Full wwPDB X-ray Structure Validation Report (i)

Jan 28, 2025 – 12:04 PM EST

PDB ID	:	9CSC
Title	:	CtfAB Native Acetoacetate-CoA Transferase protein
Authors	:	Buhrman, G.; Bing, R.
Deposited on	:	2024-07-23
Resolution	:	2.00 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

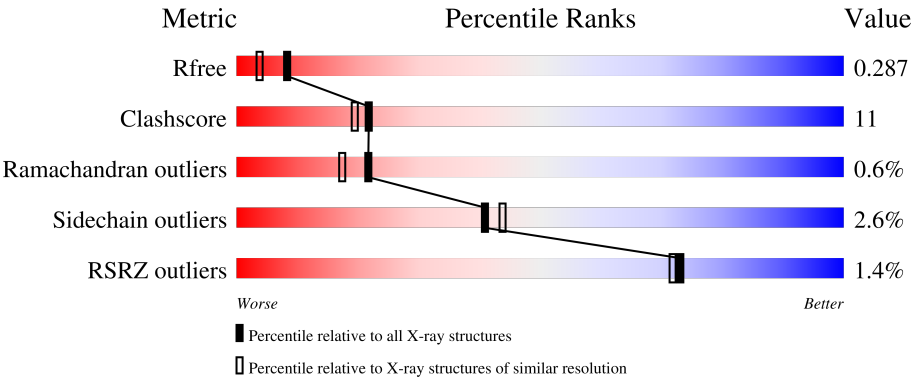
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

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 2.00 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}	164625	9409 (2.00-2.00)
Clashscore	180529	10737 (2.00-2.00)
Ramachandran outliers	177936	10628 (2.00-2.00)
Sidechain outliers	177891	10627 (2.00-2.00)
RSRZ outliers	164620	9409 (2.00-2.00)

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	B	215	2% 78% 20% ·
1	C	215	2% 70% 27% ·
2	A	217	80% 18% ·
2	D	217	75% 23% ·

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 13565 atoms, of which 6717 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 3-oxoacid CoA-transferase, B subunit.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	B	214	Total	C	H	N	O	S	0	1	0
			3213	1013	1635	259	299	7			
1	C	214	Total	C	H	N	O	S	0	1	0
			3250	1022	1658	260	302	8			

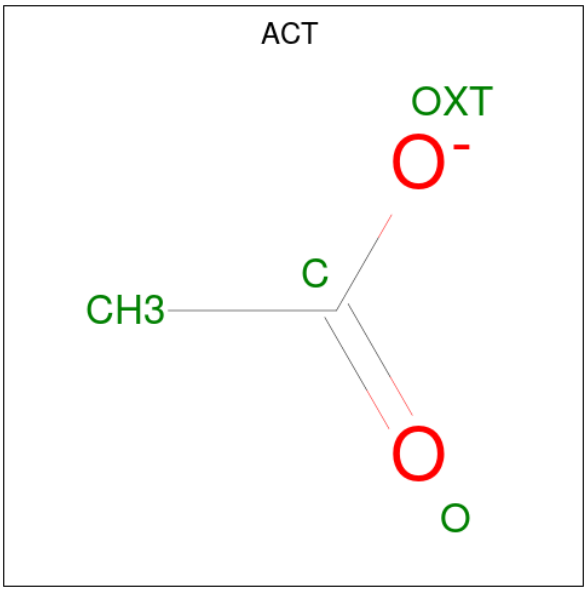
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	215	ALA	-	expression tag	UNP A6LM39
C	215	ALA	-	expression tag	UNP A6LM39

- Molecule 2 is a protein called 3-oxoacid CoA-transferase, A subunit.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	A	213	Total	C	H	N	O	S	0	1	0
			3322	1030	1712	267	308	5			
2	D	213	Total	C	H	N	O	S	0	1	0
			3322	1030	1712	267	308	5			

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0

- Molecule 4 is water.

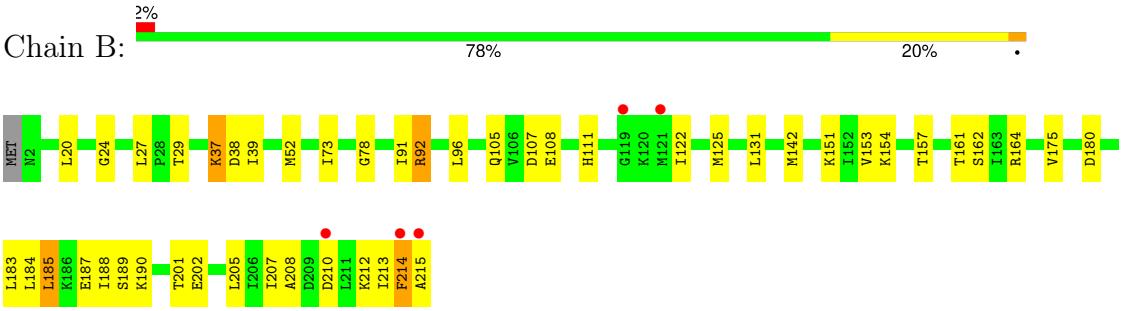
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	116	Total O 116 116	0	0
4	A	112	Total O 112 112	0	0
4	C	116	Total O 116 116	0	0
4	D	98	Total O 98 98	0	0

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.

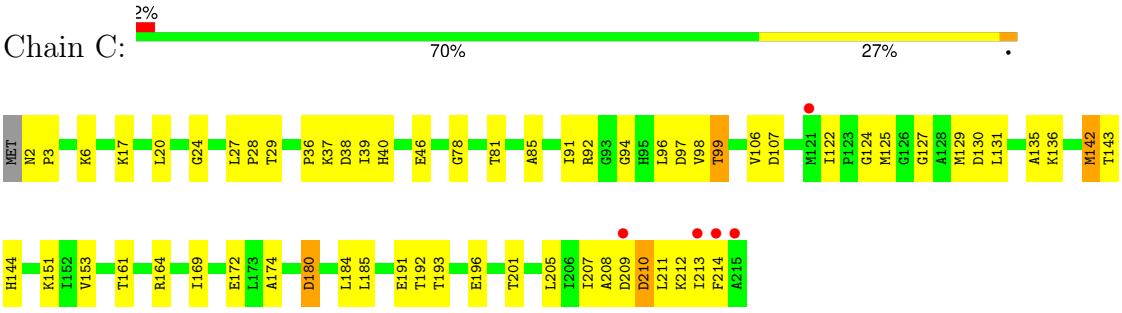
• Molecule 1: 3-oxoacid CoA-transferase, B subunit

Chain B:



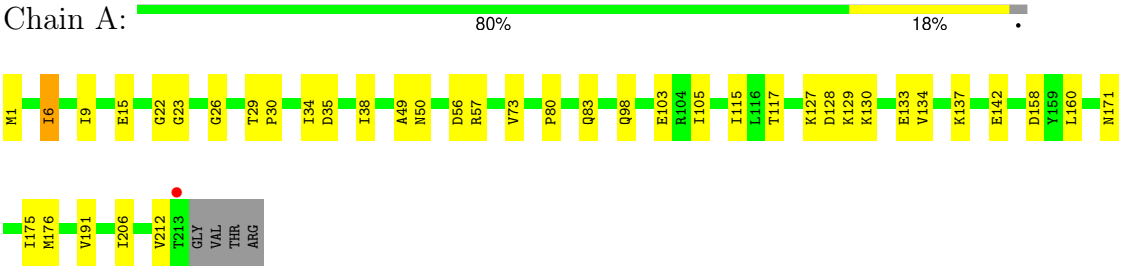
• Molecule 1: 3-oxoacid CoA-transferase, B subunit

Chain C:



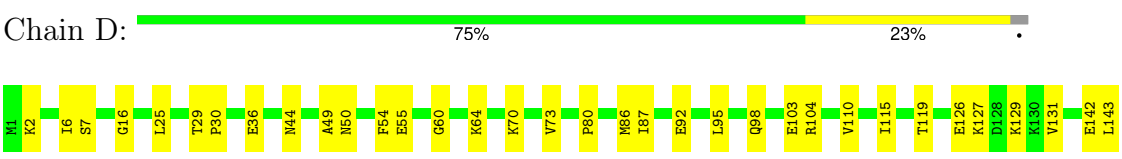
• Molecule 2: 3-oxoacid CoA-transferase, A subunit

Chain A:



• Molecule 2: 3-oxoacid CoA-transferase, A subunit

Chain D:




K153
A154
A157
D158
Y159
L160
G161
N162
L167
N171
I175
K181
V191
T203
I206
I207
V208
V212
T213
GLY
VAL
THR
ARG

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	131.42Å 131.42Å 158.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.36 – 2.00 38.36 – 2.00	Depositor EDS
% Data completeness (in resolution range)	96.3 (38.36-2.00) 95.2 (38.36-2.00)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.25 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.222 , 0.286 0.223 , 0.287	Depositor DCC
R_{free} test set	91972 reflections (2.17%)	wwPDB-VP
Wilson B-factor (Å^2)	22.3	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 41.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.40$, $< L^2 > = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	13565	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.93% 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: ACT

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	B	0.63	0/1605	0.83	2/2177 (0.1%)
1	C	0.62	0/1619	0.83	1/2193 (0.0%)
2	A	0.66	0/1631	0.86	1/2213 (0.0%)
2	D	0.69	0/1631	0.83	1/2212 (0.0%)
All	All	0.65	0/6486	0.84	5/8795 (0.1%)

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	C	0	1
All	All	0	2

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	142	MET	CG-SD-CE	8.27	113.43	100.20
1	B	96	LEU	CB-CG-CD2	-6.05	100.72	111.00
1	B	185	LEU	CB-CG-CD2	-5.66	101.38	111.00
2	A	176	MET	CG-SD-CE	5.29	108.67	100.20
2	D	212	VAL	C-N-CA	5.26	134.85	121.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	92	ARG	Sidechain
1	C	92	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	B	1578	1635	1636	41	0
1	C	1592	1658	1659	47	0
2	A	1610	1712	1714	28	0
2	D	1610	1712	1714	38	0
3	A	4	0	3	1	0
3	B	4	0	3	0	0
3	C	4	0	3	0	0
3	D	4	0	3	1	0
4	A	112	0	0	5	0
4	B	116	0	0	3	0
4	C	116	0	0	3	0
4	D	98	0	0	4	0
All	All	6848	6717	6735	139	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 11.

All (139) 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:B:185:LEU:HD21	1:B:188:ILE:HD11	1.49	0.91
2:D:2:LYS:NZ	4:D:401:HOH:O	2.01	0.88
2:D:103:GLU:HB3	2:D:115:ILE:HD13	1.62	0.80
1:B:37:LYS:O	1:B:38:ASP:HB2	1.82	0.78
2:A:80:PRO:HA	2:A:83:GLN:HE21	1.50	0.77
1:B:105:GLN:HE22	1:B:157:THR:HG22	1.51	0.76
1:C:122:ILE:HD12	2:D:86:MET:CE	2.16	0.76
1:C:212:LYS:NZ	4:C:401:HOH:O	2.14	0.73
2:A:29[B]:THR:HG21	4:A:433:HOH:O	1.88	0.72
1:B:202:GLU:OE1	4:B:401:HOH:O	2.09	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:184:LEU:HD11	1:C:208:ALA:HB2	1.72	0.70
1:C:130:ASP:OD1	2:D:119[A]:THR:HG21	1.92	0.69
2:D:2:LYS:HE2	2:D:208:VAL:O	1.93	0.69
1:B:184:LEU:HD11	1:B:208:ALA:HB2	1.74	0.69
2:A:35:ASP:O	4:A:401:HOH:O	2.11	0.67
1:B:185:LEU:HD23	1:B:207:ILE:HD12	1.78	0.65
2:D:29:THR:HG23	2:D:30:PRO:HD2	1.78	0.65
2:D:203:THR:HG23	2:D:207:ILE:HD11	1.79	0.63
1:B:39:ILE:HD12	4:B:412:HOH:O	1.96	0.63
1:B:24:GLY:O	1:B:29:THR:HG23	2.02	0.60
2:A:23:GLY:HA3	2:A:29[B]:THR:HG22	1.85	0.59
1:C:129:MET:HG2	1:C:161:THR:O	2.02	0.59
1:C:192:THR:HG23	1:C:193:THR:N	2.15	0.59
1:C:122:ILE:HD12	2:D:86:MET:HE3	1.84	0.59
1:C:122:ILE:HD12	2:D:86:MET:HE1	1.85	0.59
2:D:2:LYS:HE3	4:D:489:HOH:O	2.03	0.59
1:B:201:THR:HG21	1:B:205:LEU:HD21	1.85	0.58
1:C:212:LYS:C	1:C:213:ILE:HD13	2.24	0.58
1:C:24:GLY:O	1:C:29:THR:HG23	2.06	0.55
1:C:207:ILE:HD12	1:C:207:ILE:N	2.24	0.53
1:B:190:LYS:HB2	1:B:213:ILE:CG2	2.39	0.53
2:D:50:ASN:OD1	2:D:98:GLN:HG3	2.08	0.53
1:B:92:ARG:HH21	2:D:110:VAL:CG1	2.22	0.53
2:D:181:LYS:O	2:D:181:LYS:HE3	2.09	0.53
2:D:25:LEU:HD11	3:D:301:ACT:H2	1.90	0.52
2:A:160:LEU:HD12	1:C:78:GLY:HA3	1.92	0.52
1:C:91:ILE:HG23	1:C:131:LEU:HD23	1.90	0.52
1:C:17:LYS:HE3	1:C:40:HIS:H	1.74	0.52
1:C:27:LEU:HB3	1:C:28:PRO:HD3	1.92	0.52
1:B:27:LEU:HD23	1:B:27:LEU:O	2.10	0.52
1:B:213:ILE:O	1:B:214:PHE:CB	2.58	0.51
1:B:105:GLN:NE2	1:B:157:THR:HG22	2.22	0.51
1:C:180:ASP:N	1:C:180:ASP:OD1	2.44	0.51
2:D:129:LYS:HE2	2:D:142:GLU:OE1	2.10	0.51
2:A:129:LYS:HE3	2:A:142:GLU:OE2	2.11	0.50
2:D:7:SER:O	4:D:402:HOH:O	2.19	0.50
2:A:134:VAL:HG11	2:D:143:LEU:HD22	1.92	0.50
1:C:106:VAL:HG11	1:C:169:ILE:HD11	1.94	0.50
1:C:2:ASN:N	1:C:3:PRO:HD2	2.26	0.50
2:D:158:ASP:HA	2:D:191:VAL:O	2.12	0.50
2:A:23:GLY:HA3	2:A:29[B]:THR:CG2	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:158:ASP:HA	2:A:191:VAL:O	2.11	0.50
1:B:52:MET:HG3	1:B:73:ILE:HD13	1.93	0.49
1:C:24:GLY:HA2	4:C:456:HOH:O	2.12	0.49
2:A:34:ILE:O	2:A:38:ILE:HD12	2.13	0.49
1:C:122:ILE:CD1	2:D:87:ILE:HD11	2.41	0.49
1:C:124:GLY:HA2	2:D:95:LEU:HD13	1.94	0.49
1:B:161:THR:O	1:B:162:SER:HB3	2.12	0.49
1:B:190:LYS:O	1:B:190:LYS:HG2	2.13	0.49
2:A:129:LYS:HE3	2:A:142:GLU:CD	2.33	0.49
2:A:105:ILE:HG22	2:A:175:ILE:HG22	1.94	0.49
1:C:97:ASP:HA	1:C:136:LYS:HD2	1.94	0.49
1:C:107:ASP:HA	1:C:153:VAL:O	2.12	0.48
2:A:56:ASP:OD1	2:A:57:ARG:HG3	2.13	0.48
2:D:115:ILE:O	2:D:115:ILE:HG13	2.12	0.48
1:B:213:ILE:HG22	1:B:214:PHE:H	1.78	0.48
1:B:212:LYS:C	1:B:213:ILE:HD13	2.33	0.48
1:C:94:GLY:O	1:C:136:LYS:HE2	2.14	0.48
2:D:6:ILE:HG13	2:D:36:GLU:HG3	1.96	0.48
2:A:6:ILE:O	2:A:9:ILE:HG12	2.15	0.47
1:B:189:SER:HA	1:B:215:ALA:HA	1.97	0.47
1:C:96:LEU:HD21	1:C:98:VAL:O	2.15	0.47
1:B:52:MET:HG3	1:B:73:ILE:CD1	2.45	0.47
1:B:185:LEU:CD2	1:B:188:ILE:HD11	2.34	0.47
2:A:129:LYS:HE3	2:A:142:GLU:OE1	2.16	0.46
1:C:144:HIS:N	1:C:172[B]:GLU:OE2	2.40	0.46
1:B:187:GLU:O	1:B:188:ILE:HD12	2.16	0.46
2:A:133:GLU:HA	2:A:137:LYS:O	2.16	0.46
1:C:36:PRO:C	1:C:38:ASP:H	2.19	0.46
1:C:36:PRO:HB2	1:C:39:ILE:HG12	1.98	0.46
2:A:127:LYS:HD2	2:A:128:ASP:N	2.32	0.45
1:C:212:LYS:O	1:C:213:ILE:HD13	2.17	0.45
1:B:78:GLY:HA3	2:D:160:LEU:HD12	1.98	0.45
1:B:142:MET:CE	1:B:151:LYS:HE3	2.47	0.45
1:C:27:LEU:O	1:C:27:LEU:HD23	2.16	0.44
2:D:104:ARG:NH1	4:D:412:HOH:O	2.50	0.44
1:B:142:MET:HE3	1:B:151:LYS:HE3	1.98	0.44
2:A:206:ILE:HG12	1:C:20:LEU:HB2	1.99	0.44
1:B:122:ILE:HD13	4:A:500:HOH:O	2.16	0.44
2:D:49:ALA:O	2:D:73:VAL:HA	2.17	0.44
2:A:117:THR:HG23	2:A:117:THR:O	2.16	0.44
1:C:201:THR:HG21	1:C:205:LEU:HD21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:54:PHE:O	2:D:60:GLY:HA3	2.18	0.44
1:C:6:LYS:NZ	1:C:191:GLU:OE1	2.51	0.43
3:A:301:ACT:O	4:A:402:HOH:O	2.20	0.43
2:D:153:LYS:HG3	2:D:154:ALA:N	2.33	0.43
1:B:162:SER:HB2	4:A:405:HOH:O	2.19	0.43
2:A:22:GLY:O	2:A:29[B]:THR:HG22	2.18	0.43
2:A:49:ALA:O	2:A:73:VAL:HA	2.18	0.43
2:A:103:GLU:HB3	2:A:115:ILE:HD13	2.01	0.43
2:D:157:ALA:HA	2:D:162:ASN:O	2.18	0.43
1:B:190:LYS:HB2	1:B:213:ILE:HG22	2.00	0.43
1:B:24:GLY:HA2	4:B:461:HOH:O	2.19	0.43
2:A:26:GLY:HA2	2:A:29[B]:THR:HG21	2.01	0.43
2:D:126:GLU:OE2	2:D:131:VAL:HG21	2.19	0.43
2:D:55:GLU:OE2	2:D:80:PRO:HG2	2.19	0.43
2:A:6:ILE:HD12	2:A:212:VAL:HG11	2.01	0.42
1:C:193:THR:HG22	1:C:196:GLU:HB3	2.01	0.42
1:C:213:ILE:HD13	1:C:213:ILE:N	2.33	0.42
2:D:70:LYS:HG3	2:D:92:GLU:HG2	2.01	0.42
1:B:107:ASP:HA	1:B:153:VAL:O	2.18	0.42
1:B:208:ALA:HB3	1:B:210:ASP:O	2.20	0.42
1:B:92:ARG:HH21	2:D:110:VAL:HG12	1.85	0.42
1:B:175:VAL:HB	1:B:187:GLU:HB2	2.01	0.42
1:B:190:LYS:HB2	1:B:213:ILE:HG21	2.02	0.42
1:B:20:LEU:HB2	2:D:206:ILE:HG12	2.02	0.42
1:B:108:GLU:HG2	1:B:154:LYS:O	2.19	0.42
1:C:81:THR:HG21	2:D:167:LEU:HA	2.01	0.41
2:D:16:GLY:HA2	2:D:44:ASN:O	2.20	0.41
1:C:210:ASP:OD2	4:C:402:HOH:O	2.21	0.41
1:B:91:ILE:HG23	1:B:131:LEU:HD23	2.01	0.41
1:C:174:ALA:HB1	1:C:185:LEU:CD1	2.50	0.41
1:C:193:THR:HG23	1:C:196:GLU:H	1.85	0.41
1:C:143:THR:HA	1:C:172[B]:GLU:OE2	2.20	0.41
2:A:6:ILE:O	2:A:6:ILE:HG13	2.21	0.41
2:D:103:GLU:CB	2:D:115:ILE:HD13	2.42	0.41
1:B:107:ASP:OD1	1:B:111:HIS:HB2	2.21	0.41
1:B:208:ALA:CB	1:B:210:ASP:O	2.69	0.41
2:A:26:GLY:HA2	2:A:29[B]:THR:CG2	2.51	0.41
2:A:50:ASN:OD1	2:A:98:GLN:HG3	2.20	0.41
1:C:85:ALA:H	2:D:175:ILE:HD11	1.85	0.41
1:C:99:THR:OG1	1:C:135:ALA:HB2	2.20	0.41
1:B:187:GLU:C	1:B:188:ILE:HD12	2.41	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:210:ASP:O	1:C:211:LEU:C	2.59	0.41
2:A:29[A]:THR:HG23	2:A:30:PRO:HD2	2.02	0.40
1:C:122:ILE:HD11	2:D:87:ILE:HD11	2.02	0.40
1:C:184:LEU:HD12	1:C:184:LEU:C	2.41	0.40
1:C:142:MET:HE3	1:C:151:LYS:HE2	2.04	0.40
1:C:46:GLU:OE1	1:C:127:GLY:HA3	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	213/215 (99%)	205 (96%)	7 (3%)	1 (0%)	25	21
1	C	213/215 (99%)	207 (97%)	4 (2%)	2 (1%)	14	10
2	A	212/217 (98%)	208 (98%)	3 (1%)	1 (0%)	25	21
2	D	212/217 (98%)	207 (98%)	4 (2%)	1 (0%)	25	21
All	All	850/864 (98%)	827 (97%)	18 (2%)	5 (1%)	22	17

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	214	PHE
2	A	171	ASN
1	C	214	PHE
2	D	171	ASN
1	C	37	LYS

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	B	168/175 (96%)	163 (97%)	5 (3%)	36	37
1	C	171/175 (98%)	165 (96%)	6 (4%)	31	31
2	A	179/181 (99%)	175 (98%)	4 (2%)	47	51
2	D	179/181 (99%)	176 (98%)	3 (2%)	56	61
All	All	697/712 (98%)	679 (97%)	18 (3%)	41	44

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	37	LYS
1	B	125	MET
1	B	164	ARG
1	B	180	ASP
1	B	183	LEU
2	A	1	MET
2	A	6	ILE
2	A	15	GLU
2	A	130	LYS
1	C	99	THR
1	C	125	MET
1	C	164	ARG
1	C	180	ASP
1	C	209	ASP
1	C	210	ASP
2	D	64	LYS
2	D	127	LYS
2	D	181	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	83	GLN

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Mol	Chain	Res	Type
2	D	146	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	ACT	D	301	-	3,3,3	1.34	0	3,3,3	0.97	0
3	ACT	C	301	-	3,3,3	1.41	0	3,3,3	1.24	0
3	ACT	B	301	-	3,3,3	1.47	1 (33%)	3,3,3	0.72	0
3	ACT	A	301	-	3,3,3	1.20	0	3,3,3	1.65	1 (33%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	301	ACT	CH3-C	2.17	1.57	1.49

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	301	ACT	O-C-CH3	-2.22	113.41	122.53

There are no chirality outliers.

There are no torsion outliers.

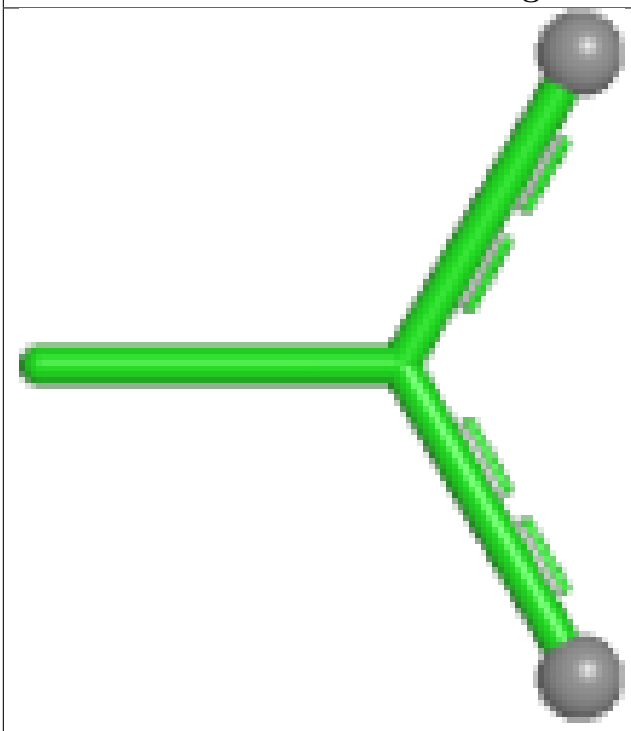
There are no ring outliers.

2 monomers are involved in 2 short contacts:

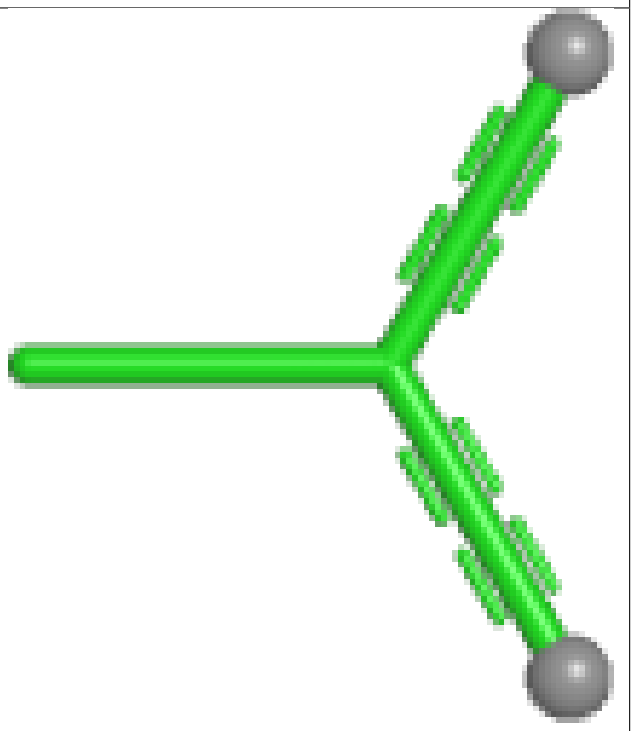
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	301	ACT	1	0
3	A	301	ACT	1	0

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.

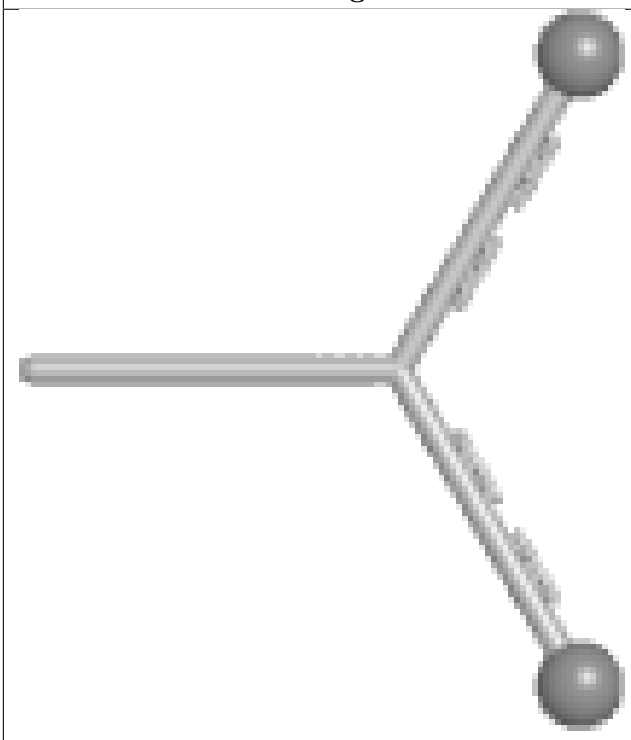
Ligand ACT D 301



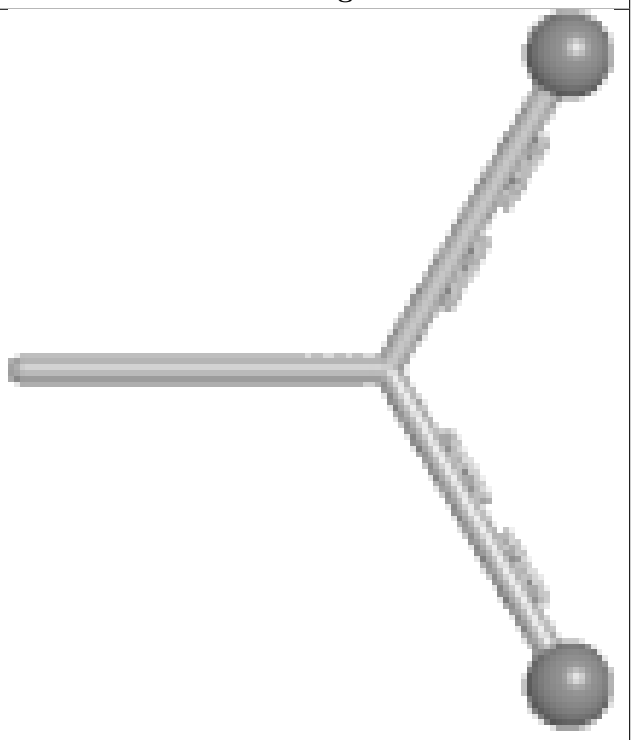
Bond lengths



Bond angles

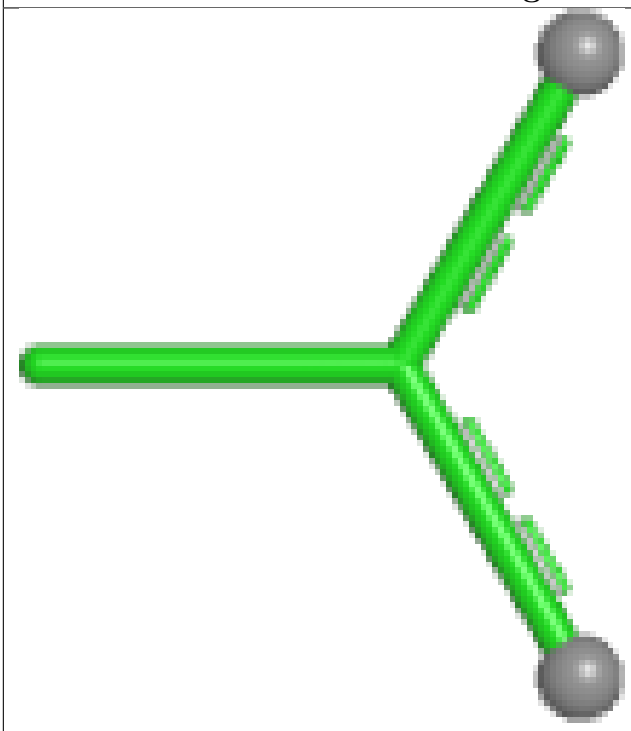


Torsions

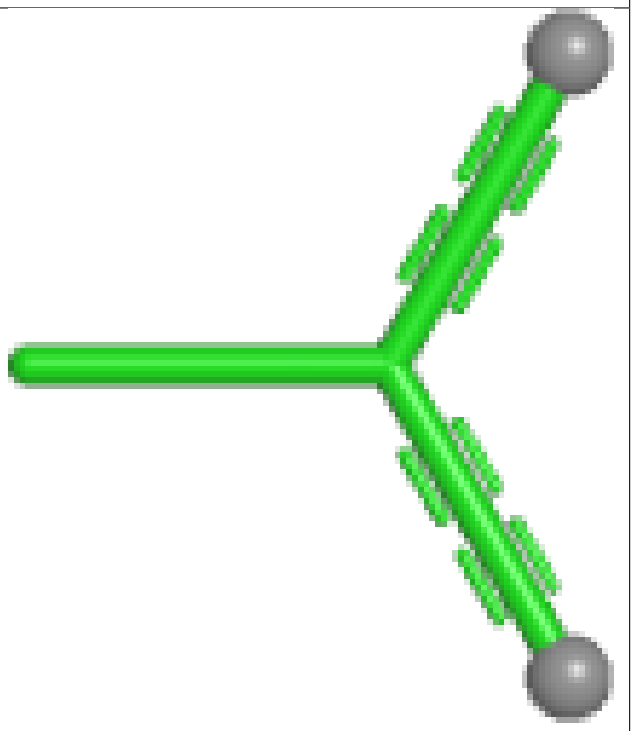


Rings

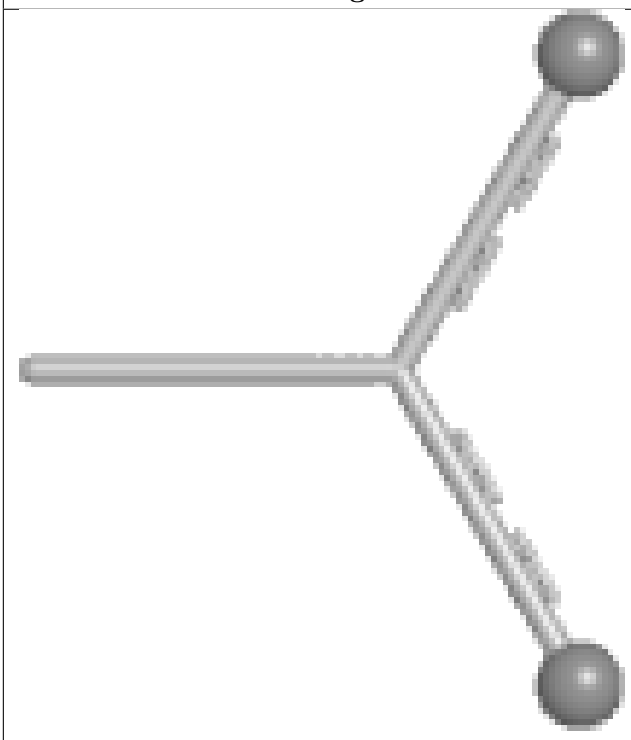
Ligand ACT C 301



Bond lengths



Bond angles



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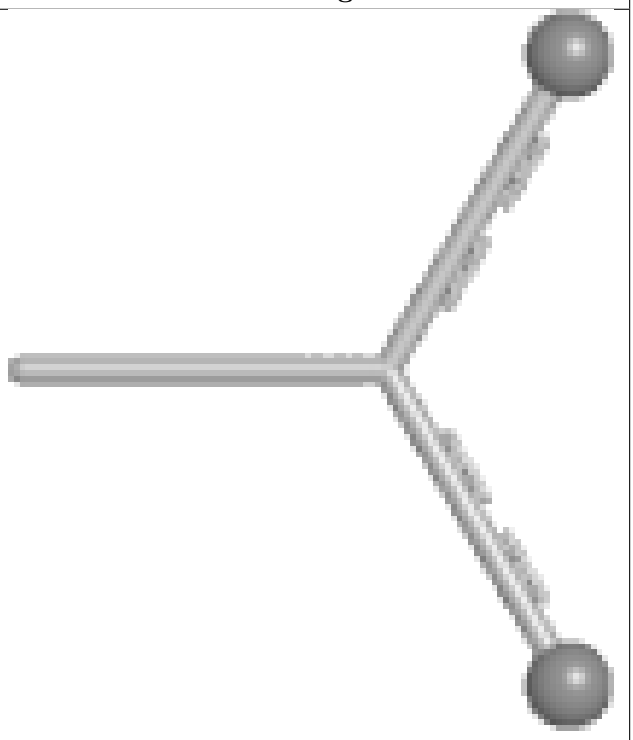
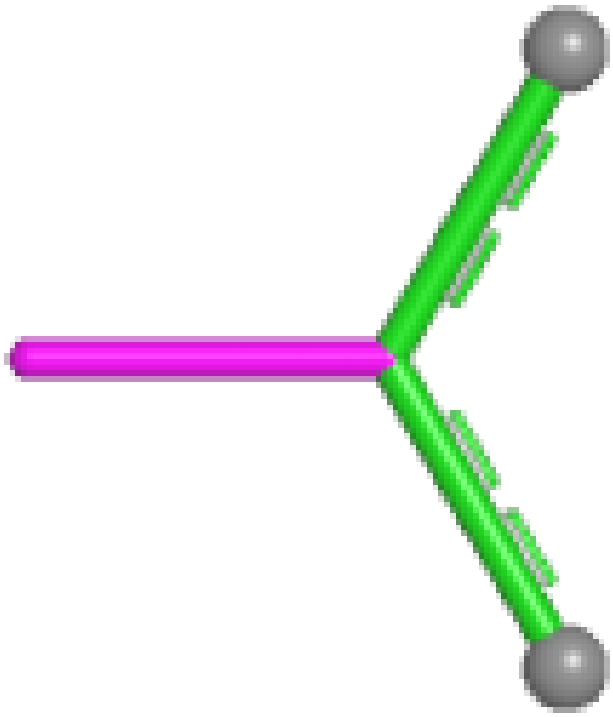
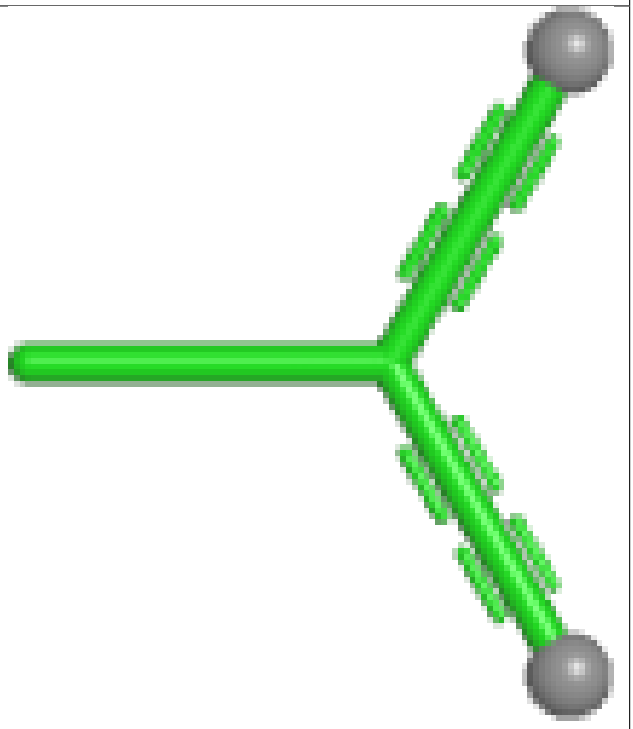


Rings

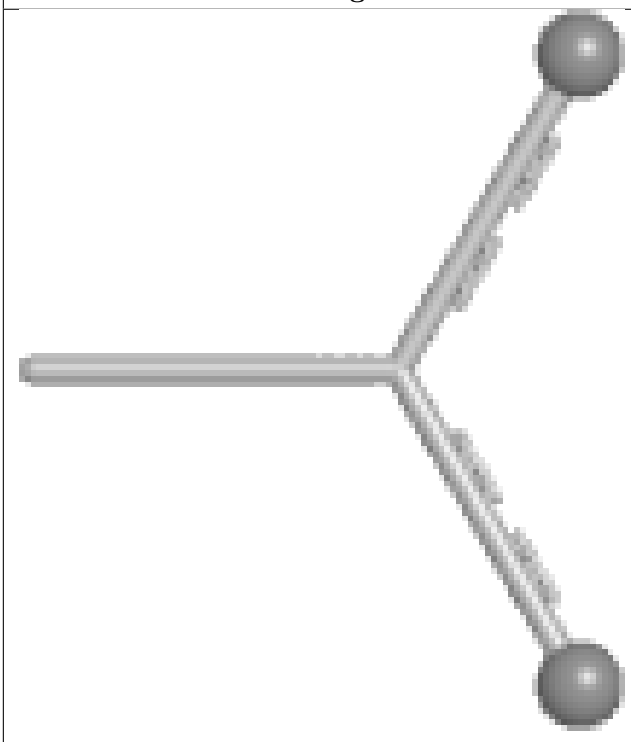
Ligand ACT B 301



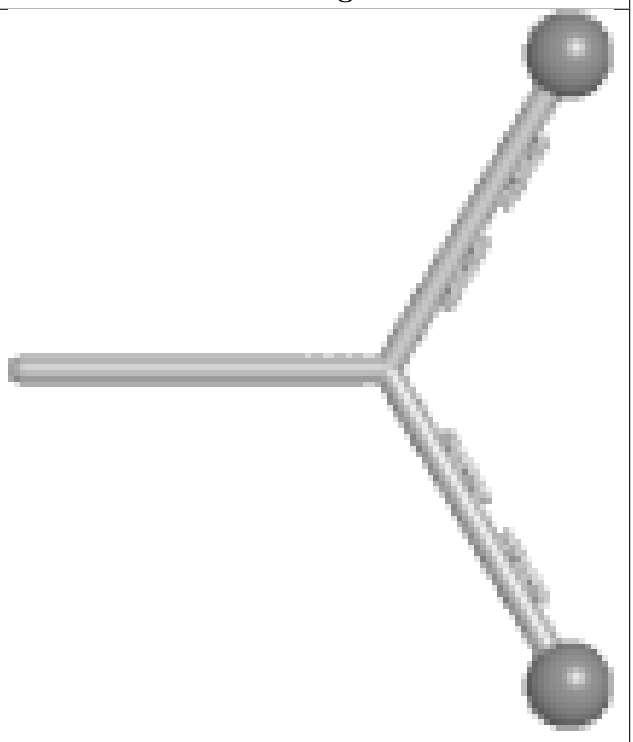
Bond lengths



Bond angles

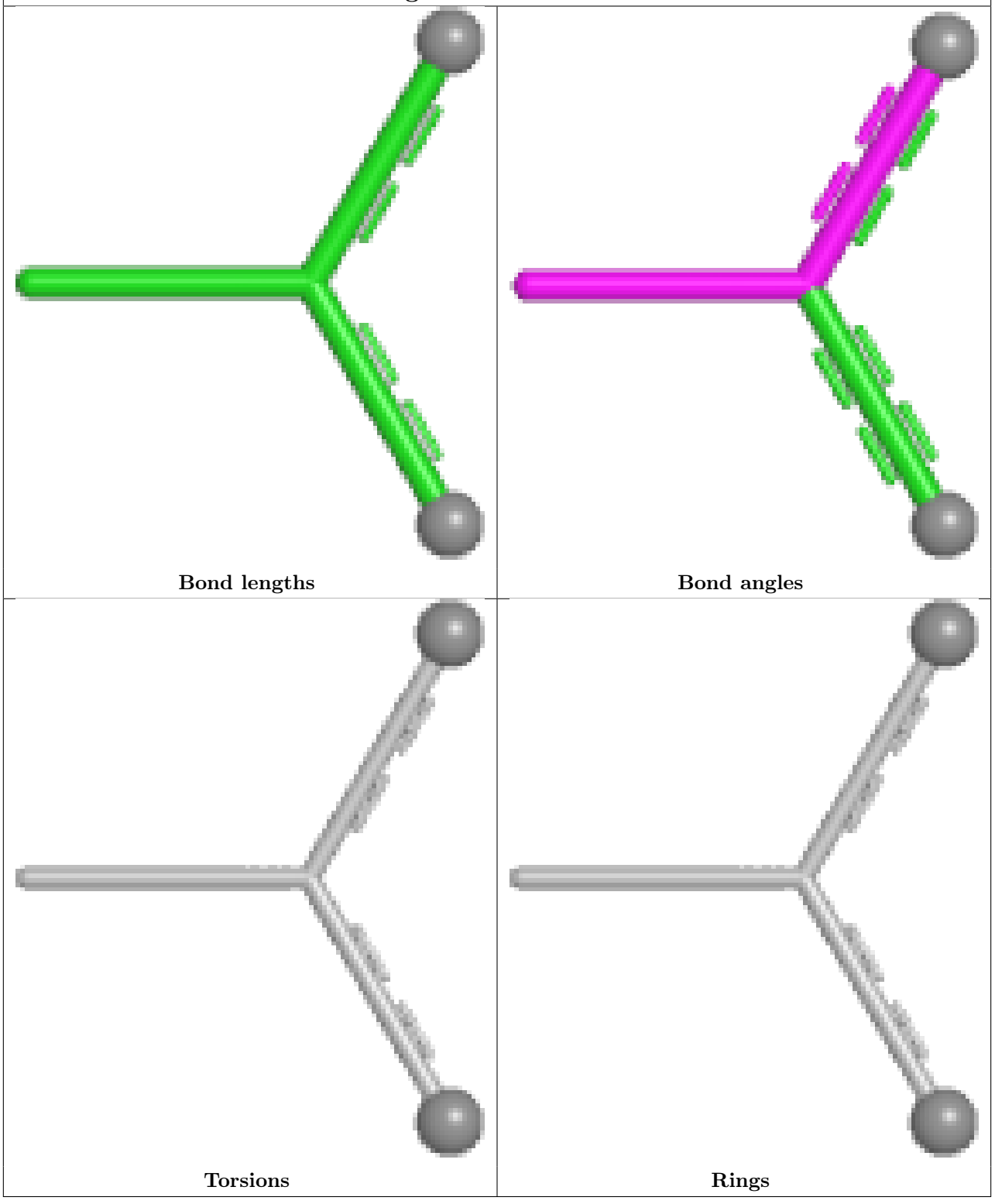


Torsions



Rings

Ligand ACT A 301



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, 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	B	214/215 (99%)	-0.05	5 (2%)	61	59	12, 31, 50, 56	1 (0%)
1	C	214/215 (99%)	0.04	5 (2%)	61	59	13, 31, 53, 63	1 (0%)
2	A	213/217 (98%)	-0.38	1 (0%)	87	86	13, 24, 45, 59	1 (0%)
2	D	213/217 (98%)	-0.32	1 (0%)	87	86	13, 25, 45, 56	1 (0%)
All	All	854/864 (98%)	-0.18	12 (1%)	73	72	12, 27, 48, 63	4 (0%)

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	214	PHE	3.8
1	C	209	ASP	3.0
2	D	213	THR	2.9
1	C	121	MET	2.8
1	B	121	MET	2.7
1	B	210	ASP	2.7
1	B	215	ALA	2.6
1	B	214	PHE	2.6
1	B	119	GLY	2.4
1	C	213	ILE	2.4
1	C	215	ALA	2.4
2	A	213	THR	2.4

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands (i)

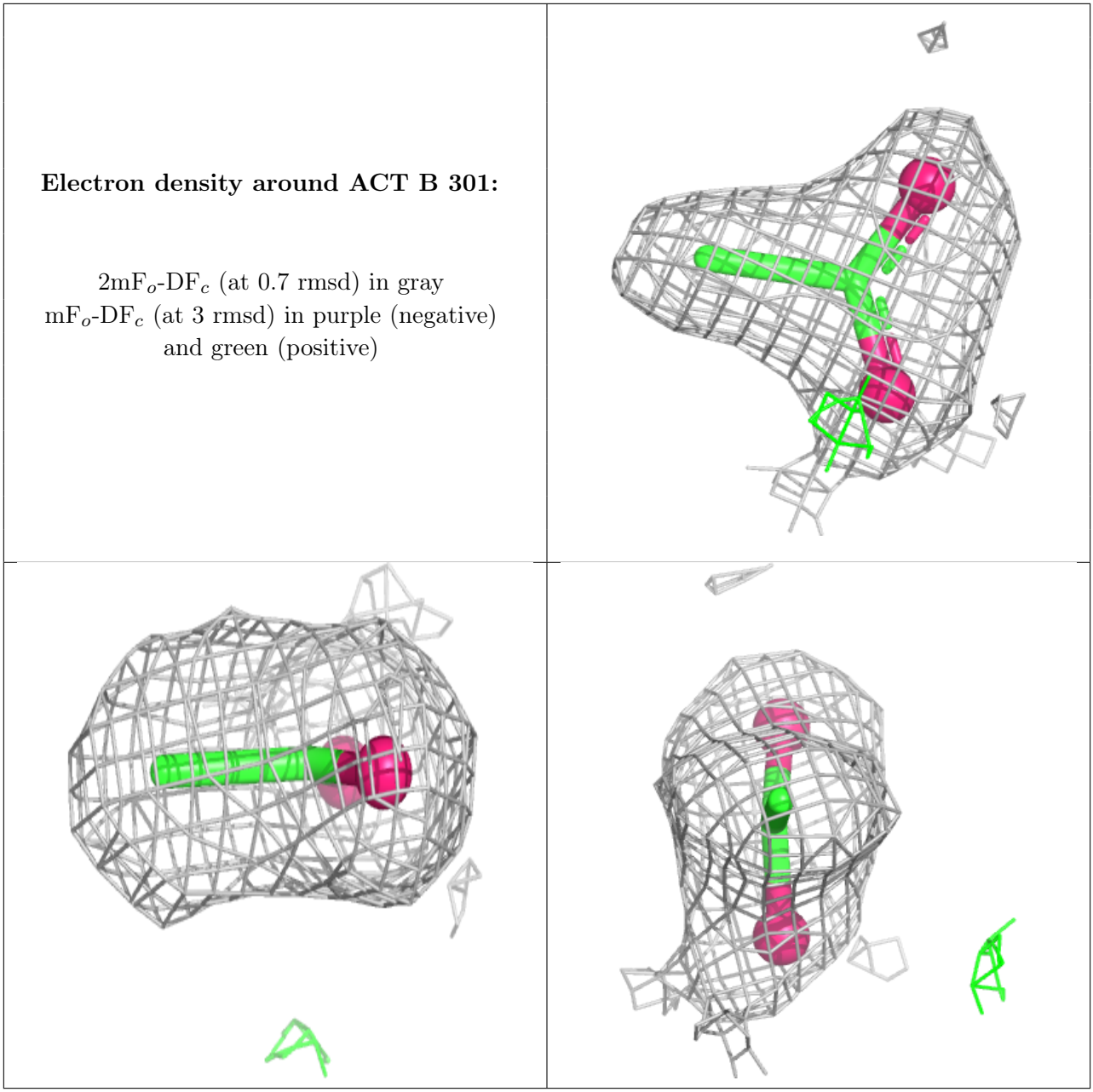
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
3	ACT	B	301	4/4	0.89	0.12	26,38,43,44	0
3	ACT	C	301	4/4	0.94	0.10	31,36,38,42	0
3	ACT	D	301	4/4	0.95	0.09	25,27,28,42	0
3	ACT	A	301	4/4	0.97	0.06	21,23,29,29	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.

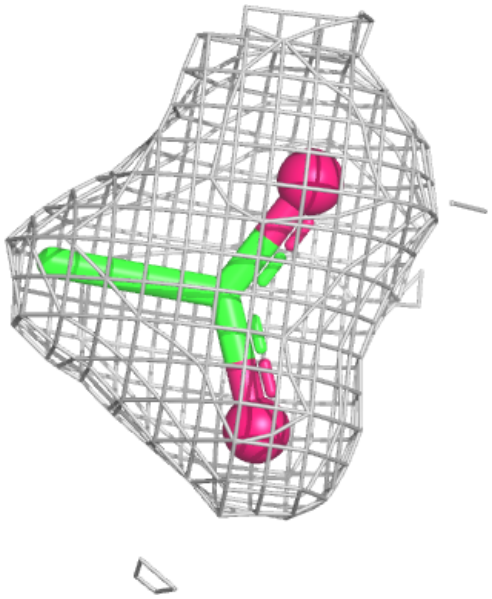
Electron density around ACT B 301:

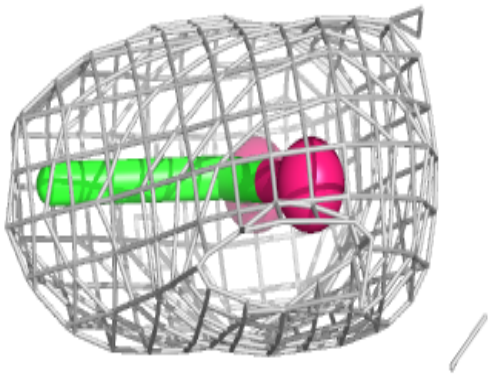
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

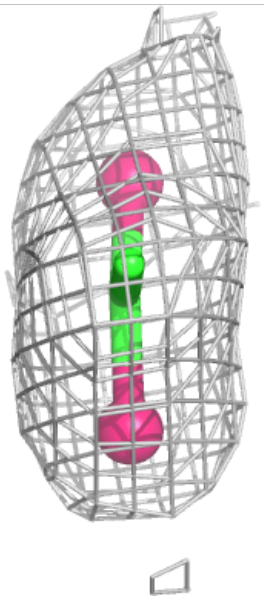


Electron density around ACT C 301:

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

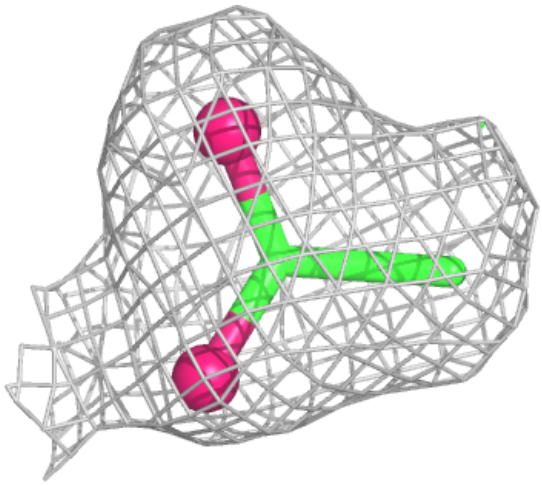


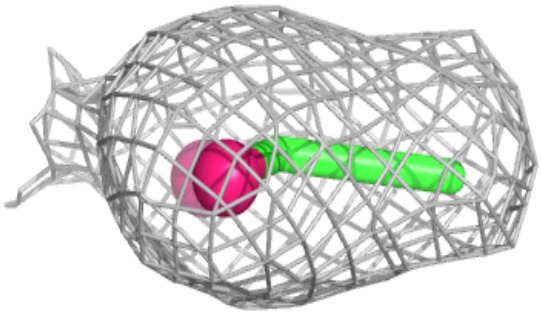


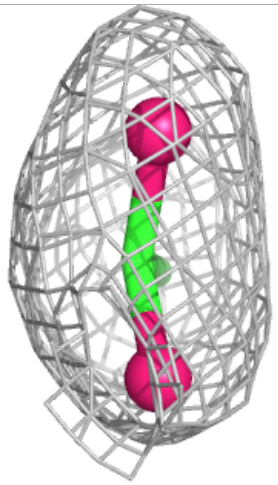


Electron density around ACT D 301:

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

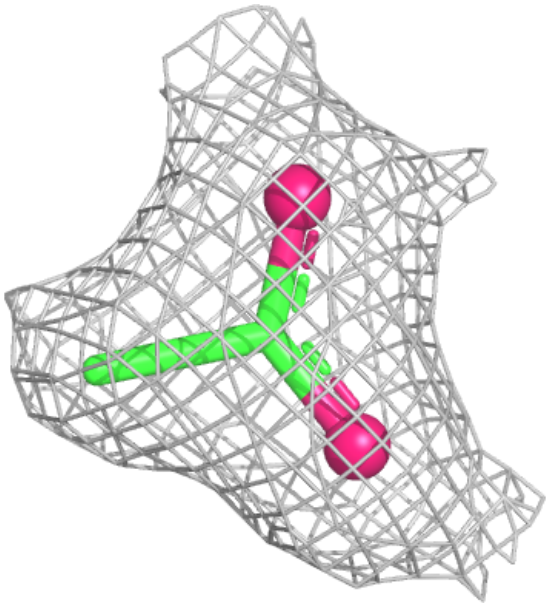


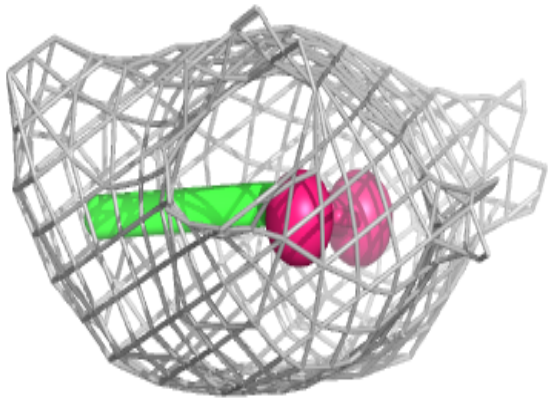


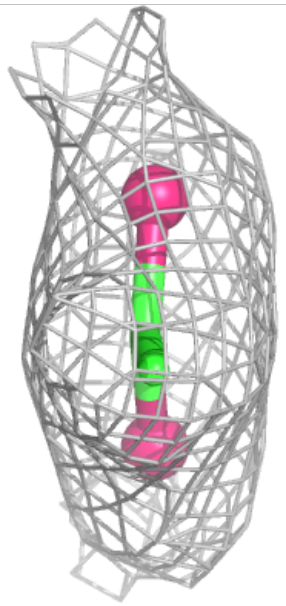


Electron density around ACT A 301:

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







6.5 Other polymers

There are no such residues in this entry.