Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 10:33 pm BST

PDB ID	:	3LYA
Title	:	Crystal structure of the periplasmic domain of CadC in the presence of K2ReCl6
Authors	:	Eichinger, A.; Skerra, A.
Deposited on	:	2010-02-26
Resolution	:	2.30 Å(reported)

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

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

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

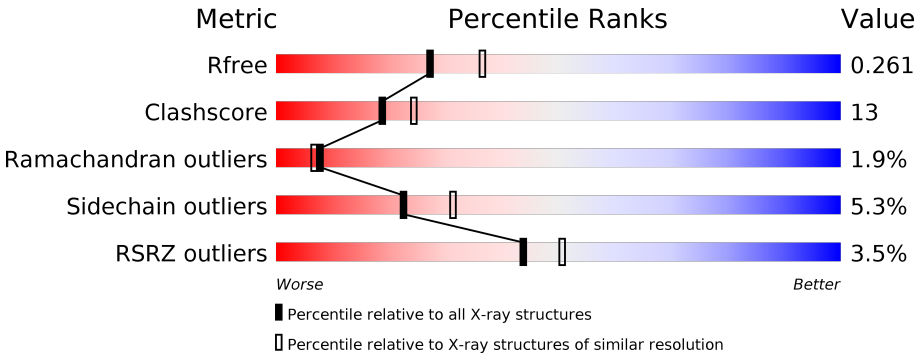
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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 <=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	372	3%, 71%, 12%, 15%

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	RHE	A	1	-	-	X	-
2	RHE	A	16	-	-	X	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	RHE	A	3	-	-	X	-
2	RHE	A	4	-	-	X	-
2	RHE	A	9	-	-	X	-

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2674 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 Transcriptional activator cadC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	318	2528	1606	426	486	10	431	0	0

There are 47 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	141	GLY	-	EXPRESSION TAG	UNP P23890
A	142	SER	-	EXPRESSION TAG	UNP P23890
A	143	GLY	-	EXPRESSION TAG	UNP P23890
A	144	MET	-	EXPRESSION TAG	UNP P23890
A	145	LYS	-	EXPRESSION TAG	UNP P23890
A	146	GLU	-	EXPRESSION TAG	UNP P23890
A	147	THR	-	EXPRESSION TAG	UNP P23890
A	148	ALA	-	EXPRESSION TAG	UNP P23890
A	149	ALA	-	EXPRESSION TAG	UNP P23890
A	150	ALA	-	EXPRESSION TAG	UNP P23890
A	151	LYS	-	EXPRESSION TAG	UNP P23890
A	152	PHE	-	EXPRESSION TAG	UNP P23890
A	153	GLU	-	EXPRESSION TAG	UNP P23890
A	154	ARG	-	EXPRESSION TAG	UNP P23890
A	155	GLN	-	EXPRESSION TAG	UNP P23890
A	156	HIS	-	EXPRESSION TAG	UNP P23890
A	157	MET	-	EXPRESSION TAG	UNP P23890
A	158	ASP	-	EXPRESSION TAG	UNP P23890
A	159	SER	-	EXPRESSION TAG	UNP P23890
A	160	PRO	-	EXPRESSION TAG	UNP P23890
A	161	ASP	-	EXPRESSION TAG	UNP P23890
A	162	LEU	-	EXPRESSION TAG	UNP P23890
A	163	GLY	-	EXPRESSION TAG	UNP P23890
A	164	THR	-	EXPRESSION TAG	UNP P23890
A	165	ASP	-	EXPRESSION TAG	UNP P23890
A	166	ASP	-	EXPRESSION TAG	UNP P23890
A	167	ASP	-	EXPRESSION TAG	UNP P23890

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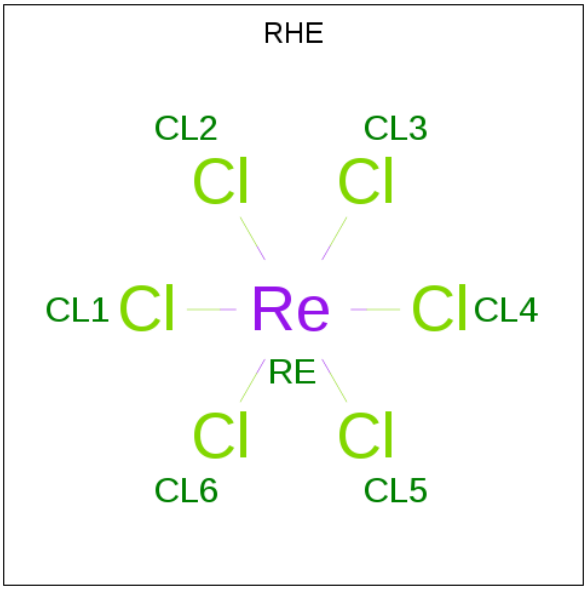
Chain	Residue	Modelled	Actual	Comment	Reference
A	168	ASP	-	EXPRESSION TAG	UNP P23890
A	169	LYS	-	EXPRESSION TAG	UNP P23890
A	170	ALA	-	EXPRESSION TAG	UNP P23890
A	171	MET	-	EXPRESSION TAG	UNP P23890
A	172	ALA	-	EXPRESSION TAG	UNP P23890
A	173	HIS	-	EXPRESSION TAG	UNP P23890
A	174	HIS	-	EXPRESSION TAG	UNP P23890
A	175	HIS	-	EXPRESSION TAG	UNP P23890
A	176	HIS	-	EXPRESSION TAG	UNP P23890
A	177	HIS	-	EXPRESSION TAG	UNP P23890
A	178	HIS	-	EXPRESSION TAG	UNP P23890
A	179	SER	-	EXPRESSION TAG	UNP P23890
A	180	SER	-	EXPRESSION TAG	UNP P23890
A	181	GLY	-	EXPRESSION TAG	UNP P23890
A	182	HIS	-	EXPRESSION TAG	UNP P23890
A	183	ILE	-	EXPRESSION TAG	UNP P23890
A	184	GLU	-	EXPRESSION TAG	UNP P23890
A	185	GLY	-	EXPRESSION TAG	UNP P23890
A	186	ARG	-	EXPRESSION TAG	UNP P23890
A	187	HIS	-	EXPRESSION TAG	UNP P23890

- Molecule 2 is rhenium (IV) hexachloride (three-letter code: RHE) (formula: Cl_6Re).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Cl Re 7 6 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Cl Re 7 6 1	0	0
2	A	1	Total Cl Re 7 6 1	0	0
2	A	1	Total Cl Re 7 6 1	0	0
2	A	1	Total Cl Re 7 6 1	0	0
2	A	1	Total Cl Re 7 6 1	0	0
2	A	1	Total Cl Re 7 6 1	0	0
2	A	1	Total Cl Re 7 6 1	0	0
2	A	1	Total Cl Re 7 6 1	0	0
2	A	1	Total Cl Re 7 6 1	0	0
2	A	1	Total Cl Re 7 6 1	0	0
2	A	1	Total Cl Re 7 6 1	0	0
2	A	1	Total Cl Re 7 6 1	0	0
2	A	1	Total Cl Re 7 6 1	0	0
2	A	1	Total Cl Re 7 6 1	0	0
2	A	1	Total Cl Re 7 6 1	0	0

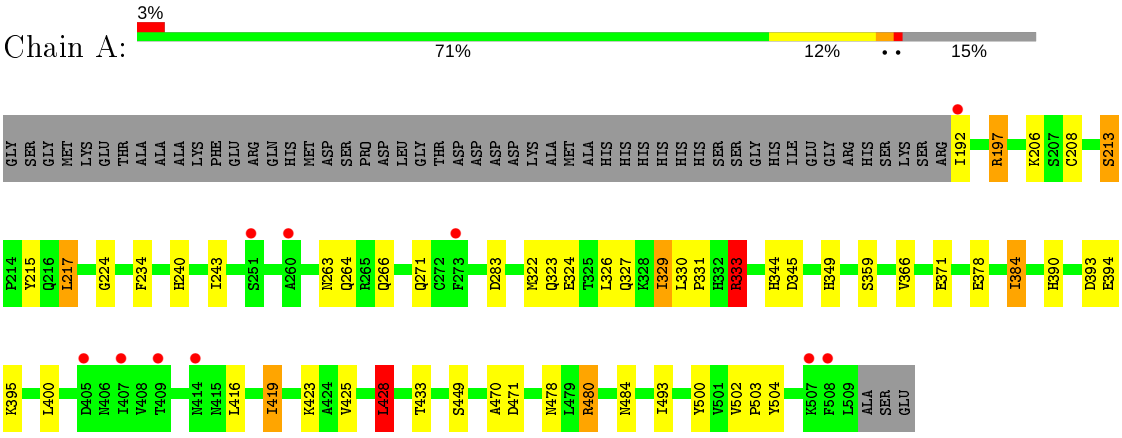
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	34	Total O 34 34	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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: Transcriptional activator cadC



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α, β, γ	80.56Å 80.56Å 199.78Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	69.77 – 2.30 39.49 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.5 (69.77-2.30) 98.6 (39.49-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) >$ [1]	5.90 (at 2.29Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.230 , 0.271 0.230 , 0.261	Depositor DCC
R_{free} test set	897 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å^2)	30.0	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 48.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	2674	wwPDB-VP
Average B, all atoms (Å^2)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.70% 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: RHE

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	0.80	0/2578	0.86	8/3503 (0.2%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	480	ARG	NE-CZ-NH2	-11.96	114.32	120.30
1	A	333	ARG	NE-CZ-NH1	9.23	124.92	120.30
1	A	480	ARG	NE-CZ-NH1	8.60	124.60	120.30
1	A	333	ARG	NE-CZ-NH2	-8.51	116.04	120.30
1	A	197	ARG	NE-CZ-NH2	-7.69	116.45	120.30
1	A	428	LEU	CA-CB-CG	7.28	132.04	115.30
1	A	480	ARG	CG-CD-NE	-6.98	97.15	111.80
1	A	480	ARG	CD-NE-CZ	5.07	130.69	123.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2528	0	2508	55	3
2	A	112	0	0	35	2
3	A	34	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	2674	0	2508	56	3

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 13.

All (56) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:470:ALA:HB1	2:A:9:RHE:CL6	1.91	1.07
1:A:470:ALA:CB	2:A:9:RHE:CL6	2.44	1.03
1:A:395:LYS:N	2:A:16:RHE:CL4	2.35	0.96
1:A:503:PRO:HG2	2:A:9:RHE:CL5	2.04	0.93
1:A:393:ASP:OD1	2:A:16:RHE:CL4	2.27	0.89
1:A:480:ARG:NH2	1:A:484:ASN:HD22	1.75	0.85
1:A:333:ARG:HD3	2:A:1:RHE:CL4	2.15	0.83
1:A:503:PRO:HD2	2:A:9:RHE:CL2	2.15	0.83
1:A:504:TYR:CB	2:A:9:RHE:CL4	2.66	0.80
1:A:470:ALA:HB3	2:A:9:RHE:CL6	2.18	0.79
1:A:394:GLU:N	2:A:16:RHE:CL4	2.52	0.79
1:A:480:ARG:HH22	1:A:484:ASN:HD22	1.31	0.78
1:A:393:ASP:C	2:A:16:RHE:CL4	2.60	0.77
1:A:504:TYR:HB3	2:A:9:RHE:CL4	2.24	0.75
2:A:4:RHE:CL5	3:A:515:HOH:O	2.44	0.72
1:A:504:TYR:HB2	2:A:9:RHE:CL4	2.27	0.72
1:A:344:HIS:HE1	2:A:3:RHE:CL3	2.11	0.71
1:A:323:GLN:O	1:A:327:GLN:HG2	1.94	0.67
1:A:234:PHE:CB	1:A:322:MET:HE2	2.25	0.67
1:A:395:LYS:HB3	2:A:16:RHE:CL6	2.35	0.63
1:A:371:GLU:HG2	2:A:1:RHE:CL3	2.36	0.63
1:A:234:PHE:HB2	1:A:322:MET:CE	2.32	0.60
1:A:480:ARG:HH22	1:A:484:ASN:ND2	2.01	0.59
1:A:502:VAL:C	2:A:9:RHE:CL3	2.78	0.58
1:A:345:ASP:O	1:A:349:HIS:HD2	1.87	0.57
1:A:234:PHE:HB2	1:A:322:MET:HE1	1.85	0.57
1:A:390:HIS:NE2	2:A:4:RHE:CL4	2.75	0.56
1:A:366:VAL:HG11	2:A:6:RHE:CL1	2.43	0.56
1:A:333:ARG:HG2	2:A:1:RHE:CL4	2.44	0.55
1:A:234:PHE:CB	1:A:322:MET:CE	2.84	0.55
1:A:504:TYR:HB3	2:A:9:RHE:CL3	2.46	0.53
1:A:344:HIS:CE1	2:A:3:RHE:CL3	2.97	0.53
1:A:393:ASP:HA	2:A:16:RHE:CL4	2.47	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:502:VAL:CA	2:A:9:RHE:CL3	2.96	0.51
1:A:333:ARG:CD	2:A:1:RHE:CL4	2.94	0.50
1:A:384:ILE:HD13	1:A:425:VAL:HB	1.94	0.49
1:A:502:VAL:HA	2:A:9:RHE:CL3	2.49	0.49
1:A:234:PHE:CG	1:A:322:MET:HE2	2.48	0.48
1:A:371:GLU:CG	2:A:1:RHE:CL2	2.99	0.48
1:A:393:ASP:CA	2:A:16:RHE:CL4	2.99	0.48
1:A:502:VAL:HG12	2:A:9:RHE:CL3	2.52	0.47
1:A:449:SER:HB2	2:A:3:RHE:CL2	2.53	0.45
1:A:329:ILE:CD1	1:A:416:LEU:HD22	2.45	0.45
1:A:504:TYR:N	2:A:9:RHE:CL3	2.83	0.45
1:A:419:ILE:O	1:A:423:LYS:HG3	2.16	0.45
1:A:428:LEU:HD12	1:A:493:ILE:HG21	1.98	0.44
1:A:371:GLU:HG3	2:A:1:RHE:CL2	2.55	0.43
1:A:322:MET:HE2	1:A:322:MET:HB2	1.77	0.43
1:A:331:PRO:HA	2:A:1:RHE:CL5	2.55	0.43
1:A:217:LEU:HD22	1:A:217:LEU:HA	1.91	0.42
1:A:493:ILE:HD13	1:A:493:ILE:HG21	1.81	0.42
1:A:224:GLY:HA3	1:A:243:ILE:HD11	2.02	0.41
1:A:329:ILE:HG22	1:A:330:LEU:HG	2.02	0.41
1:A:326:LEU:HD23	1:A:326:LEU:N	2.35	0.41
1:A:240:HIS:HD2	1:A:478:ASN:O	2.04	0.41
1:A:502:VAL:CG1	2:A:9:RHE:CL3	3.06	0.41

All (3) 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:A:324:GLU:OE1	1:A:500:TYR:OH[5_454]	2.03	0.17
1:A:359:SER:O	2:A:16:RHE:CL2[12_575]	2.05	0.15
1:A:283:ASP:OD2	2:A:9:RHE:CL1[12_565]	2.14	0.06

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	316/372 (85%)	296 (94%)	14 (4%)	6 (2%)	8 7

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	208	CYS
1	A	264	GLN
1	A	266	GLN
1	A	213	SER
1	A	271	GLN
1	A	206	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	A	281/324 (87%)	266 (95%)	15 (5%)	22 31

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

Mol	Chain	Res	Type
1	A	192	ILE
1	A	197	ARG
1	A	213	SER
1	A	215	TYR
1	A	217	LEU
1	A	263	ASN
1	A	329	ILE
1	A	333	ARG
1	A	378	GLU
1	A	384	ILE
1	A	400	LEU
1	A	419	ILE
1	A	428	LEU

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Mol	Chain	Res	Type
1	A	433	THR
1	A	471	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	240	HIS
1	A	332	HIS
1	A	349	HIS
1	A	387	HIS
1	A	396	GLN
1	A	484	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry

16 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	RHE	A	15	-	6,6,6	0.52	0	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	RHE	A	4	-	6,6,6	0.67	0	-		
2	RHE	A	3	-	6,6,6	2.35	3 (50%)	-		
2	RHE	A	11	-	6,6,6	0.97	0	-		
2	RHE	A	16	-	6,6,6	0.56	0	-		
2	RHE	A	12	-	6,6,6	0.58	0	-		
2	RHE	A	9	-	6,6,6	0.31	0	-		
2	RHE	A	5	-	6,6,6	1.09	0	-		
2	RHE	A	14	-	6,6,6	0.54	0	-		
2	RHE	A	13	-	6,6,6	0.63	0	-		
2	RHE	A	1	-	6,6,6	1.62	1 (16%)	-		
2	RHE	A	10	-	6,6,6	0.89	0	-		
2	RHE	A	6	-	6,6,6	0.68	0	-		
2	RHE	A	2	-	6,6,6	2.01	2 (33%)	-		
2	RHE	A	8	-	6,6,6	1.10	0	-		
2	RHE	A	7	-	6,6,6	1.21	1 (16%)	-		

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	3	RHE	RE-CL6	4.63	2.49	2.36
2	A	1	RHE	RE-CL2	-3.07	2.27	2.36
2	A	2	RHE	RE-CL1	-3.06	2.27	2.36
2	A	2	RHE	RE-CL3	-3.01	2.27	2.36
2	A	3	RHE	RE-CL5	-2.32	2.29	2.36
2	A	7	RHE	RE-CL6	2.29	2.42	2.36
2	A	3	RHE	RE-CL2	2.04	2.42	2.36

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

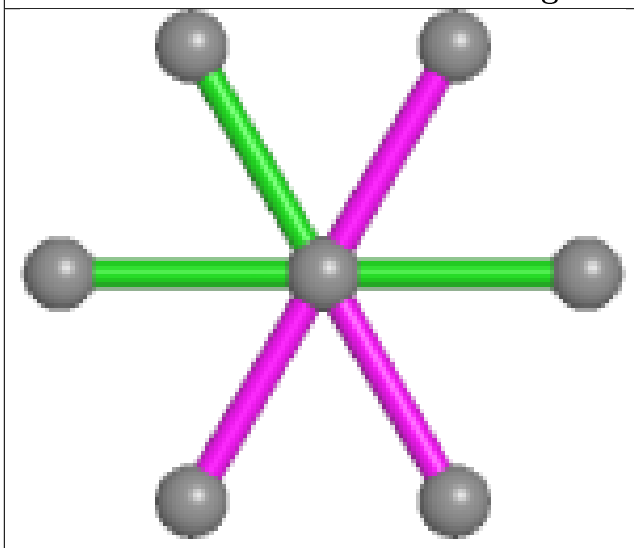
There are no ring outliers.

6 monomers are involved in 37 short contacts:

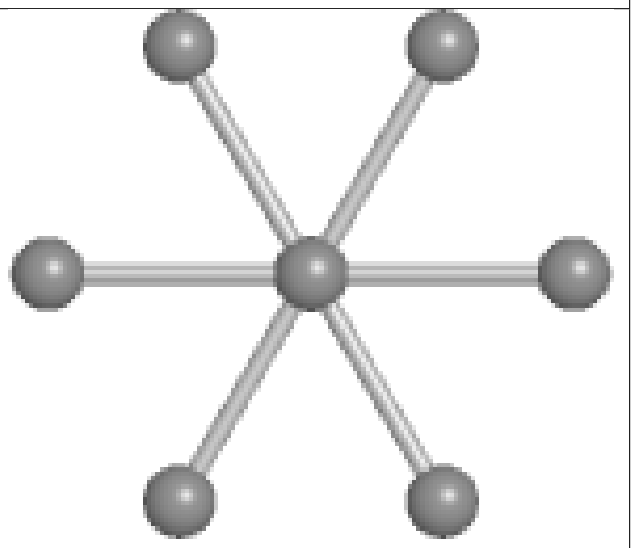
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	4	RHE	2	0
2	A	3	RHE	3	0
2	A	16	RHE	7	1
2	A	9	RHE	15	1
2	A	1	RHE	7	0
2	A	6	RHE	1	0

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.

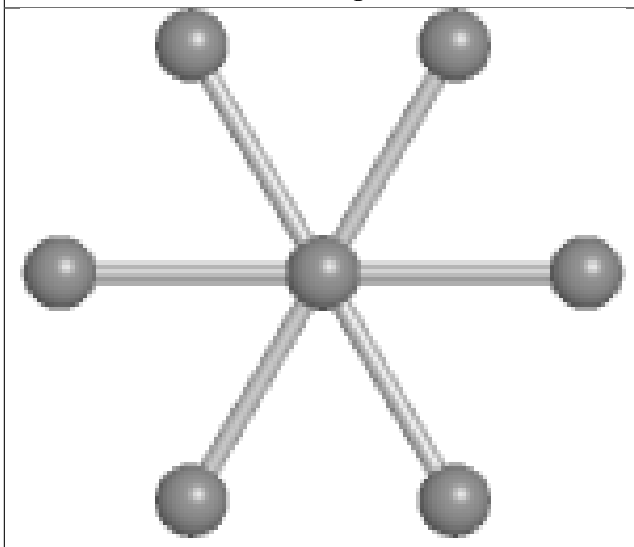
Ligand RHE A 3



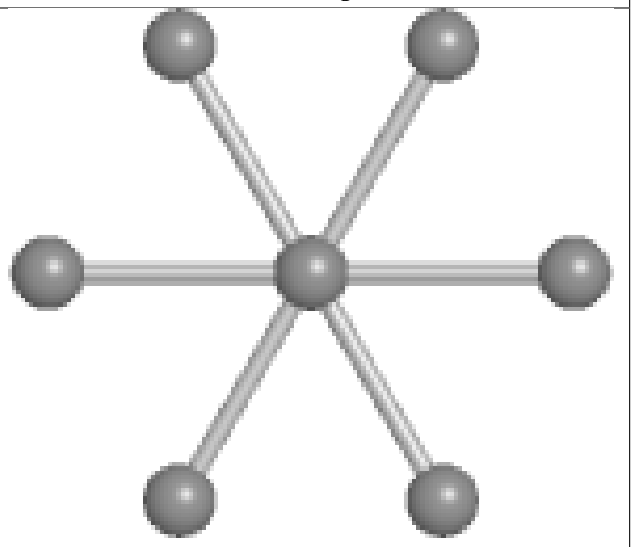
Bond lengths



Bond angles

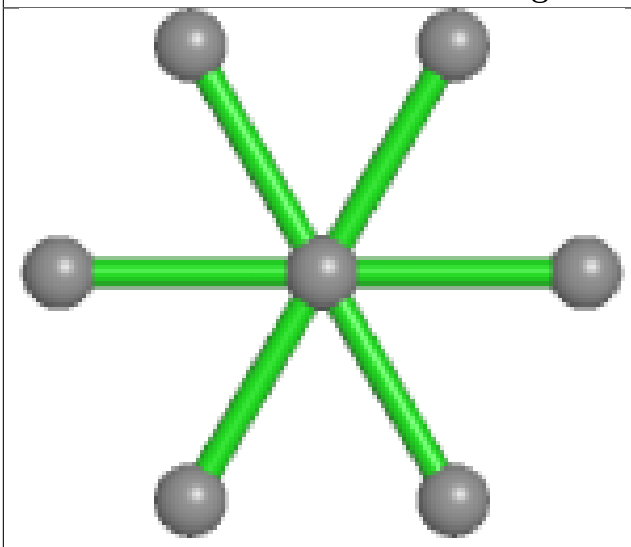


Torsions

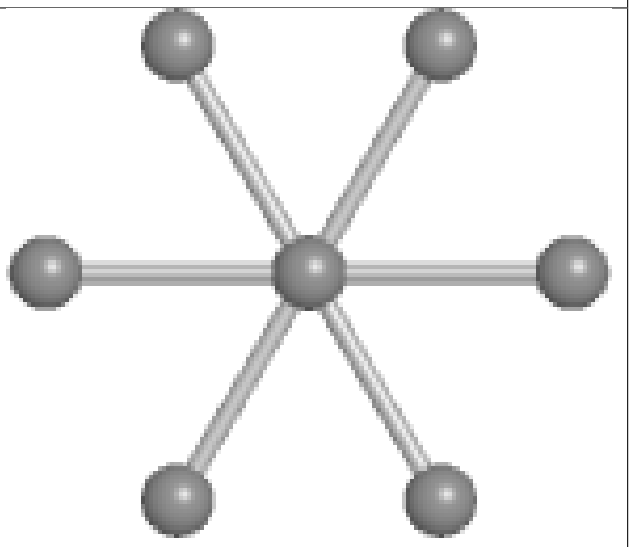


Rings

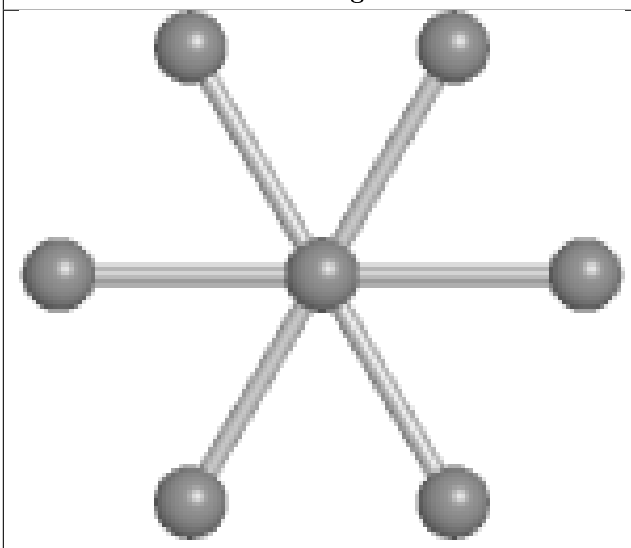
Ligand RHE A 16



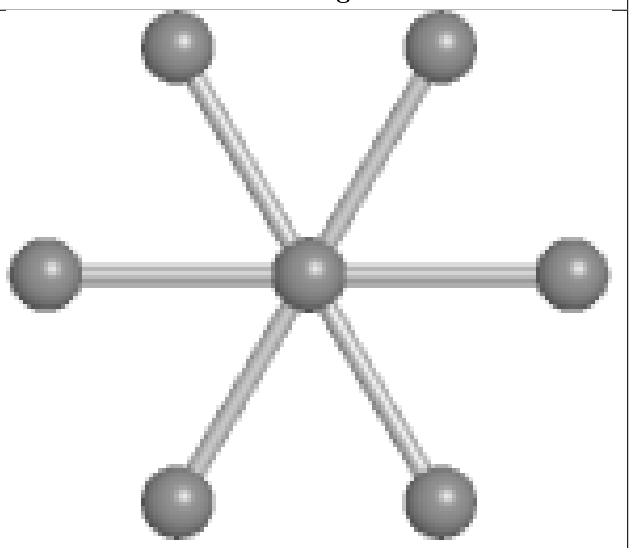
Bond lengths



Bond angles

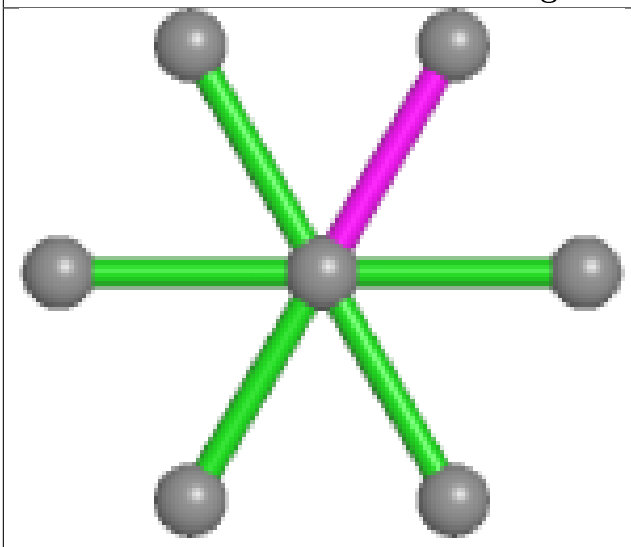


Torsions

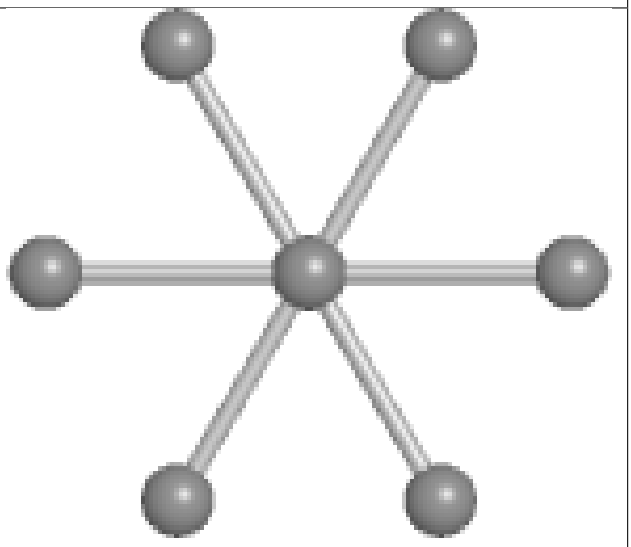


Rings

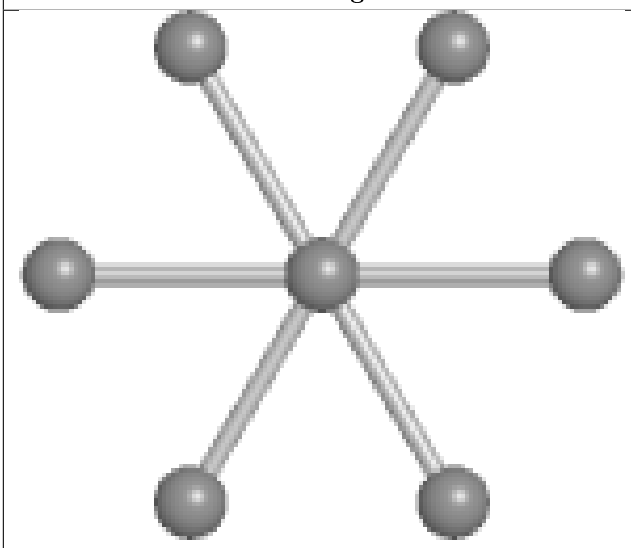
Ligand RHE A 1



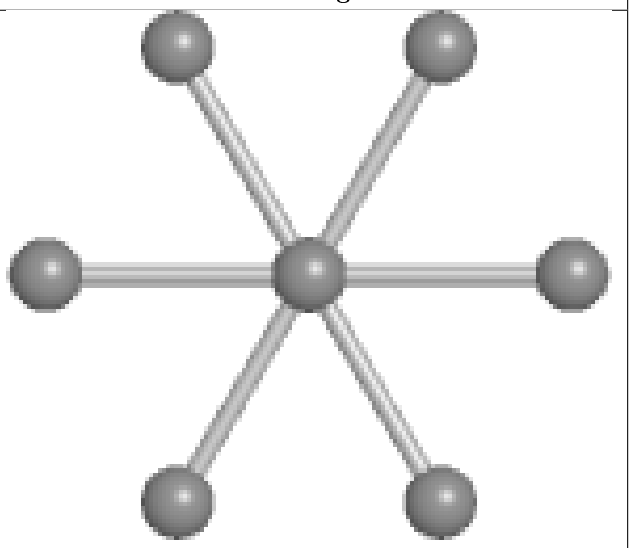
Bond lengths



Bond angles

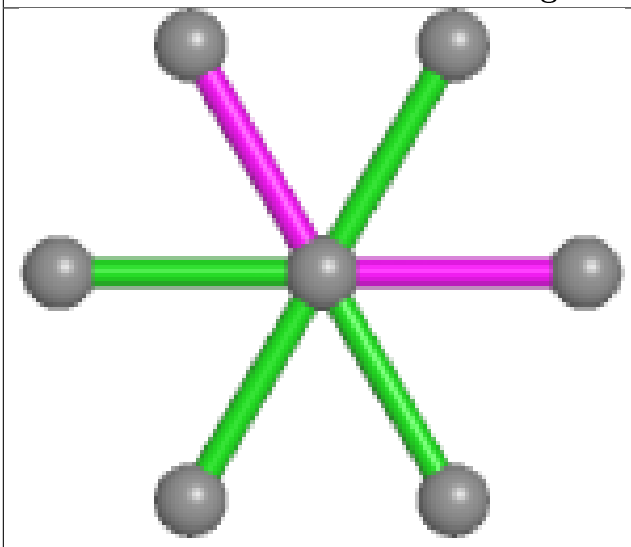


Torsions

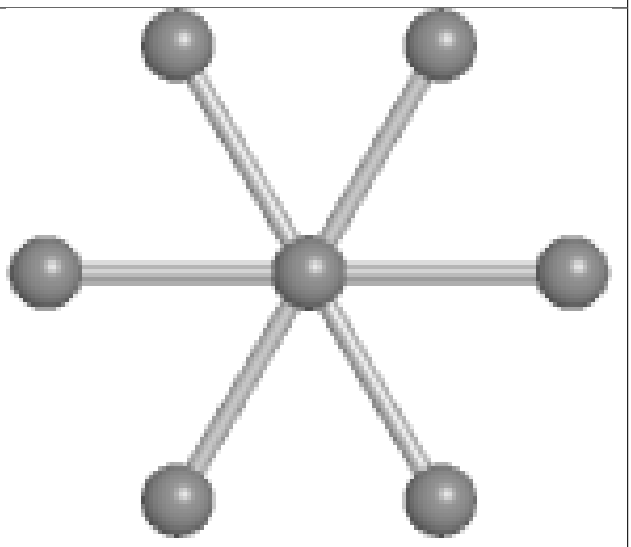


Rings

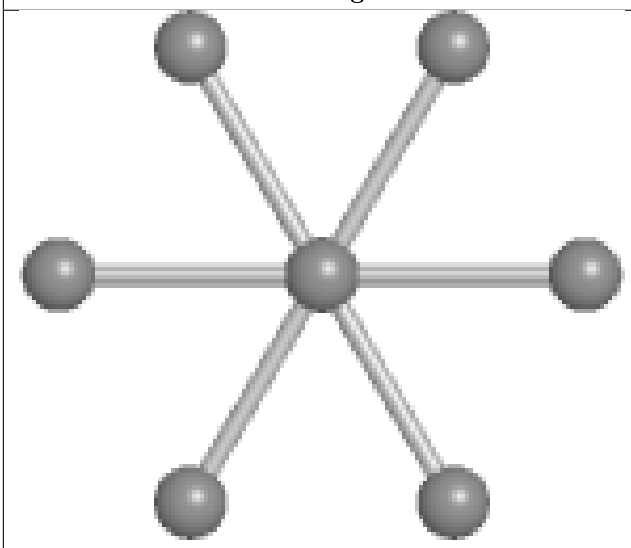
Ligand RHE A 2



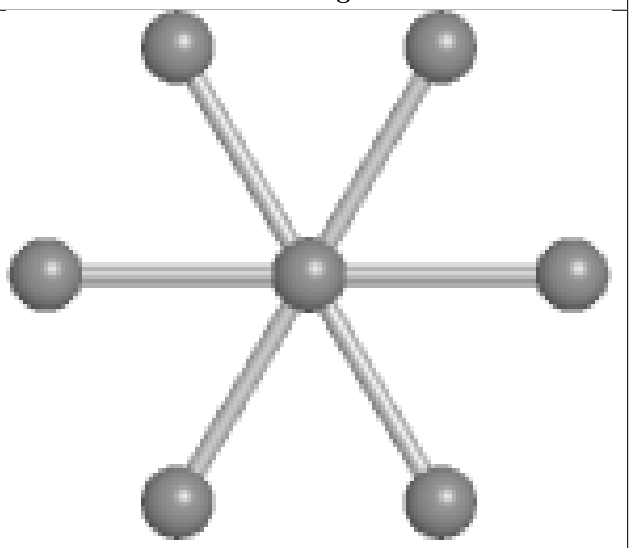
Bond lengths



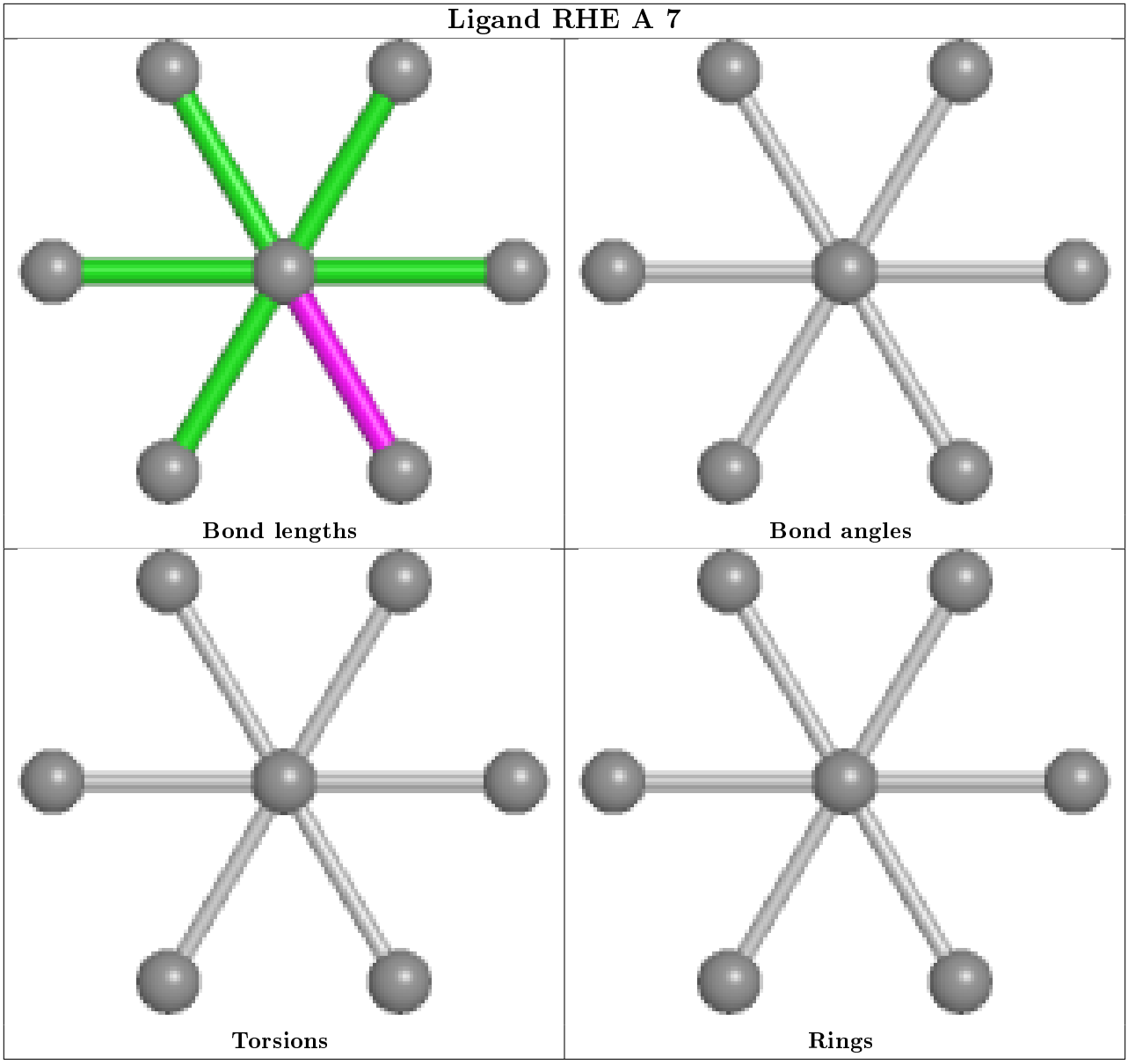
Bond angles



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	286/372 (76%)	0.02	10 (3%) 44 51	8, 20, 35, 42	49 (17%)

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	260	ALA	3.9
1	A	508	PHE	3.8
1	A	192	ILE	3.7
1	A	507	LYS	3.6
1	A	405	ASP	2.6
1	A	409	THR	2.3
1	A	251	SER	2.2
1	A	407	ILE	2.1
1	A	414	ASN	2.1
1	A	273	PHE	2.0

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 carbohydrates in this entry.

6.4 Ligands

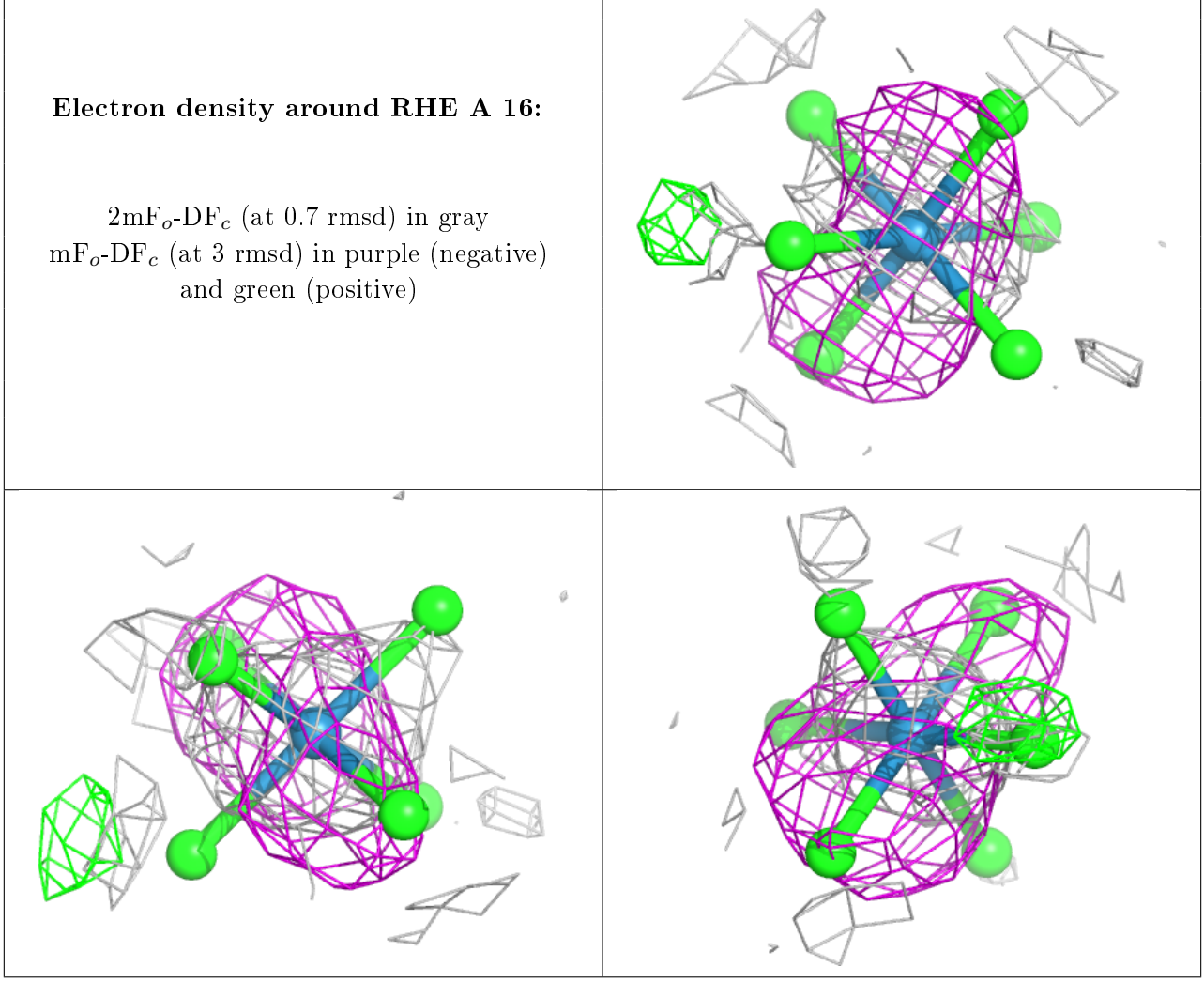
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	RHE	A	16	7/7	0.74	0.66	67,68,70,71	7
2	RHE	A	15	7/7	0.85	0.31	91,91,92,92	7
2	RHE	A	13	7/7	0.88	0.26	68,72,74,75	7
2	RHE	A	12	7/7	0.92	0.14	49,49,56,57	7
2	RHE	A	11	7/7	0.93	0.22	42,44,44,46	7
2	RHE	A	8	7/7	0.93	0.18	36,40,44,44	7
2	RHE	A	10	7/7	0.94	0.23	29,31,35,36	7
2	RHE	A	14	7/7	0.96	0.27	79,81,82,82	7
2	RHE	A	9	7/7	0.96	0.45	44,57,61,61	7
2	RHE	A	3	7/7	0.98	0.10	29,31,35,40	0
2	RHE	A	5	7/7	0.98	0.22	31,36,38,38	7
2	RHE	A	7	7/7	0.98	0.25	56,59,62,62	0
2	RHE	A	2	7/7	0.99	0.07	11,18,19,20	0
2	RHE	A	4	7/7	0.99	0.16	28,32,36,38	7
2	RHE	A	6	7/7	0.99	0.19	49,55,56,60	0
2	RHE	A	1	7/7	1.00	0.06	13,21,25,27	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.

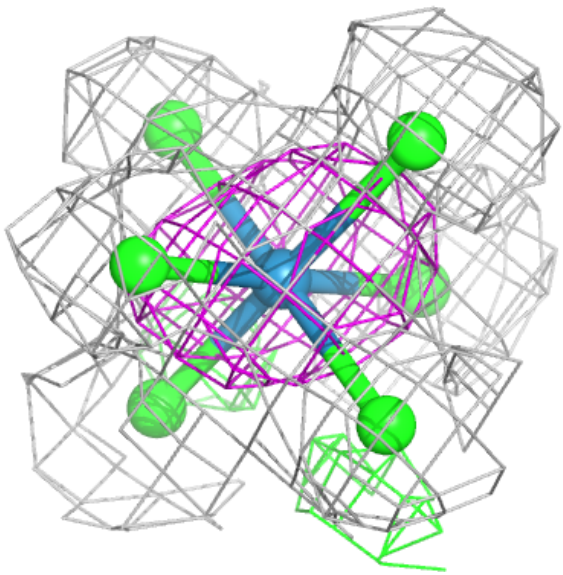
Electron density around RHE A 16:

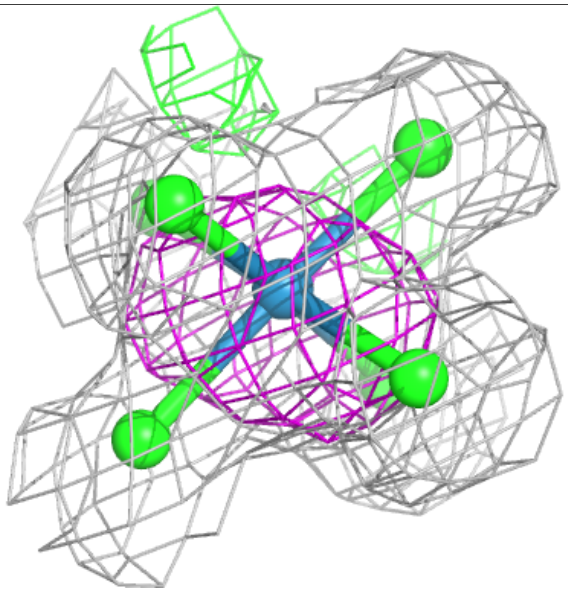
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

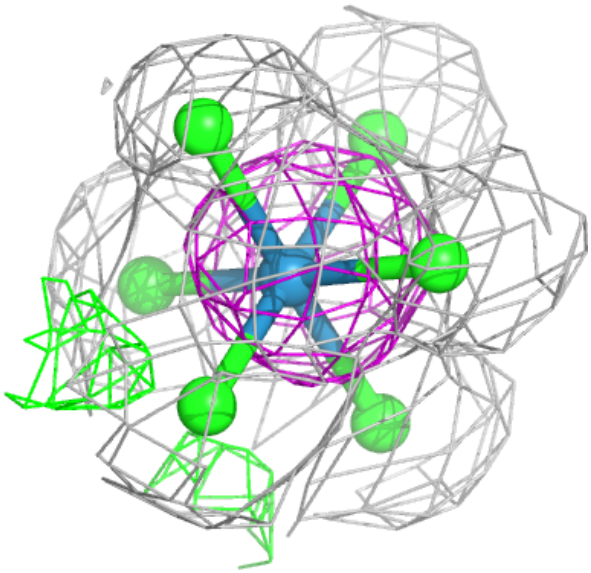


Electron density around RHE A 3:

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

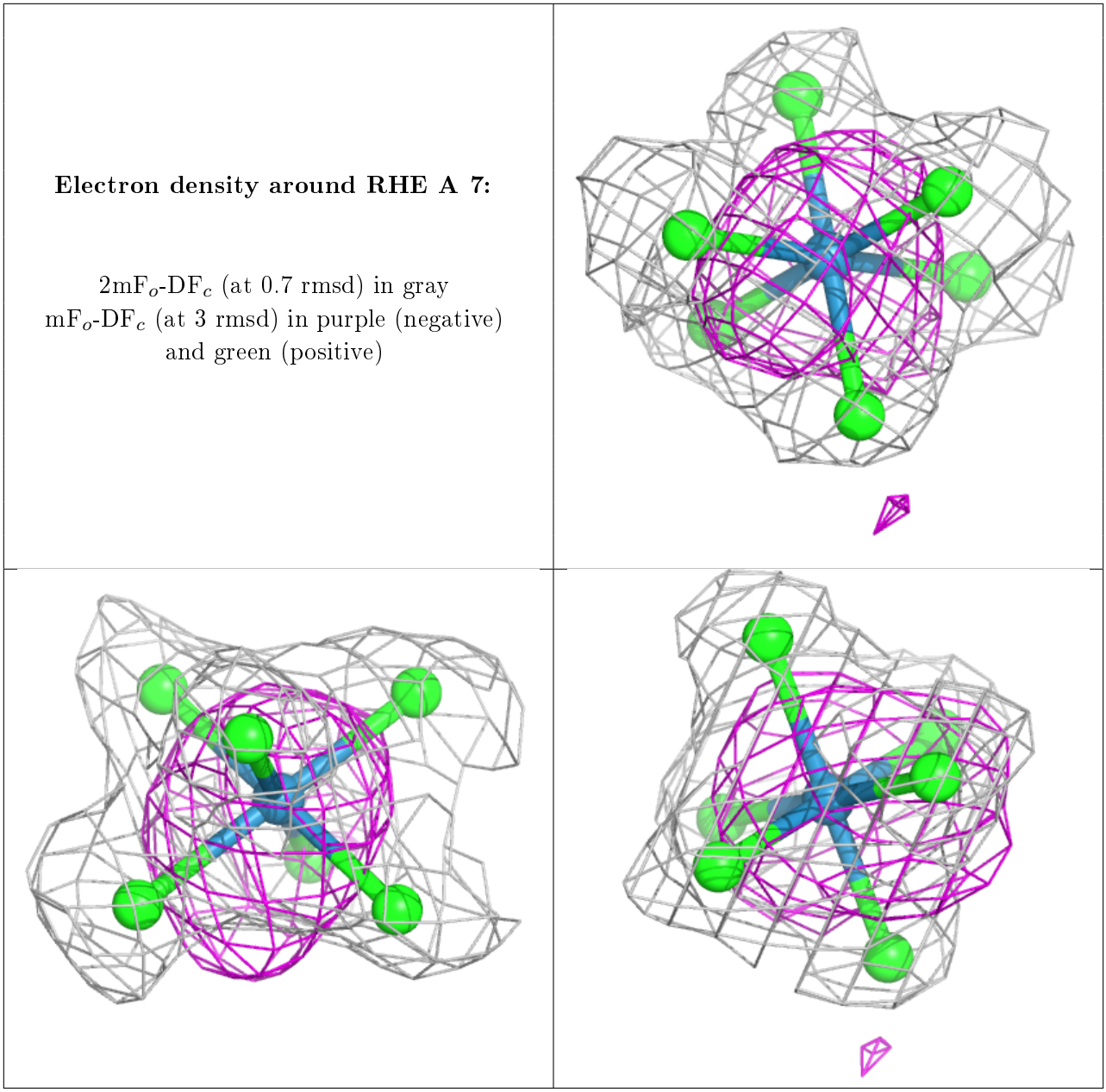






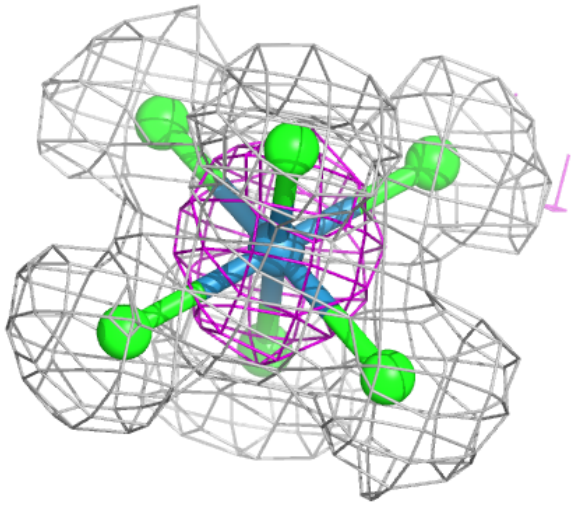
Electron density around RHE A 7:

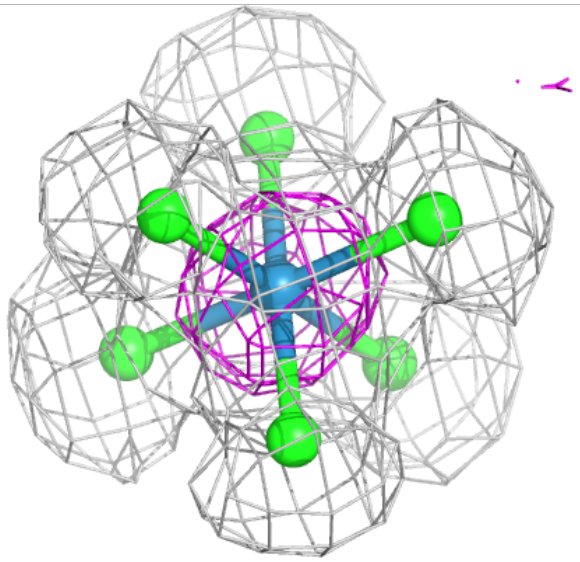
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

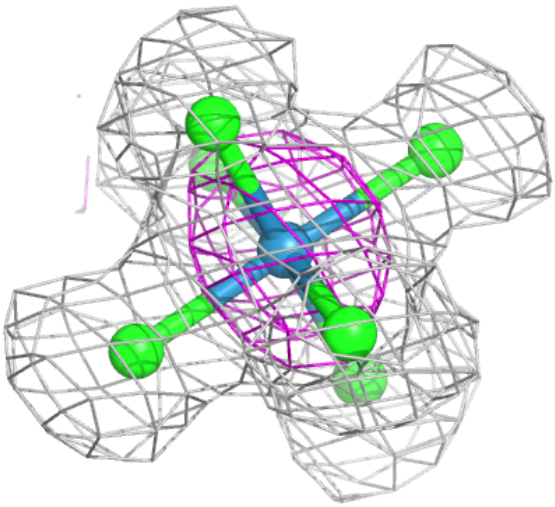


Electron density around RHE A 2:

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

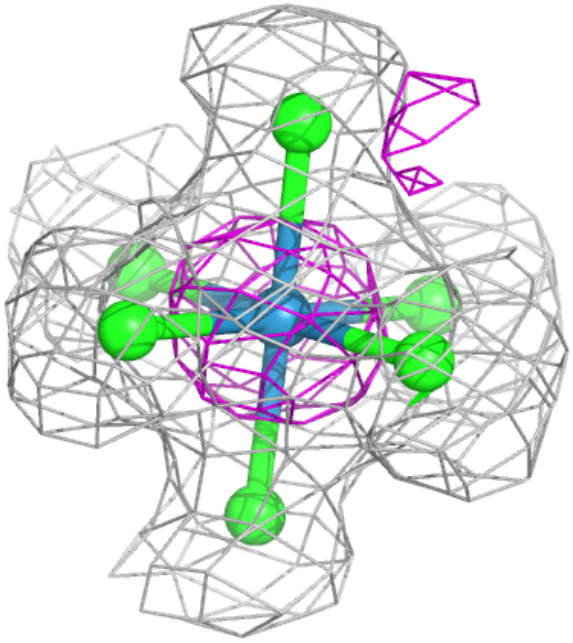


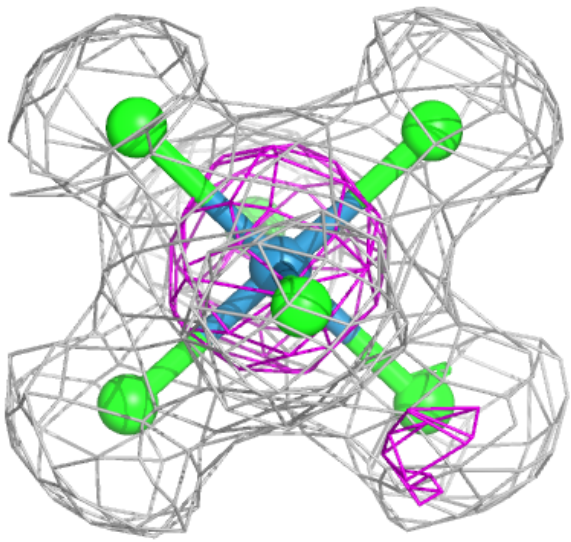


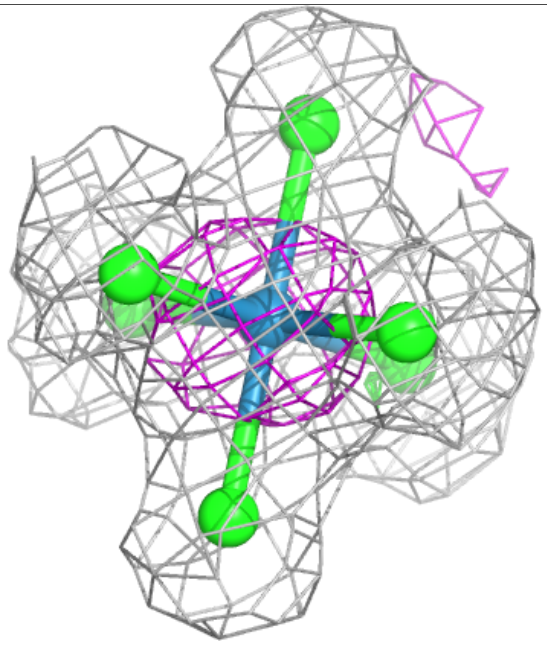


Electron density around RHE A 1:

$2mF_o$-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.