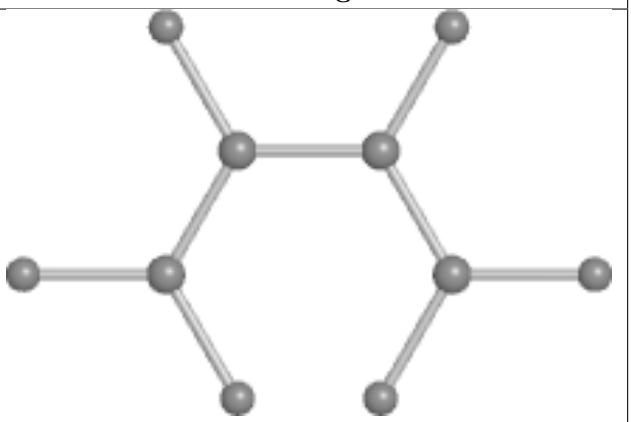
Bond lengths



Bond angles

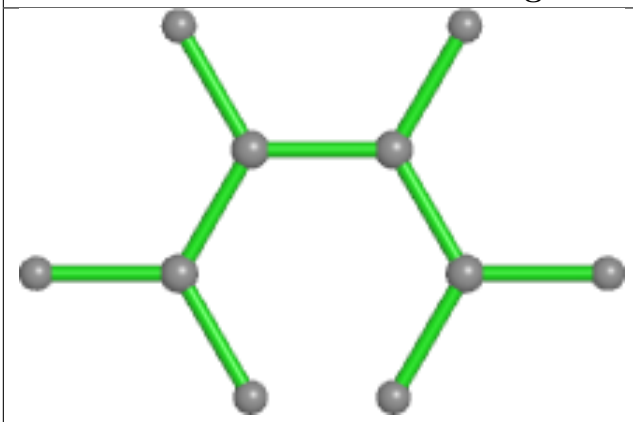


Torsions

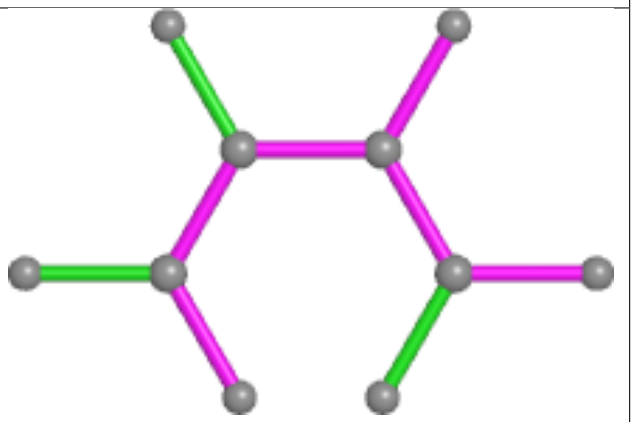


Rings

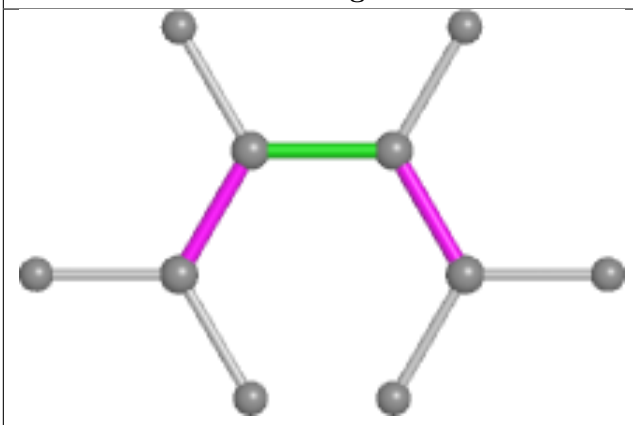
Ligand TAR E 401



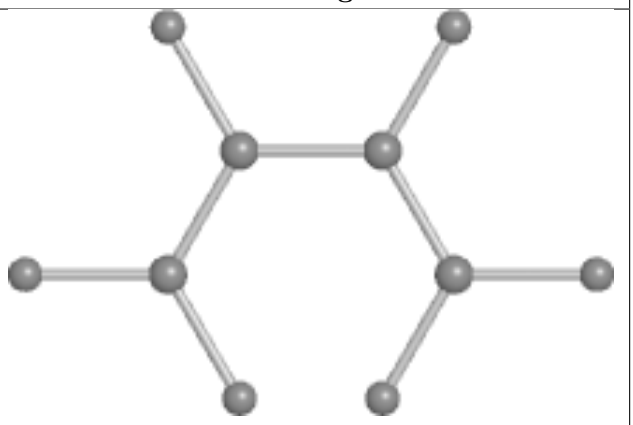
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 95^{th} 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	265/350 (75%)	-0.14	5 (1%)	66	63	42, 55, 81, 102	0
1	B	260/350 (74%)	-0.13	8 (3%)	49	45	43, 58, 84, 102	0
1	C	263/350 (75%)	0.00	12 (4%)	32	30	47, 62, 91, 104	0
1	D	259/350 (74%)	-0.15	9 (3%)	44	40	43, 57, 85, 100	0
1	E	265/350 (75%)	-0.15	6 (2%)	60	56	42, 55, 83, 99	0
1	F	258/350 (73%)	-0.14	8 (3%)	49	45	41, 55, 81, 97	0
1	G	263/350 (75%)	0.03	11 (4%)	36	33	46, 64, 91, 106	0
1	H	258/350 (73%)	-0.12	8 (3%)	49	45	48, 60, 89, 101	0
All	All	2091/2800 (74%)	-0.10	67 (3%)	47	44	41, 58, 87, 106	0

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	255	ALA	5.3
1	H	221	GLY	5.3
1	C	252	ALA	4.9
1	G	84	ASP	4.4
1	A	26	ASN	4.1
1	C	292	TRP	4.1
1	E	84	ASP	3.9
1	C	84	ASP	3.8
1	A	84	ASP	3.6
1	E	27	GLU	3.5
1	C	27	GLU	3.4
1	G	27	GLU	3.3
1	G	253	THR	3.2
1	A	27	GLU	3.2
1	E	221	GLY	3.2
1	F	255	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	253	THR	3.1
1	H	84	ASP	3.0
1	H	259	LEU	3.0
1	C	255	ALA	2.9
1	B	289	GLY	2.9
1	C	256	LYS	2.9
1	G	292	TRP	2.9
1	A	253	THR	2.8
1	D	253	THR	2.8
1	H	26	ASN	2.8
1	H	255	ALA	2.8
1	F	253	THR	2.8
1	G	175	GLU	2.7
1	G	85	ASP	2.7
1	H	254	GLU	2.6
1	H	256	LYS	2.6
1	D	276	ASP	2.6
1	A	259	LEU	2.6
1	G	254	GLU	2.6
1	H	253	THR	2.5
1	E	82	ALA	2.5
1	D	254	GLU	2.5
1	C	294	VAL	2.5
1	B	175	GLU	2.4
1	C	85	ASP	2.4
1	F	252	ALA	2.4
1	B	258	GLU	2.4
1	C	259	LEU	2.4
1	D	222	ILE	2.3
1	E	85	ASP	2.3
1	D	221	GLY	2.3
1	C	253	THR	2.3
1	B	252	ALA	2.2
1	B	255	ALA	2.2
1	F	288	SER	2.2
1	D	84	ASP	2.1
1	C	254	GLU	2.1
1	F	276	ASP	2.1
1	C	83	SER	2.1
1	D	25	LYS	2.1
1	B	290	ARG	2.1
1	D	27	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	F	289	GLY	2.1
1	G	145	GLY	2.1
1	G	252	ALA	2.1
1	E	253	THR	2.1
1	F	84	ASP	2.0
1	D	24	PRO	2.0
1	B	256	LYS	2.0
1	F	256	LYS	2.0
1	G	259	LEU	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, 95^{th} 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.

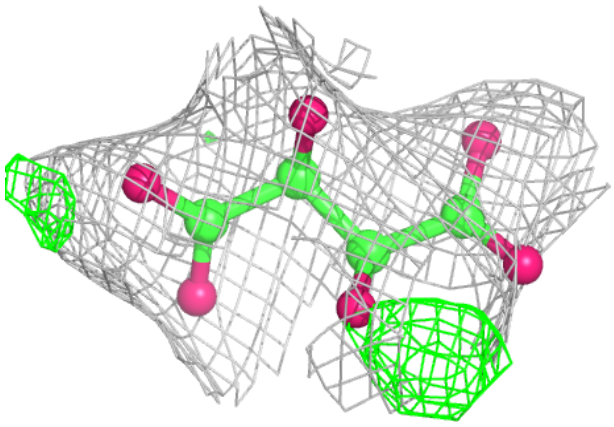
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	TAR	C	401	10/10	0.79	0.17	82,94,98,100	0
2	TAR	G	401	10/10	0.81	0.17	83,92,100,100	0
2	TAR	A	401	10/10	0.87	0.16	73,79,91,91	0
2	TAR	E	401	10/10	0.88	0.15	70,83,88,95	0
2	TAR	H	401	10/10	0.88	0.13	81,90,94,104	0
3	PEG	B	402	7/7	0.88	0.20	60,69,71,72	0
2	TAR	F	401	10/10	0.89	0.15	74,82,91,93	0
2	TAR	D	401	10/10	0.89	0.15	75,85,87,90	0
3	PEG	H	402	7/7	0.89	0.23	65,71,77,79	0
3	PEG	D	402	7/7	0.90	0.14	60,64,69,76	0
2	TAR	B	401	10/10	0.91	0.15	76,84,89,90	0
3	PEG	F	402	7/7	0.92	0.33	70,72,74,78	0

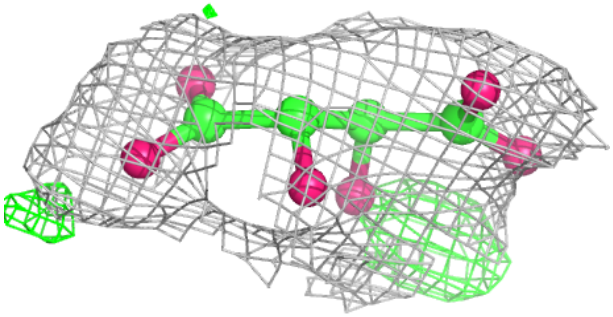
The following is a graphical depiction of the model fit to experimental electron density of all

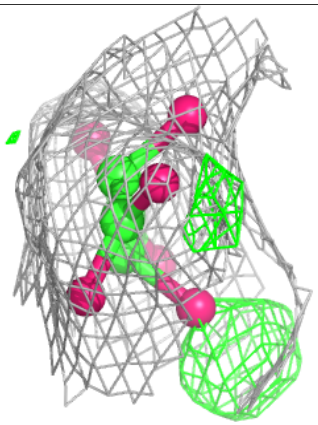
instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around TAR 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)

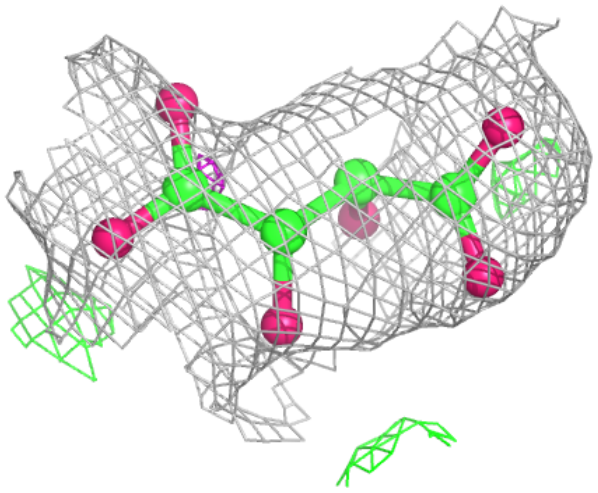


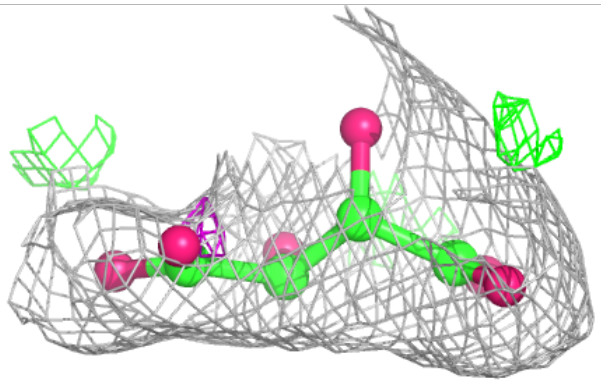


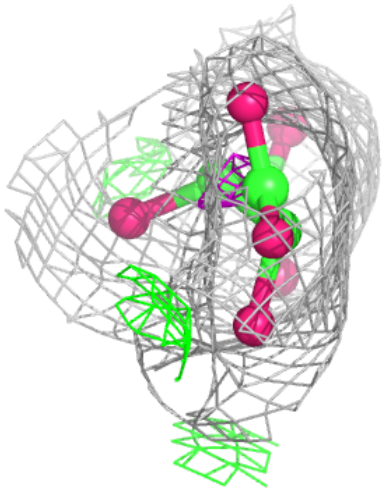


Electron density around TAR G 401:

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

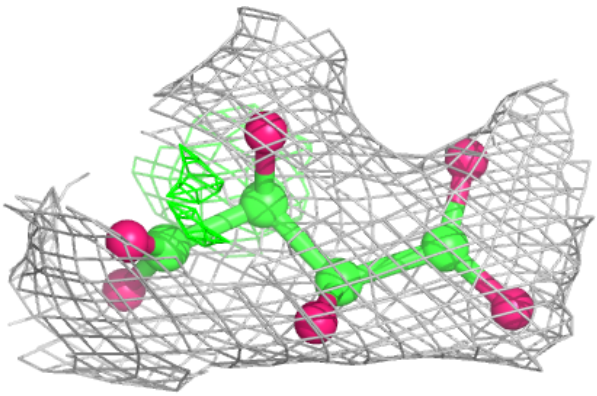


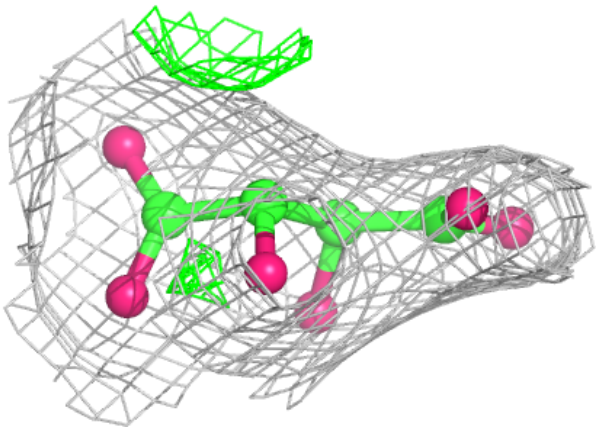


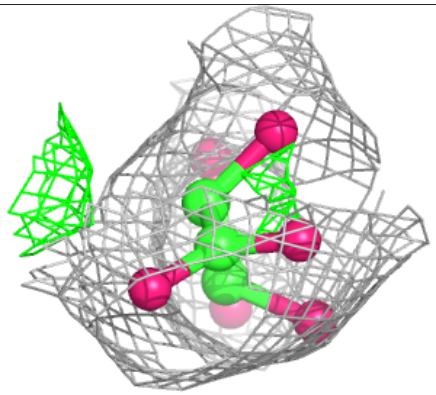


Electron density around TAR A 401:

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

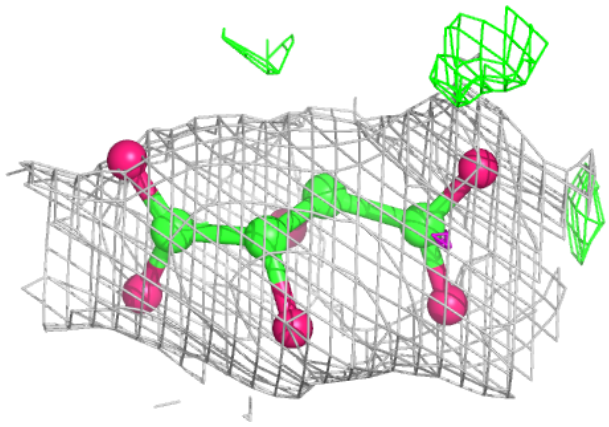


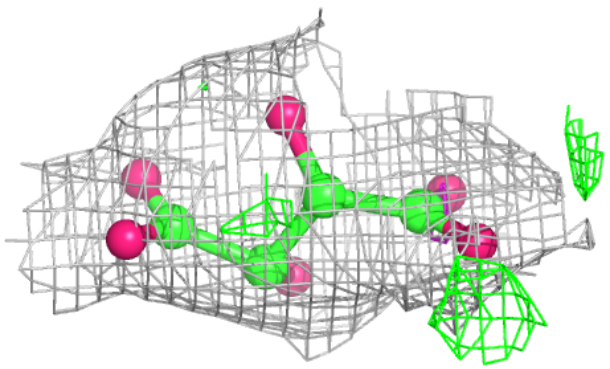


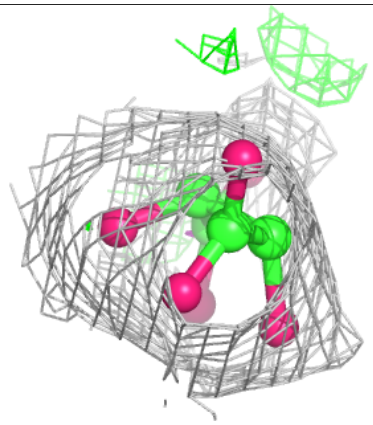


Electron density around TAR E 401:

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

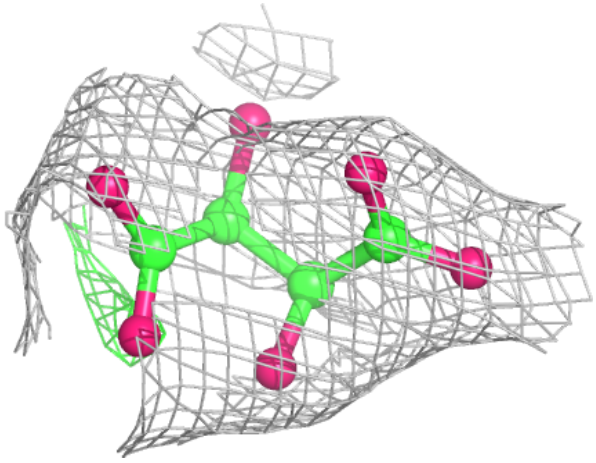


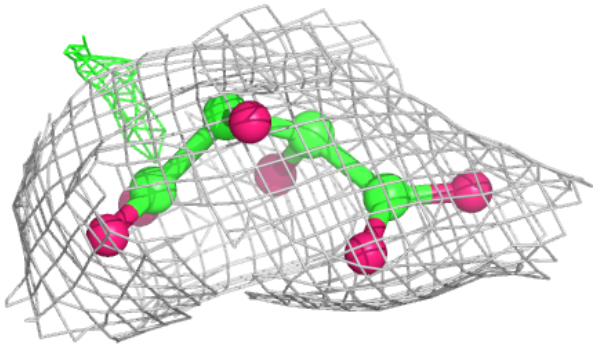


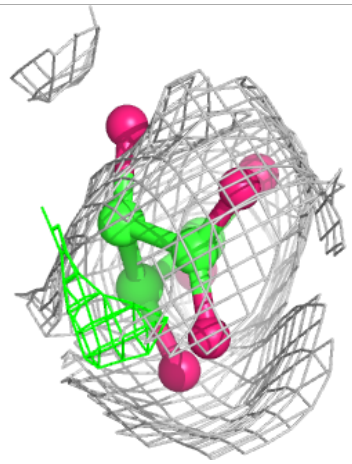


Electron density around TAR H 401:

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

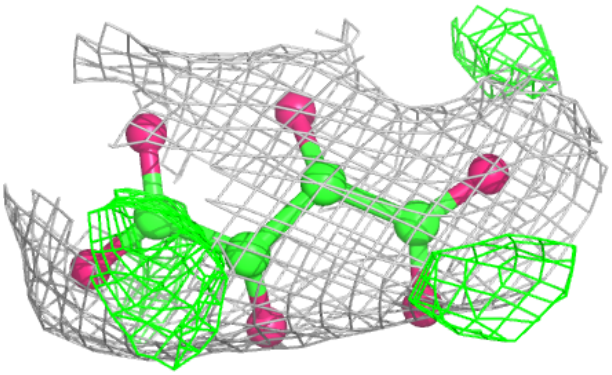


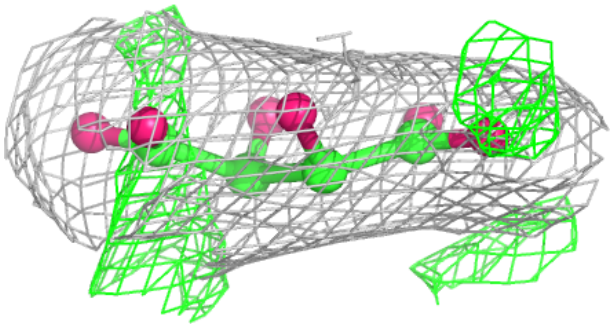


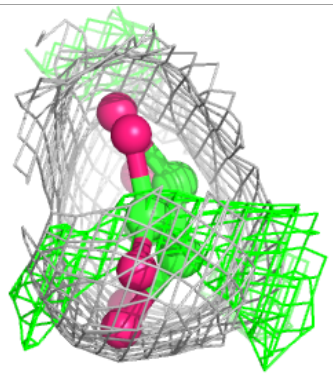


Electron density around TAR F 401:

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

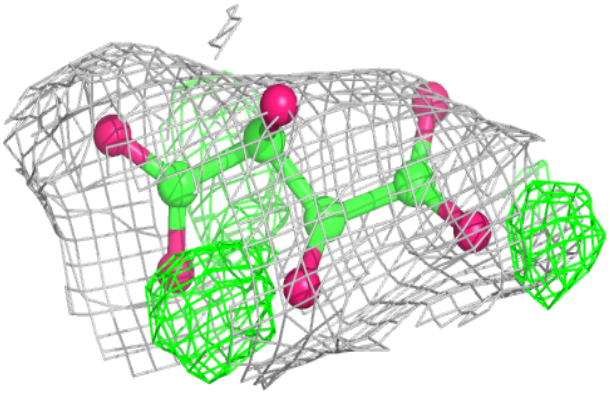


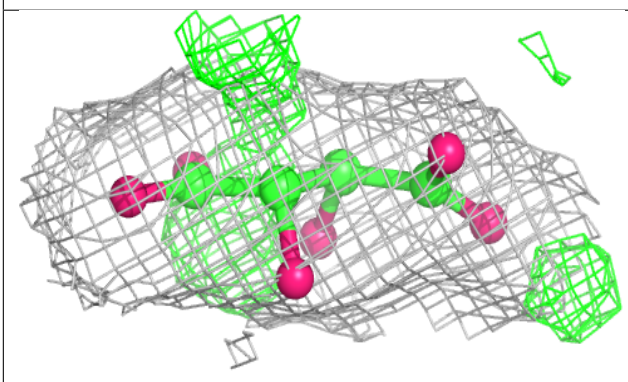


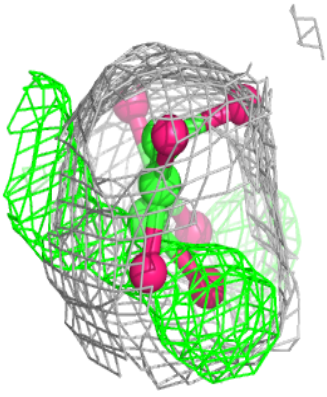


Electron density around TAR D 401:

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

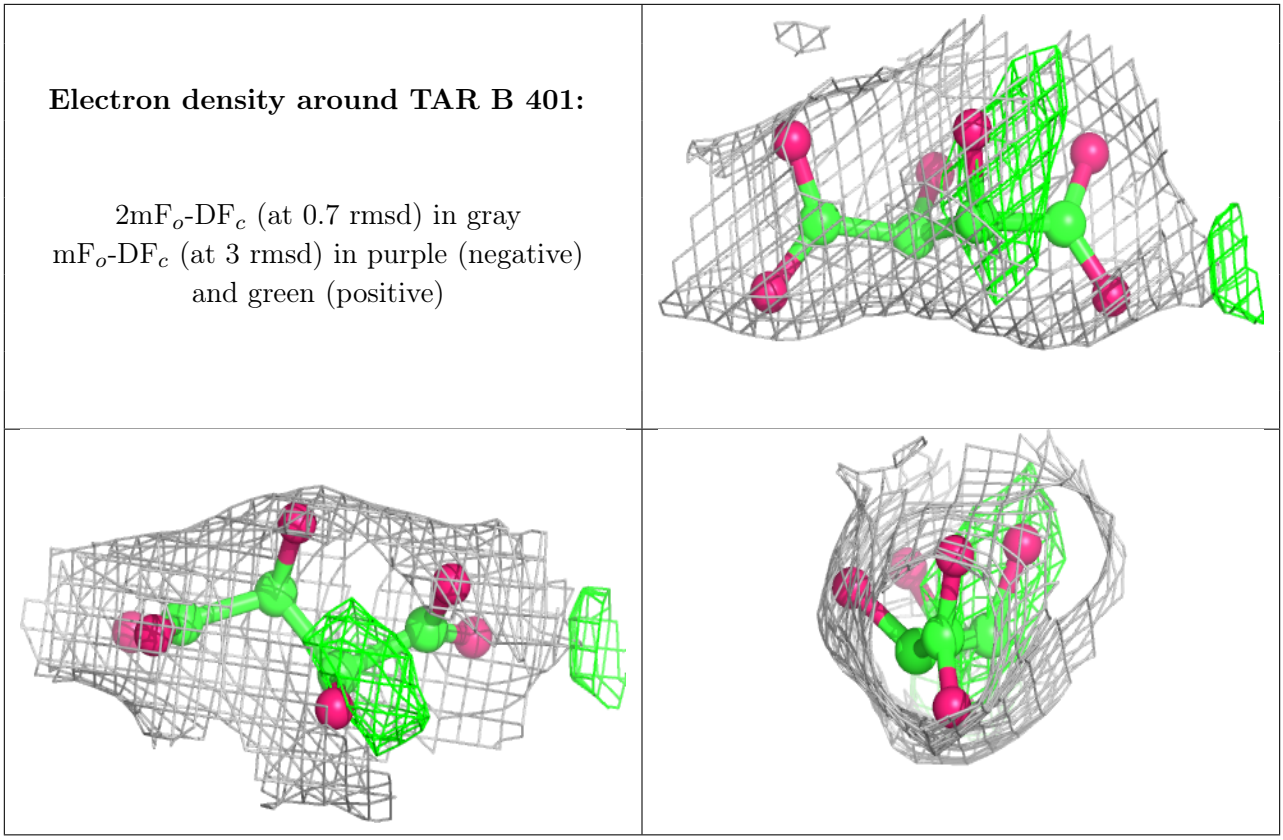






Electron density around TAR B 401:

$2mF_o$-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.