Full wwPDB X-ray Structure Validation Report (i)

Dec 7, 2023 – 02:09 pm GMT

PDB ID : 2W4I
Title : Crystal structure of Helicobacter pylori glutamate racemase in complex with D-Glutamate and an inhibitor
Authors : Lundqvist, T.
Deposited on : 2008-11-25
Resolution : 1.87 Å(reported)

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

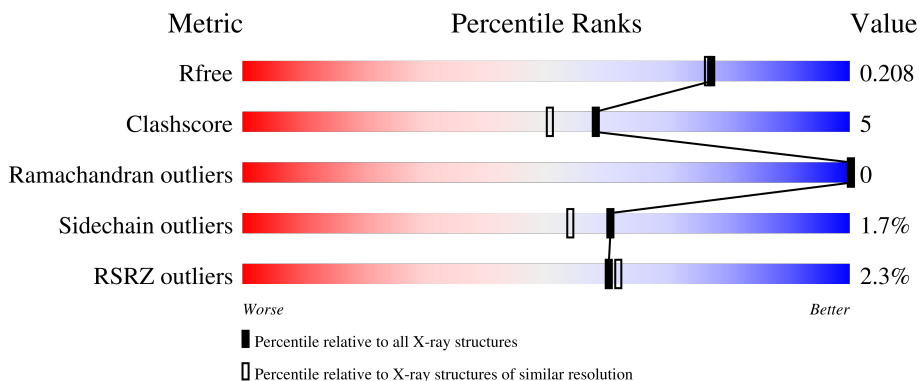|		
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance ⓘ

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

The reported resolution of this entry is 1.87 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	Percentile Ranks	Value
Rfree		0.208
Clashscore		5
Ramachandran outliers		0
Sidechain outliers		1.7%
RSRZ outliers		2.3%

Worse   *Better*

▊ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	9470 (1.90-1.86)
Clashscore	141614	10282 (1.90-1.86)
Ramachandran outliers	138981	10152 (1.90-1.86)
Sidechain outliers	138945	10152 (1.90-1.86)
RSRZ outliers	127900	9303 (1.90-1.86)

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	255	% · 95% 5%
1	B	255	3% 88% 11%
1	E	255	4% 91% 9%
1	F	255	2% 91% 9%

WORLDWIDE PDB
PROTEIN DATA BANK

2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 9466 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 GLUTAMATE RACEMASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	255	Total	C	N	O	S	0	0	0
			2012	1319	318	367	8			
1	B	254	Total	C	N	O	S	0	0	0
			2003	1313	317	365	8			
1	E	254	Total	C	N	O	S	0	0	0
			2003	1313	317	365	8			
1	F	254	Total	C	N	O	S	0	0	0
			2003	1313	317	365	8			

- Molecule 2 is D-GLUTAMIC ACID (three-letter code: DGL) (formula: $C_5H_9NO_4$).
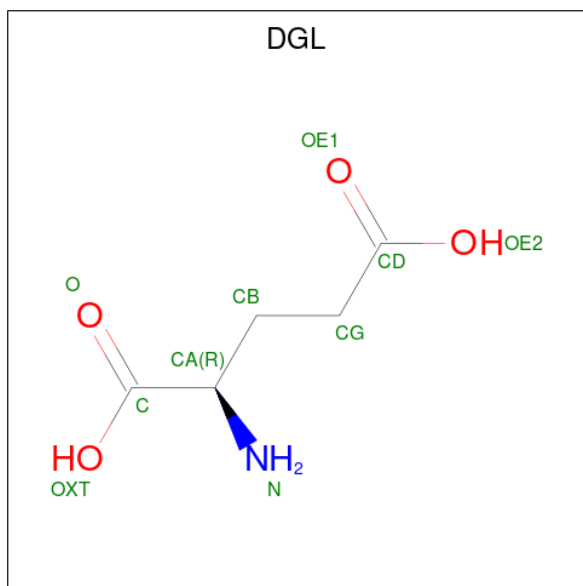
DGL

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			10	5	1	4		
2	B	1	Total	C	N	O	0	0
			10	5	1	4		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	E	1	Total 10	C 5	N 1	O 4	0	0
2	F	1	Total 10	C 5	N 1	O 4	0	0

- Molecule 3 is 1-[(3S)-5-PHENYL-3-THIOPHEN-2-YL-3H-1,4-BENZODIAZEPIN-2-YL]AZ ETIDIN-3-OL (three-letter code: VGA) (formula: $C_{22}H_{19}N_3OS$).
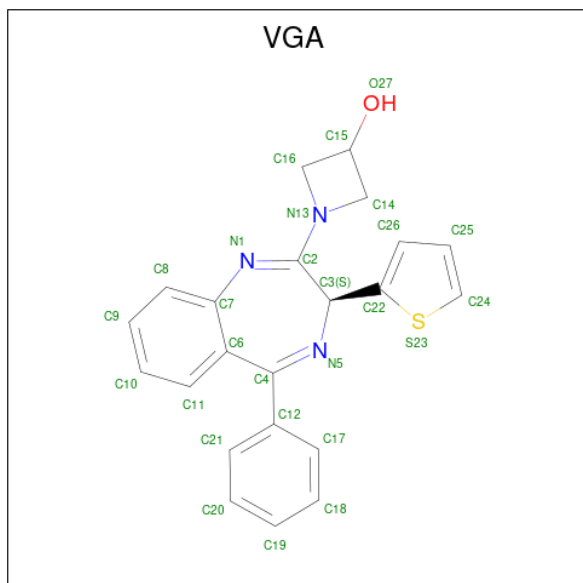
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total 27	C 22	N 3	O 1	S 1	0	0
3	E	1	Total 27	C 22	N 3	O 1	S 1	0	0

- Molecule 4 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	390	Total 390	O 390	0	0
4	B	328	Total 328	O 328	0	0
4	E	328	Total 328	O 328	0	0
4	F	305	Total 305	O 305	0	0

3 Residue-property plots ⓘ

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.
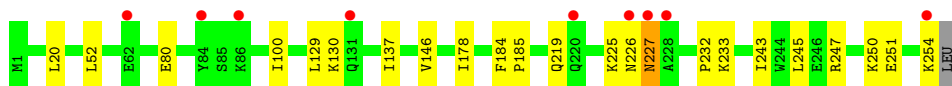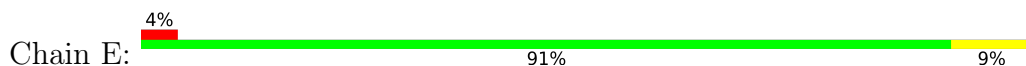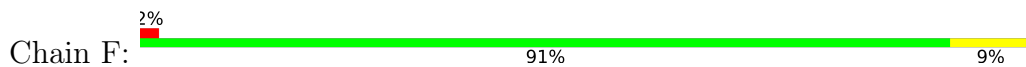
• Molecule 1: GLUTAMATE RACEMASE

Chain A:

• Molecule 1: GLUTAMATE RACEMASE

Chain B:
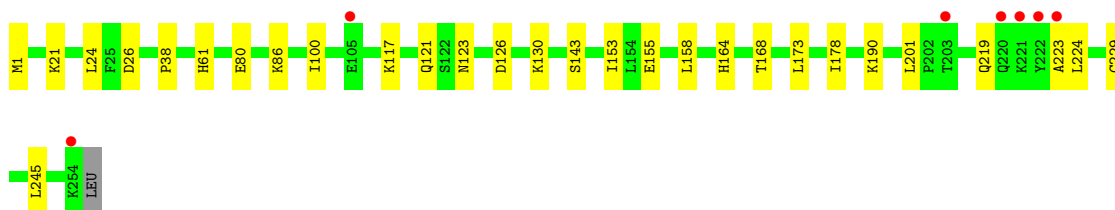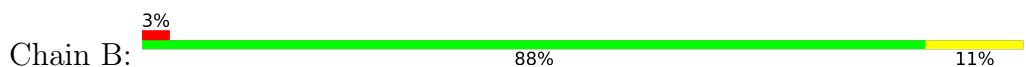
• Molecule 1: GLUTAMATE RACEMASE

Chain E:

• Molecule 1: GLUTAMATE RACEMASE

Chain F:

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	59.07Å 93.98Å 101.30Å 90.00° 91.46° 90.00°	Depositor
Resolution (Å)	24.67 – 1.87 24.67 – 1.87	Depositor EDS
% Data completeness (in resolution range)	100.0 (24.67-1.87) 97.6 (24.67-1.87)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.64 (at 1.88Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.156 , 0.209 0.155 , 0.208	Depositor DCC
R_{free} test set	4456 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	15.0	Xtriage
Anisotropy	0.076	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 63.9	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.028 for h,-k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	9466	wwPDB-VP
Average B, all atoms (Å^2)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.84% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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: DGL, VGA

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	0.68	0/2060	0.64	0/2795
1	B	0.66	1/2051 (0.0%)	0.64	0/2784
1	E	0.67	0/2051	0.60	0/2784
1	F	0.64	0/2051	0.61	0/2784
All	All	0.66	1/8213 (0.0%)	0.62	0/11147

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	229	CYS	CB-SG	-5.23	1.73	1.81

There are no bond angle outliers.

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	2012	0	2055	8	0
1	B	2003	0	2044	28	0
1	E	2003	0	2044	15	0
1	F	2003	0	2044	21	0
2	A	10	0	7	0	0
2	B	10	0	7	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	10	0	7	0	0
2	F	10	0	7	0	0
3	B	27	0	19	5	0
3	E	27	0	19	5	0
4	A	390	0	0	5	0
4	B	328	0	0	12	1
4	E	328	0	0	3	0
4	F	305	0	0	10	1
All	All	9466	0	8253	78	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 5.

All (78) 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:117:LYS:HD3	4:B:2213:HOH:O	1.68	0.92
1:F:248:GLN:HG3	4:F:2297:HOH:O	1.73	0.89
1:F:233:LYS:HE3	4:F:2042:HOH:O	1.76	0.84
4:A:2244:HOH:O	3:B:1256:VGA:H17	1.80	0.82
1:A:247:ARG:HD3	4:A:2377:HOH:O	1.77	0.82
1:B:219:GLN:NE2	4:B:2287:HOH:O	2.12	0.82
1:B:164:HIS:CE1	1:B:168:THR:HG21	2.16	0.81
1:B:223:ALA:HB3	4:B:2290:HOH:O	1.83	0.77
1:B:80:GLU:HG2	4:B:2128:HOH:O	1.85	0.75
1:B:61:HIS:HD2	4:B:2005:HOH:O	1.70	0.74
1:B:26:ASP:HB2	4:B:2003:HOH:O	1.87	0.73
1:F:219:GLN:NE2	1:F:226:ASN:HD21	1.86	0.73
1:B:155:GLU:HG2	1:B:190:LYS:HE3	1.74	0.69
1:B:130:LYS:HG2	4:B:2196:HOH:O	1.94	0.68
1:B:173:LEU:HD21	1:B:201:LEU:HD21	1.77	0.66
1:B:86:LYS:NZ	4:B:2137:HOH:O	2.29	0.66
1:B:164:HIS:CE1	1:B:168:THR:CG2	2.79	0.65
1:F:173:LEU:HD21	1:F:201:LEU:HD21	1.79	0.64
1:B:164:HIS:NE2	1:B:168:THR:HG21	2.12	0.64
3:B:1256:VGA:H21	3:B:1256:VGA:C11	2.27	0.63
1:F:21:LYS:HG3	4:F:2016:HOH:O	1.98	0.63
1:E:232:PRO:HD2	4:E:2005:HOH:O	1.99	0.61
1:B:164:HIS:O	1:B:168:THR:HG23	2.00	0.60
1:A:230:THR:HG22	4:A:2350:HOH:O	2.02	0.60
1:A:121:GLN:HG3	4:A:2212:HOH:O	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:117:LYS:CD	4:B:2213:HOH:O	2.37	0.59
1:B:219:GLN:HG3	1:B:224:LEU:O	2.02	0.59
3:E:1256:VGA:C11	3:E:1256:VGA:H21	2.33	0.59
1:F:61:HIS:HD2	4:F:2004:HOH:O	1.88	0.56
1:F:17:LYS:HG2	1:F:21:LYS:HE3	1.89	0.55
1:B:117:LYS:CG	4:B:2213:HOH:O	2.55	0.55
1:F:17:LYS:HG2	1:F:21:LYS:CE	2.37	0.54
1:A:173:LEU:HD12	1:A:174:PRO:HD2	1.89	0.53
1:F:82:GLN:HG2	4:F:2147:HOH:O	2.08	0.53
1:F:219:GLN:HE21	1:F:226:ASN:HD21	1.52	0.53
3:B:1256:VGA:C11	3:B:1256:VGA:C21	2.86	0.52
1:F:94:GLU:HB3	4:F:2056:HOH:O	2.09	0.52
1:F:131:GLN:HG2	4:F:2076:HOH:O	2.09	0.51
1:A:243:ILE:O	1:A:247:ARG:HG3	2.10	0.51
1:E:226:ASN:O	1:E:227:ASN:ND2	2.42	0.51
1:E:219:GLN:NE2	1:E:226:ASN:OD1	2.44	0.51
1:B:117:LYS:HG3	1:B:143:SER:OG	2.12	0.49
1:E:247:ARG:HA	1:E:250:LYS:HE3	1.95	0.49
1:B:153:ILE:HD13	1:B:158:LEU:HD23	1.95	0.49
1:E:243:ILE:HG12	4:E:2307:HOH:O	2.13	0.48
1:B:117:LYS:O	1:B:121:GLN:HG3	2.14	0.48
1:F:17:LYS:HE2	1:F:21:LYS:HE2	1.96	0.48
1:F:177:ILE:HB	1:F:207:LEU:HD22	1.93	0.48
1:F:248:GLN:CG	4:F:2297:HOH:O	2.45	0.48
1:B:1:MET:HE3	4:B:2031:HOH:O	2.13	0.48
4:A:2244:HOH:O	3:B:1256:VGA:C17	2.48	0.47
1:E:100:ILE:HD11	1:E:178:ILE:CD1	2.44	0.47
1:B:164:HIS:CD2	1:B:168:THR:HG21	2.49	0.47
1:F:252:TRP:HA	4:F:2305:HOH:O	2.16	0.46
1:A:86:LYS:HA	1:A:86:LYS:HD3	1.59	0.46
3:E:1256:VGA:C11	3:E:1256:VGA:C21	2.92	0.45
3:E:1256:VGA:C8	1:F:38:PRO:HB3	2.47	0.45
1:B:155:GLU:HG2	1:B:190:LYS:CE	2.46	0.45
1:E:100:ILE:HD11	1:E:178:ILE:HD11	1.99	0.45
1:F:216:GLU:HG2	4:F:2273:HOH:O	2.16	0.44
1:F:110:PRO:HG2	1:F:175:GLU:HG3	2.00	0.44
1:E:52:LEU:HD21	1:E:80:GLU:HG3	2.00	0.44
1:E:146:VAL:HG12	3:E:1256:VGA:S23	2.58	0.43
1:F:78:LEU:O	1:F:82:GLN:HG3	2.18	0.43
1:B:100:ILE:CD1	1:B:178:ILE:HD11	2.49	0.42
1:A:144:LEU:HD11	1:B:153:ILE:HD12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:24:LEU:HB3	1:B:224:LEU:HD13	2.01	0.42
1:E:20:LEU:HD22	1:E:232:PRO:HG3	2.01	0.42
1:E:251:GLU:HB2	4:E:2312:HOH:O	2.20	0.42
1:E:100:ILE:HD13	1:E:129:LEU:HD21	2.03	0.41
1:E:130:LYS:HG3	1:E:137:ILE:HD12	2.03	0.41
1:F:189:GLN:OE1	1:F:189:GLN:HA	2.21	0.41
1:E:184:PHE:N	1:E:185:PRO:CD	2.84	0.41
1:B:38:PRO:HB3	3:B:1256:VGA:C8	2.51	0.40
1:A:17:LYS:NZ	1:A:254:LYS:HG3	2.36	0.40
1:E:100:ILE:CD1	1:E:178:ILE:HD11	2.51	0.40
3:E:1256:VGA:C22	3:E:1256:VGA:C16	2.99	0.40
1:B:61:HIS:HE1	4:B:2099:HOH:O	2.05	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)
4:B:2004:HOH:O	4:F:2003:HOH:O[2_546]	2.12	0.08

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	253/255 (99%)	249 (98%)	4 (2%)	0	100	100
1	B	252/255 (99%)	245 (97%)	7 (3%)	0	100	100
1	E	252/255 (99%)	244 (97%)	8 (3%)	0	100	100
1	F	252/255 (99%)	247 (98%)	5 (2%)	0	100	100
All	All	1009/1020 (99%)	985 (98%)	24 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	219/219 (100%)	215 (98%)	4 (2%)	59	52
1	B	218/219 (100%)	214 (98%)	4 (2%)	59	52
1	E	218/219 (100%)	213 (98%)	5 (2%)	50	41
1	F	218/219 (100%)	216 (99%)	2 (1%)	78	76
All	All	873/876 (100%)	858 (98%)	15 (2%)	60	54

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

Mol	Chain	Res	Type
1	A	170	LEU
1	A	224	LEU
1	A	245	LEU
1	A	255	LEU
1	B	21	LYS
1	B	123	ASN
1	B	126	ASP
1	B	245	LEU
1	E	225	LYS
1	E	227	ASN
1	E	233	LYS
1	E	245	LEU
1	E	254	LYS
1	F	229	CYS
1	F	245	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	103	GLN
1	A	121	GLN
1	A	164	HIS
1	A	227	ASN

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Mol	Chain	Res	Type
1	A	248	GLN
1	B	61	HIS
1	B	123	ASN
1	B	219	GLN
1	E	219	GLN
1	E	226	ASN
1	F	61	HIS
1	F	121	GLN
1	F	198	HIS
1	F	219	GLN
1	F	220	GLN
1	F	248	GLN

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 ⓘ

6 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	DGL	A	1256	-	8,9,9	0.99	0	10,11,11	1.19	1 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
3	VGA	B	1256	-	27,31,31	1.17	3 (11%)	27,44,44	1.46	5 (18%)
2	DGL	E	1255	-	8,9,9	0.97	0	10,11,11	1.39	1 (10%)
2	DGL	B	1255	-	8,9,9	1.11	0	10,11,11	1.12	0
2	DGL	F	1255	-	8,9,9	0.89	0	10,11,11	1.52	2 (20%)
3	VGA	E	1256	-	27,31,31	1.02	3 (11%)	27,44,44	1.39	4 (14%)

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	DGL	A	1256	-	-	3/9/9/9	-
3	VGA	B	1256	-	-	2/4/36/36	0/4/5/5
2	DGL	E	1255	-	-	2/9/9/9	-
2	DGL	B	1255	-	-	2/9/9/9	-
2	DGL	F	1255	-	-	2/9/9/9	-
3	VGA	E	1256	-	-	2/4/36/36	0/4/5/5

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1256	VGA	C22-C3	-3.31	1.49	1.52
3	B	1256	VGA	C14-N13	2.67	1.49	1.47
3	E	1256	VGA	C22-C3	-2.60	1.50	1.52
3	B	1256	VGA	C2-N13	2.32	1.38	1.34
3	E	1256	VGA	C2-N13	2.30	1.38	1.34
3	E	1256	VGA	C14-N13	2.14	1.48	1.47

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	1256	VGA	C25-C24-S23	-4.24	109.54	112.98
3	B	1256	VGA	C25-C24-S23	-3.47	110.17	112.98
3	E	1256	VGA	C8-C7-C6	-3.26	115.77	119.16
2	F	1255	DGL	OXT-C-CA	2.99	123.57	113.38
3	B	1256	VGA	C6-C4-C12	-2.85	114.80	118.11
3	B	1256	VGA	C8-C7-C6	-2.73	116.32	119.16
3	B	1256	VGA	C9-C8-C7	2.54	123.76	118.98
3	E	1256	VGA	C9-C8-C7	2.28	123.27	118.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	1256	VGA	C9-C10-C11	-2.27	116.73	120.19
2	A	1256	DGL	OXT-C-CA	2.23	120.99	113.38
2	E	1255	DGL	OXT-C-CA	2.19	120.83	113.38
2	F	1255	DGL	OXT-C-O	-2.13	119.26	124.09
3	E	1256	VGA	C9-C10-C11	-2.07	117.04	120.19

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	1256	VGA	C17-C12-C4-C6
3	B	1256	VGA	C17-C12-C4-C6
3	E	1256	VGA	C21-C12-C4-C6
3	B	1256	VGA	C21-C12-C4-C6
2	E	1255	DGL	OE2-CD-CG-CB
2	A	1256	DGL	OE1-CD-CG-CB
2	B	1255	DGL	OE2-CD-CG-CB
2	A	1256	DGL	OE2-CD-CG-CB
2	F	1255	DGL	OE2-CD-CG-CB
2	E	1255	DGL	OE1-CD-CG-CB
2	B	1255	DGL	OE1-CD-CG-CB
2	F	1255	DGL	OE1-CD-CG-CB
2	A	1256	DGL	CA-CB-CG-CD

There are no ring outliers.

2 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1256	VGA	5	0
3	E	1256	VGA	5	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 VGA B 1256

Bond lengths

Bond angles

Torsions

Rings

Ligand VGA E 1256

Bond lengths

Bond angles

Torsions

Rings
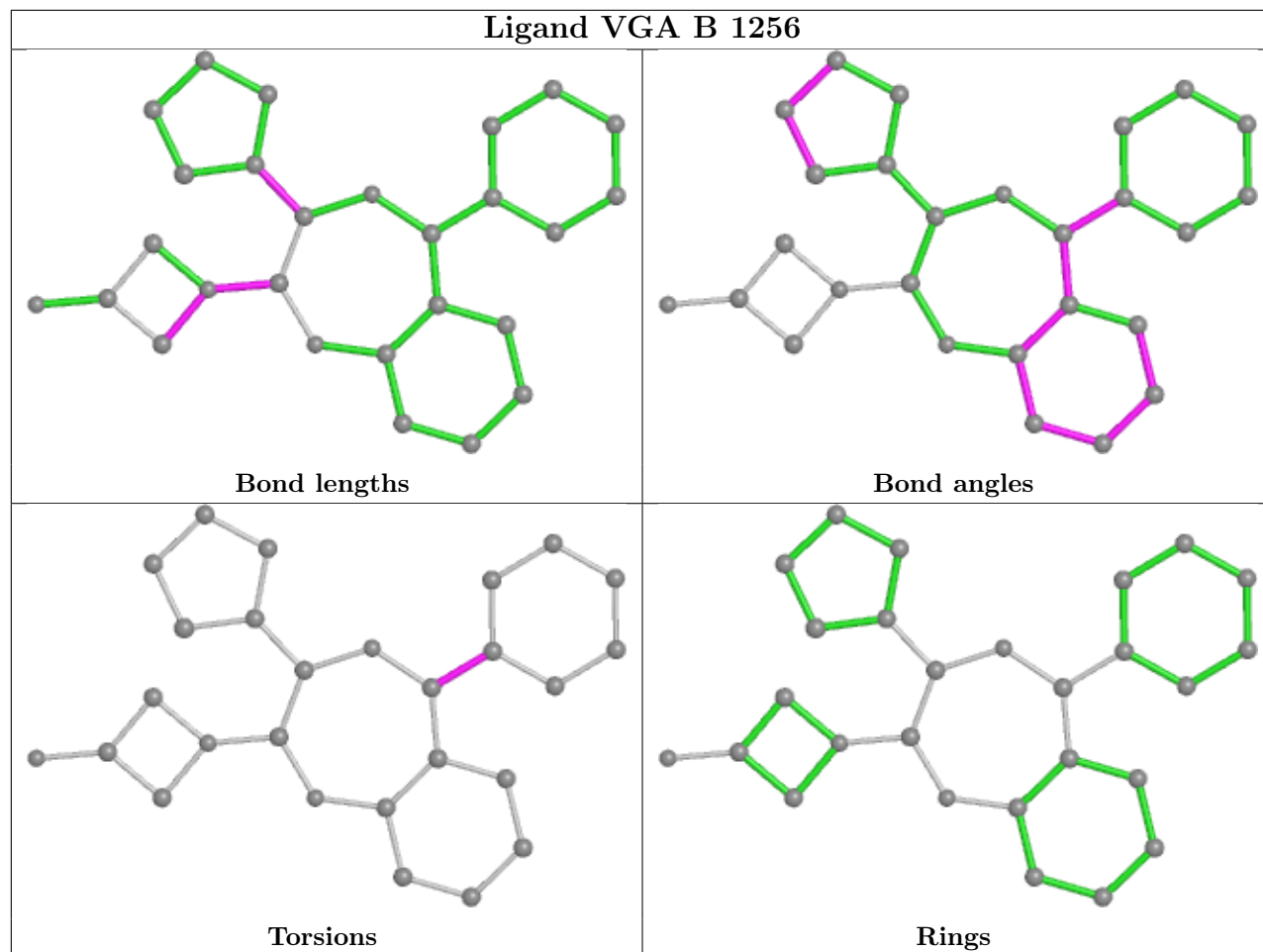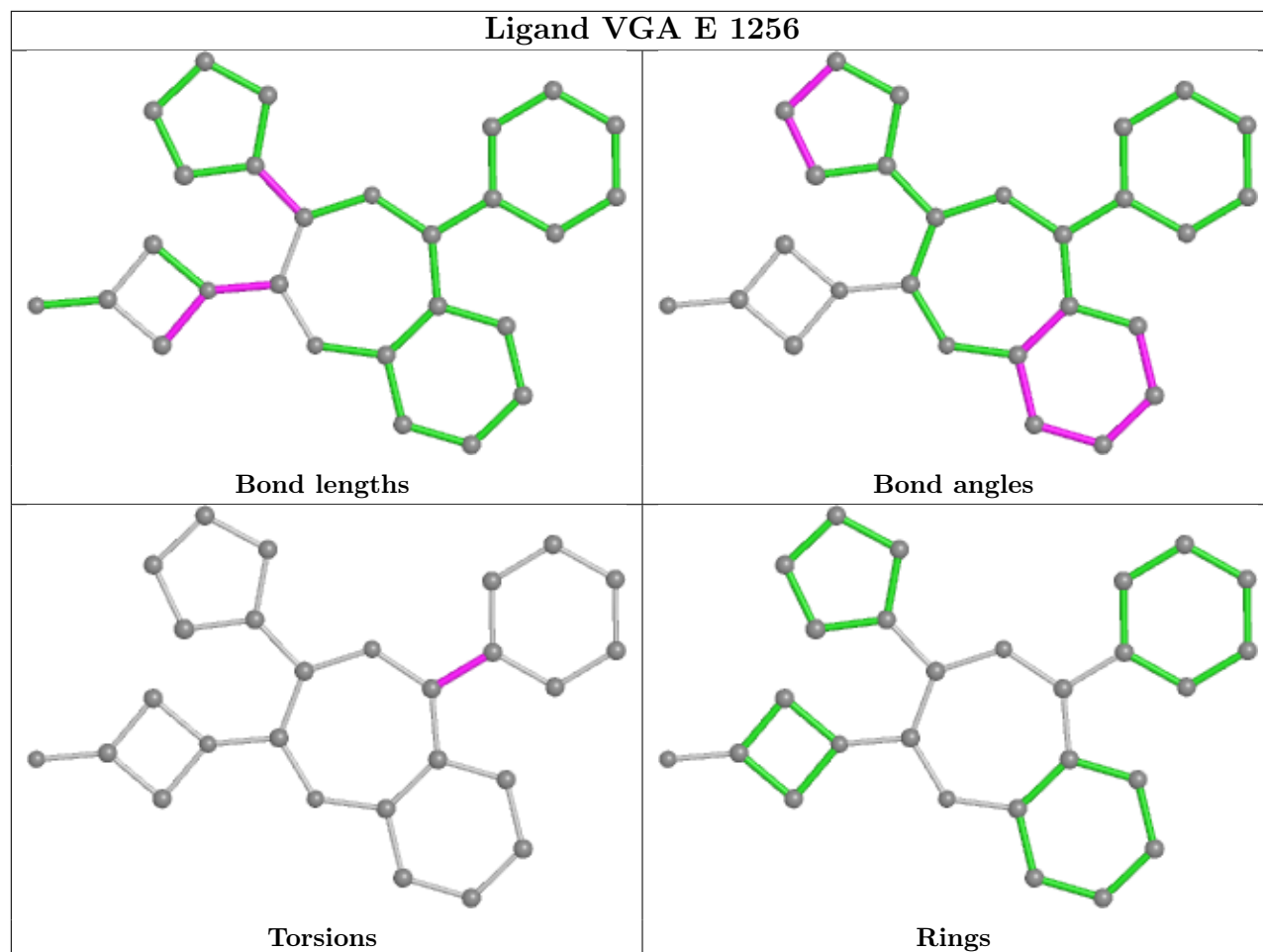
5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	255/255 (100%)	-0.34	3 (1%)	79	80	6, 12, 21, 29	0
1	B	254/255 (99%)	-0.22	7 (2%)	53	54	5, 13, 30, 37	0
1	E	254/255 (99%)	-0.13	9 (3%)	44	45	6, 13, 29, 45	0
1	F	254/255 (99%)	-0.10	4 (1%)	72	74	7, 15, 31, 37	0
All	All	1017/1020 (99%)	-0.20	23 (2%)	60	62	5, 13, 29, 45	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	226	ASN	5.6
1	B	222	TYR	4.4
1	E	254	LYS	4.4
1	A	255	LEU	3.9
1	E	84	TYR	3.5
1	A	84	TYR	3.3
1	F	171	GLU	3.1
1	E	227	ASN	3.1
1	B	254	LYS	2.8
1	B	220	GLN	2.8
1	F	254	LYS	2.7
1	B	105	GLU	2.7
1	E	220	GLN	2.5
1	F	105	GLU	2.4
1	E	86	LYS	2.3
1	E	62	GLU	2.3
1	A	135	LEU	2.2
1	E	131	GLN	2.2
1	F	225	LYS	2.1
1	B	203	THR	2.1
1	E	228	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	223	ALA	2.0
1	B	221	LYS	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 monosaccharides in this entry.

6.4 Ligands ⓘ

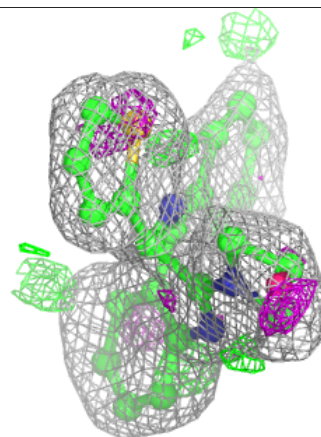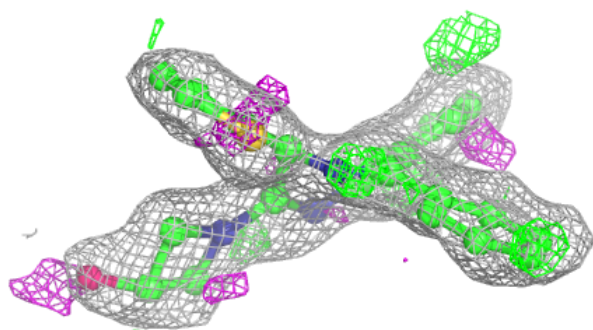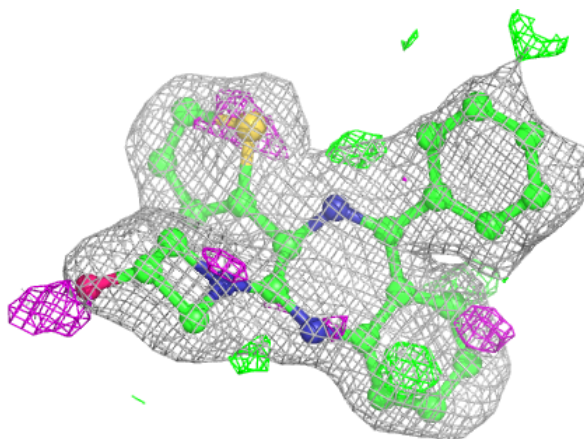In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.
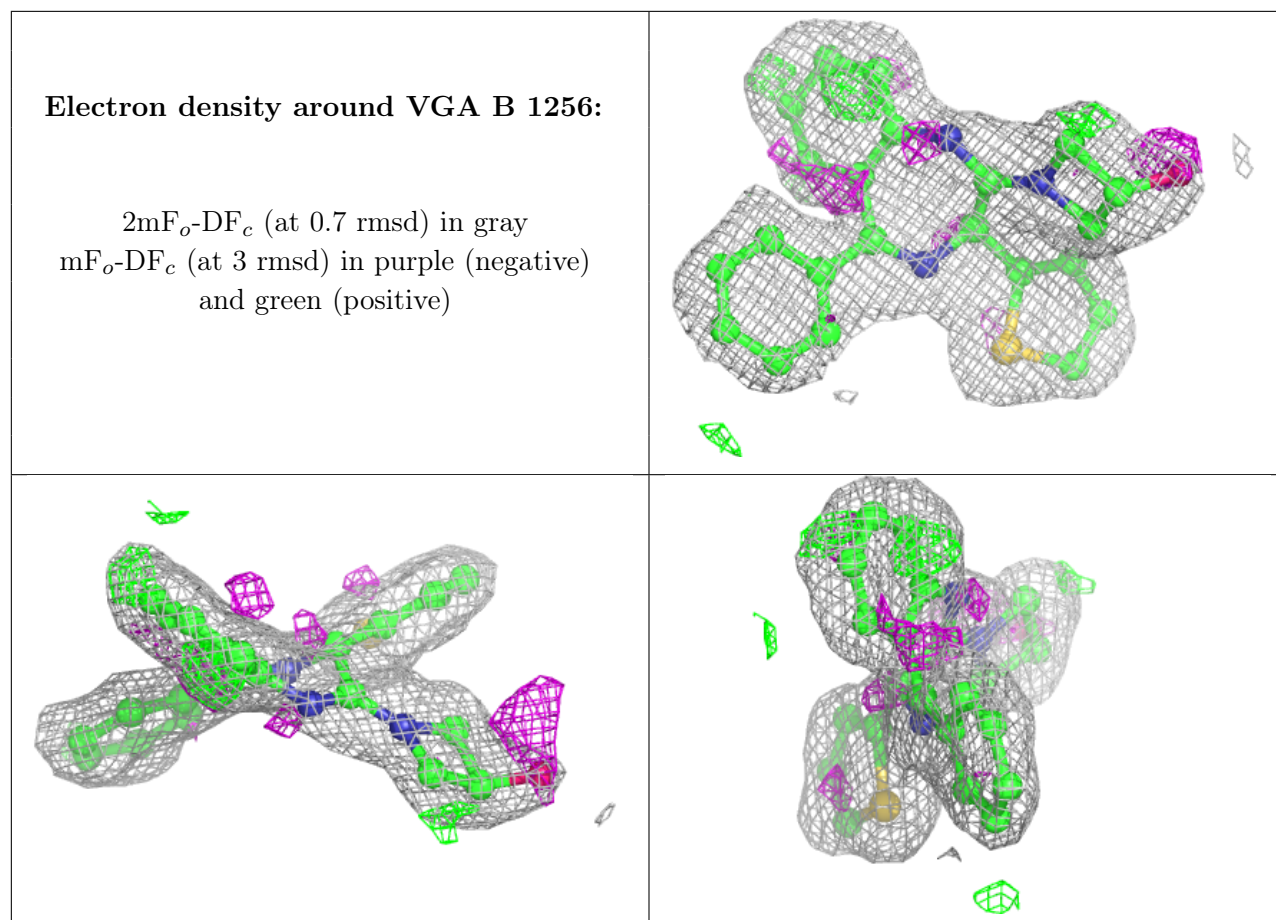
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	VGA	E	1256	27/27	0.87	0.15	20,24,27,30	0
3	VGA	B	1256	27/27	0.88	0.15	16,22,26,30	0
2	DGL	B	1255	10/10	0.97	0.10	5,7,8,9	0
2	DGL	E	1255	10/10	0.98	0.10	6,7,8,9	0
2	DGL	F	1255	10/10	0.98	0.12	5,7,9,9	0
2	DGL	A	1256	10/10	0.99	0.11	7,8,8,9	0

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 VGA E 1256:

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

Electron density around VGA B 1256:

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

6.5 Other polymers ⓘ

There are no such residues in this entry.