



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:56 AM UTC

PDB ID : 4GR1 / pdb_00004gr1
Title : THE BINDING OF THE RETRO-ANALOGUE OF GLUTATHIONE
DISULFIDE TO GLUTATHIONE REDUCTASE
Authors : Schulz, G.E.; Janes, W.
Deposited on : 1990-03-26
Resolution : 2.40 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

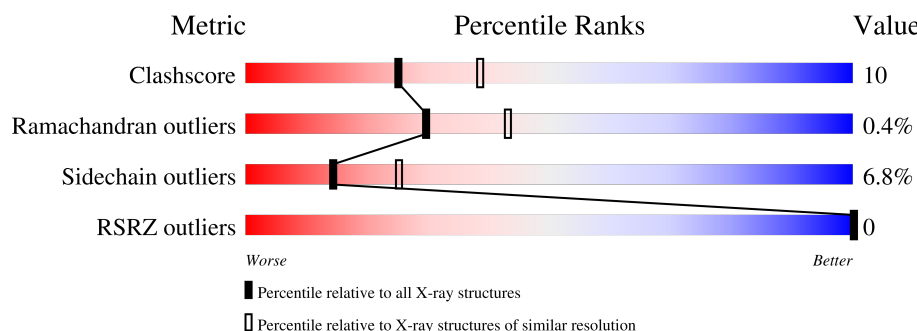
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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))
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	478	

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
4	RGS	A	481	-	X	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4111 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 GLUTATHIONE REDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	461	3499	2212	603	660	24	0	0	0

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



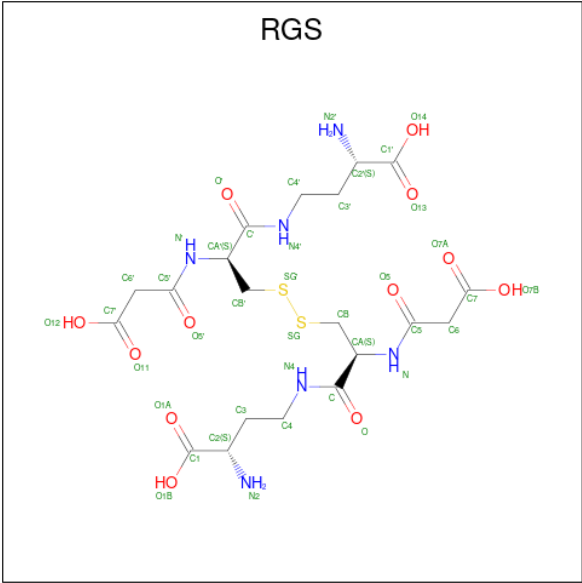
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	P		
2	A	1	5	4	1	0	0

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 4 is 4N-MALONYL-CYSTEINYL-2,4-DIAMINO BUTYRATE DISULFIDE (CCD ID: RGS) (formula: C₂₀H₃₂N₆O₁₂S₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			40	20	6	12	2		

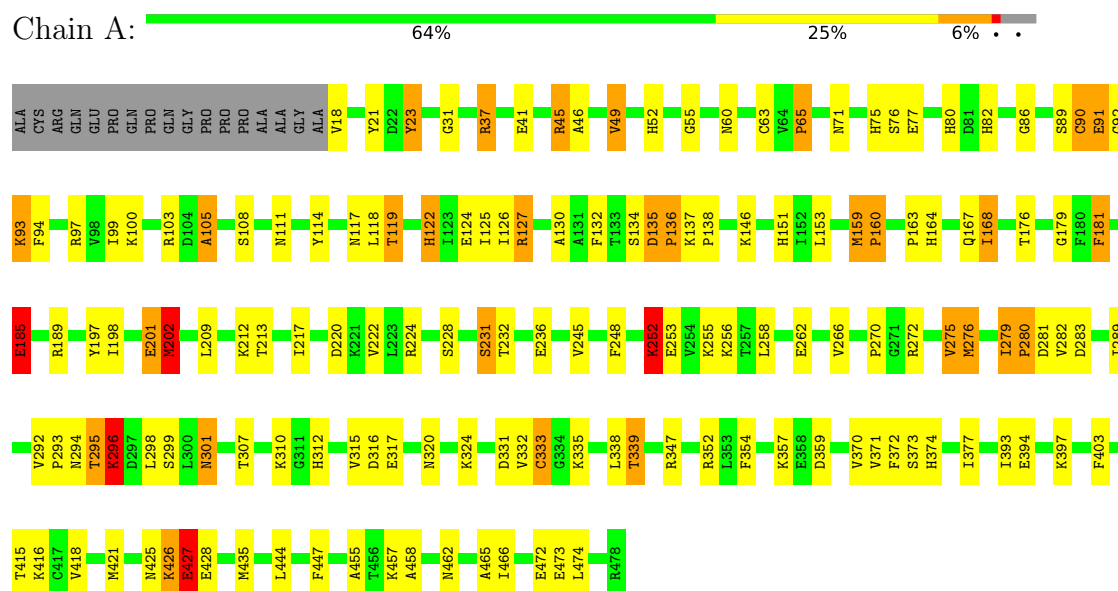
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	514	Total 514	O 514	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: GLUTATHIONE REDUCTASE



4 Data and refinement statistics

Property	Value	Source
Space group	B 1 1 2	Depositor
Cell constants a, b, c, α , β , γ	119.80Å 84.50Å 63.20Å 90.00° 90.00° 58.70°	Depositor
Resolution (Å)	(Not available) – 2.40 72.20 – 2.42	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-2.40) 99.1 (72.20-2.42)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	TNT	Depositor
R, R_{free}	0.151 , (Not available) (Not available) , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	22.7	Xtriage
Anisotropy	0.236	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 113.9	EDS
L-test for twinning ¹	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4111	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.41% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: RGS, FAD, PO4

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	1.60	17/3566 (0.5%)	1.93	82/4824 (1.7%)

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	125	ILE	C-O	-6.71	1.16	1.24
1	A	126	ILE	C-O	-6.04	1.17	1.24
1	A	339	THR	C-O	-5.86	1.19	1.24
1	A	331	ASP	CG-OD2	5.75	1.36	1.25
1	A	352	ARG	C-O	-5.67	1.17	1.24
1	A	168	ILE	CA-C	-5.65	1.47	1.52
1	A	103	ARG	N-CA	-5.55	1.39	1.46
1	A	97	ARG	NE-CZ	5.53	1.39	1.33
1	A	168	ILE	CA-CB	-5.38	1.47	1.54
1	A	127	ARG	NE-CZ	5.37	1.39	1.33
1	A	347	ARG	C-O	-5.29	1.18	1.24
1	A	97	ARG	C-N	-5.20	1.27	1.33
1	A	252	LYS	N-CA	-5.08	1.39	1.46
1	A	179	GLY	C-O	-5.05	1.17	1.23
1	A	359	ASP	CG-OD2	5.04	1.34	1.25
1	A	45	ARG	CZ-NH2	5.03	1.40	1.33
1	A	428	GLU	CA-C	-5.03	1.47	1.53

All (82) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	91	GLU	CA-C-N	-12.25	97.40	121.41
1	A	91	GLU	C-N-CA	-12.25	97.40	121.41
1	A	159	MET	CB-CA-C	-10.17	94.21	109.97
1	A	94	PHE	CA-C-N	-8.89	110.49	123.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	94	PHE	C-N-CA	-8.89	110.49	123.11
1	A	181	PHE	CA-CB-CG	-8.13	105.67	113.80
1	A	415	THR	N-CA-C	-7.74	97.61	109.14
1	A	310	LYS	N-CA-CB	7.62	122.10	110.44
1	A	91	GLU	N-CA-C	7.55	122.67	113.38
1	A	295	THR	CA-C-O	7.47	127.28	118.69
1	A	444	LEU	N-CA-C	7.40	118.99	111.07
1	A	97	ARG	N-CA-CB	7.40	121.75	110.28
1	A	80	HIS	N-CA-CB	7.34	121.66	110.28
1	A	272	ARG	N-CA-CB	-7.20	100.40	111.56
1	A	37	ARG	NE-CZ-NH2	7.13	125.62	119.20
1	A	294	ASN	N-CA-CB	-6.86	101.31	110.57
1	A	52	HIS	CA-CB-CG	-6.83	106.97	113.80
1	A	213	THR	N-CA-C	6.82	120.56	109.59
1	A	41	GLU	N-CA-CB	6.76	120.63	110.22
1	A	282	VAL	CB-CA-C	6.70	119.07	110.96
1	A	71	ASN	CA-CB-CG	6.49	119.09	112.60
1	A	280	PRO	CB-CA-C	-6.48	100.87	111.56
1	A	122	HIS	CA-CB-CG	-6.46	107.34	113.80
1	A	21	TYR	CA-C-O	-6.38	114.09	121.49
1	A	462	ASN	CA-CB-CG	-6.30	106.30	112.60
1	A	103	ARG	N-CA-C	-6.29	104.34	111.14
1	A	316	ASP	CA-CB-CG	6.29	118.89	112.60
1	A	333	CYS	N-CA-C	-6.25	105.66	113.28
1	A	228	SER	CA-C-O	6.24	127.06	119.38
1	A	427	GLU	CB-CG-CD	6.21	123.17	112.60
1	A	279	ILE	N-CA-CB	6.21	119.66	111.40
1	A	99	ILE	CA-C-N	-6.13	111.58	120.29
1	A	99	ILE	C-N-CA	-6.13	111.58	120.29
1	A	270	PRO	N-CA-CB	6.06	108.39	103.36
1	A	201	GLU	N-CA-CB	6.05	118.84	110.07
1	A	135	ASP	N-CA-CB	6.04	118.63	109.75
1	A	60	ASN	N-CA-C	5.98	118.70	111.40
1	A	372	PHE	CA-CB-CG	-5.97	107.83	113.80
1	A	55	GLY	N-CA-C	-5.93	106.86	113.79
1	A	275	VAL	CB-CA-C	5.84	119.50	110.50
1	A	135	ASP	CA-C-O	5.84	125.68	120.02
1	A	37	ARG	NE-CZ-NH1	-5.75	115.75	121.50
1	A	245	VAL	CB-CA-C	-5.63	104.10	111.25
1	A	159	MET	N-CA-CB	5.56	119.10	111.25
1	A	126	ILE	CA-C-O	-5.54	114.60	120.53
1	A	338	LEU	CA-C-N	5.54	126.64	119.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	338	LEU	C-N-CA	5.54	126.64	119.78
1	A	18	VAL	N-CA-CB	5.46	120.79	111.50
1	A	92	GLY	N-CA-C	5.46	126.11	113.18
1	A	37	ARG	CD-NE-CZ	5.45	132.03	124.40
1	A	31	GLY	CA-C-N	5.44	125.98	119.94
1	A	31	GLY	C-N-CA	5.44	125.98	119.94
1	A	301	ASN	CA-CB-CG	-5.40	107.20	112.60
1	A	94	PHE	CA-CB-CG	-5.39	108.41	113.80
1	A	65	PRO	N-CA-CB	5.38	109.20	103.39
1	A	176	THR	CA-C-O	-5.35	114.78	121.46
1	A	49	VAL	O-C-N	-5.34	116.86	122.95
1	A	111	ASN	N-CA-CB	5.34	118.44	110.22
1	A	231	SER	N-CA-CB	5.33	118.53	110.28
1	A	354	PHE	CA-CB-CG	-5.32	108.48	113.80
1	A	97	ARG	N-CA-C	5.28	117.95	111.82
1	A	455	ALA	N-CA-CB	-5.26	102.59	110.17
1	A	255	LYS	CA-C-N	5.25	129.41	122.42
1	A	255	LYS	C-N-CA	5.25	129.41	122.42
1	A	248	PHE	CA-CB-CG	-5.24	108.56	113.80
1	A	119	THR	N-CA-CB	5.22	117.72	109.94
1	A	416	LYS	N-CA-CB	-5.18	102.81	111.20
1	A	86	GLY	CA-C-O	5.17	124.92	119.03
1	A	132	PHE	CA-CB-CG	-5.15	108.65	113.80
1	A	76	SER	CA-CB-OG	-5.14	100.81	111.10
1	A	118	LEU	N-CA-C	-5.09	105.64	111.14
1	A	151	HIS	CA-CB-CG	-5.08	108.72	113.80
1	A	153	LEU	CA-C-N	-5.07	116.03	122.37
1	A	153	LEU	C-N-CA	-5.07	116.03	122.37
1	A	296	LYS	CA-C-N	-5.06	114.58	122.73
1	A	296	LYS	C-N-CA	-5.06	114.58	122.73
1	A	185	GLU	CB-CG-CD	5.05	121.19	112.60
1	A	105	ALA	O-C-N	5.04	127.46	122.12
1	A	217	ILE	O-C-N	-5.01	117.77	123.18
1	A	160	PRO	N-CA-CB	5.00	107.76	103.36
1	A	23	TYR	N-CA-CB	-5.00	102.07	110.32
1	A	202	MET	CA-C-O	-5.00	115.57	120.82

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	3499	0	3537	65	1
2	A	5	0	0	0	0
3	A	53	0	31	0	0
4	A	40	0	27	6	0
5	A	514	0	0	15	1
All	All	4111	0	3595	70	2

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 10.

All (70) 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:296:LYS:HB2	5:A:584:HOH:O	1.72	0.89
1:A:114:TYR:OH	4:A:481:RGS:H62	1.77	0.84
1:A:224:ARG:HD2	5:A:982:HOH:O	1.88	0.73
1:A:77:GLU:OE1	1:A:374:HIS:ND1	2.23	0.72
1:A:127:ARG:HD2	5:A:723:HOH:O	1.90	0.71
1:A:93:LYS:O	1:A:93:LYS:HG2	1.92	0.69
1:A:373:SER:HB2	5:A:989:HOH:O	1.93	0.67
1:A:185:GLU:HG3	5:A:805:HOH:O	1.95	0.67
1:A:202:MET:HA	1:A:202:MET:HE2	1.77	0.66
1:A:292:VAL:HG23	1:A:293:PRO:HD2	1.77	0.66
1:A:45:ARG:NH1	1:A:124:GLU:OE2	2.28	0.66
1:A:293:PRO:HG3	1:A:312:HIS:CD2	2.31	0.64
1:A:100:LYS:HG2	1:A:100:LYS:O	1.98	0.64
1:A:135:ASP:HB3	1:A:136:PRO:HD2	1.78	0.64
4:A:481:RGS:N4'	4:A:481:RGS:HA	2.13	0.64
1:A:198:ILE:O	1:A:202:MET:HG2	2.01	0.61
1:A:315:VAL:HA	1:A:320:ASN:O	2.02	0.59
1:A:266:VAL:HG22	1:A:276:MET:HG2	1.85	0.59
1:A:236:GLU:HG2	5:A:926:HOH:O	2.03	0.58
1:A:164:HIS:HB2	5:A:922:HOH:O	2.04	0.57
1:A:232:THR:O	1:A:236:GLU:HG3	2.05	0.57
1:A:159:MET:HB3	1:A:160:PRO:CD	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:45:ARG:HH12	1:A:124:GLU:HB2	1.71	0.56
1:A:370:VAL:HA	1:A:377:ILE:O	2.08	0.53
1:A:307:THR:HA	1:A:312:HIS:O	2.09	0.52
1:A:159:MET:HB3	1:A:160:PRO:HD2	1.90	0.52
1:A:91:GLU:O	1:A:91:GLU:HG3	2.09	0.51
1:A:197:TYR:O	1:A:201:GLU:HG3	2.11	0.51
1:A:220:ASP:OD2	1:A:220:ASP:N	2.45	0.50
1:A:280:PRO:O	1:A:281:ASP:HB2	2.11	0.50
1:A:418:VAL:O	1:A:418:VAL:HG23	2.11	0.50
1:A:163:PRO:HD3	1:A:289:ILE:HD11	1.93	0.50
1:A:222:VAL:O	1:A:231:SER:HB2	2.12	0.50
1:A:357:LYS:NZ	5:A:789:HOH:O	2.46	0.47
4:A:481:RGS:C	4:A:481:RGS:H4'2	2.45	0.47
1:A:447:PHE:CE1	1:A:474:LEU:HD12	2.50	0.46
1:A:458:ALA:HA	5:A:754:HOH:O	2.15	0.46
1:A:418:VAL:O	1:A:435:MET:HA	2.16	0.46
1:A:421:MET:SD	1:A:457:LYS:HD3	2.56	0.45
1:A:252:LYS:HG3	5:A:972:HOH:O	2.17	0.45
1:A:465:ALA:HB1	1:A:472:GLU:HB2	1.98	0.45
1:A:324:LYS:HE2	5:A:751:HOH:O	2.16	0.45
1:A:393:ILE:O	1:A:393:ILE:HG22	2.16	0.45
1:A:466:ILE:O	1:A:472:GLU:HB3	2.17	0.44
1:A:65:PRO:HB2	1:A:181:PHE:CE1	2.52	0.44
1:A:426:LYS:HE3	1:A:426:LYS:HB3	1.76	0.44
4:A:481:RGS:HN22	4:A:481:RGS:H41	1.54	0.44
1:A:403:PHE:CE1	1:A:473:GLU:HG3	2.53	0.44
1:A:23:TYR:O	1:A:46:ALA:HA	2.18	0.43
1:A:262:GLU:HA	1:A:279:ILE:O	2.18	0.43
1:A:371:VAL:HB	1:A:377:ILE:HB	2.01	0.43
1:A:258:LEU:HD23	1:A:258:LEU:HA	1.79	0.42
4:A:481:RGS:O1A	5:A:929:HOH:O	2.21	0.42
1:A:295:THR:CG2	1:A:332:VAL:CG2	2.98	0.42
1:A:122:HIS:CD2	5:A:941:HOH:O	2.72	0.42
1:A:427:GLU:H	1:A:427:GLU:HG2	1.38	0.42
1:A:49:VAL:HG11	1:A:130:ALA:HB2	2.01	0.42
1:A:209:LEU:HD23	1:A:209:LEU:HA	1.84	0.42
1:A:37:ARG:NH2	5:A:772:HOH:O	2.50	0.42
1:A:105:ALA:O	1:A:108:SER:HB2	2.19	0.42
1:A:135:ASP:HA	1:A:136:PRO:HD3	1.79	0.41
1:A:292:VAL:HG23	1:A:293:PRO:CD	2.47	0.41
1:A:301:ASN:ND2	1:A:301:ASN:C	2.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:117:ASN:HD22	1:A:117:ASN:HA	1.58	0.41
1:A:137:LYS:HA	1:A:138:PRO:HD3	1.94	0.41
1:A:189:ARG:N	1:A:283:ASP:OD1	2.54	0.41
1:A:298:LEU:O	1:A:299:SER:HB2	2.21	0.41
4:A:481:RGS:N4'	4:A:481:RGS:CA	2.82	0.40
1:A:168:ILE:O	1:A:168:ILE:HG22	2.15	0.40
1:A:333:CYS:HB2	5:A:525:HOH:O	2.21	0.40

All (2) 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)
5:A:580:HOH:O	5:A:580:HOH:O[2_665]	0.51	1.69
1:A:90:CYS:SG	1:A:90:CYS:SG[2_665]	1.42	0.78

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	459/478 (96%)	438 (95%)	19 (4%)	2 (0%)	30 43

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	136	PRO
1	A	425	ASN

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	382/393 (97%)	356 (93%)	26 (7%)	14	25

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	63	CYS
1	A	75	HIS
1	A	82	HIS
1	A	89	SER
1	A	90	CYS
1	A	93	LYS
1	A	119	THR
1	A	134	SER
1	A	146	LYS
1	A	167	GLN
1	A	185	GLU
1	A	202	MET
1	A	212	LYS
1	A	252	LYS
1	A	253	GLU
1	A	256	LYS
1	A	275	VAL
1	A	276	MET
1	A	296	LYS
1	A	317	GLU
1	A	335	LYS
1	A	339	THR
1	A	394	GLU
1	A	397	LYS
1	A	426	LYS
1	A	427	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	52	HIS
1	A	117	ASN
1	A	164	HIS

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Mol	Chain	Res	Type
1	A	182	GLN
1	A	233	ASN
1	A	301	ASN
1	A	365	ASN
1	A	425	ASN
1	A	436	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

3 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	PO4	A	480	-	4,4,4	1.34	0	6,6,6	0.66	0
4	RGS	A	481	-	37,39,39	4.90	26 (70%)	42,50,50	4.25	25 (59%)
3	FAD	A	479	-	58,58,58	1.59	13 (22%)	85,89,89	1.25	7 (8%)

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
4	RGS	A	481	-	-	14/51/51/51	-
3	FAD	A	479	-	-	3/34/50/50	0/6/6/6

All (39) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	481	RGS	C4-N4	-11.56	1.20	1.46
4	A	481	RGS	O5-C5	-9.68	1.04	1.23
4	A	481	RGS	C4'-N4'	-9.63	1.24	1.46
4	A	481	RGS	C6'-C7'	9.51	1.65	1.51
4	A	481	RGS	C5-N	-8.43	1.16	1.34
4	A	481	RGS	O5'-C5'	6.52	1.36	1.23
4	A	481	RGS	CA-N	-6.06	1.33	1.45
4	A	481	RGS	O12-C7'	5.75	1.49	1.30
4	A	481	RGS	C6'-C5'	5.40	1.59	1.51
4	A	481	RGS	O'-C'	5.15	1.33	1.23
4	A	481	RGS	O11-C7'	5.01	1.38	1.22
4	A	481	RGS	C6-C5	-4.93	1.45	1.51
4	A	481	RGS	C5'-N'	4.90	1.44	1.34
3	A	479	FAD	P-O3P	4.69	1.64	1.59
4	A	481	RGS	O13-C1'	4.41	1.35	1.22
4	A	481	RGS	CA-C	4.32	1.63	1.52
4	A	481	RGS	CA'-C'	4.23	1.63	1.52
4	A	481	RGS	C3'-C2'	4.05	1.61	1.53
4	A	481	RGS	C3-C2	3.93	1.61	1.53
4	A	481	RGS	C-N4	3.65	1.42	1.33
4	A	481	RGS	O7A-C7	3.59	1.33	1.22
4	A	481	RGS	C'-N4'	3.28	1.41	1.33
3	A	479	FAD	O2-C2	-3.24	1.18	1.24
3	A	479	FAD	C2A-N1A	3.05	1.39	1.33
3	A	479	FAD	C5A-C4A	2.90	1.44	1.39
3	A	479	FAD	C5A-C6A	2.72	1.48	1.41
3	A	479	FAD	O4B-C1B	2.56	1.47	1.42
4	A	481	RGS	O1B-C1	2.53	1.38	1.30
3	A	479	FAD	C2'-C3'	2.44	1.57	1.53
4	A	481	RGS	C2-N2	2.38	1.60	1.48
3	A	479	FAD	C10-N10	-2.21	1.32	1.37
3	A	479	FAD	PA-O2A	-2.21	1.45	1.55
4	A	481	RGS	O1A-C1	2.20	1.28	1.22
4	A	481	RGS	SG'-SG	-2.07	1.88	2.03
3	A	479	FAD	C6-C7	-2.04	1.36	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	479	FAD	O4-C4	-2.04	1.19	1.23
4	A	481	RGS	O-C	2.02	1.27	1.23
3	A	479	FAD	O3B-C3B	-2.02	1.38	1.43
3	A	479	FAD	C5'-C4'	2.02	1.54	1.51

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	481	RGS	CA-N-C5	14.35	157.68	121.68
4	A	481	RGS	C6-C5-N	-12.30	95.31	116.31
4	A	481	RGS	O5-C5-N	9.28	138.66	122.95
4	A	481	RGS	CB-CA-N	-6.42	94.26	111.06
4	A	481	RGS	C5-C6-C7	5.85	132.73	111.33
4	A	481	RGS	O-C-CA	-5.55	108.85	120.48
3	A	479	FAD	O4B-C1B-N9A	-5.23	98.04	108.09
4	A	481	RGS	C4'-N4'-C'	4.69	130.97	122.55
4	A	481	RGS	CA-C-N4	4.07	125.27	116.54
4	A	481	RGS	C3'-C4'-N4'	3.66	121.91	111.88
4	A	481	RGS	O7A-C7-C6	-3.57	111.96	122.11
4	A	481	RGS	O5'-C5'-N'	3.51	128.90	122.95
4	A	481	RGS	C-CA-N	-3.33	102.09	111.11
4	A	481	RGS	CB-CA-C	-3.31	102.00	109.46
4	A	481	RGS	C6'-C5'-N'	-3.29	110.69	116.31
4	A	481	RGS	C3'-C2'-N2'	3.07	118.14	110.12
4	A	481	RGS	O5-C5-C6	2.90	125.97	121.40
4	A	481	RGS	C3-C2-C1	2.74	117.72	110.45
3	A	479	FAD	O4B-C1B-C2B	-2.71	100.82	106.62
4	A	481	RGS	CB-SG-SG'	-2.56	97.22	103.86
4	A	481	RGS	CA'-CB'-SG'	-2.49	104.16	114.47
3	A	479	FAD	O4-C4-C4X	-2.45	120.07	126.53
4	A	481	RGS	O7B-C7-O7A	2.43	129.59	123.33
4	A	481	RGS	O'-C'-N4'	2.42	128.11	122.98
4	A	481	RGS	C5'-C6'-C7'	-2.35	102.75	111.33
3	A	479	FAD	C4-N3-C2	-2.32	121.52	125.64
4	A	481	RGS	O1B-C1-O1A	-2.30	118.86	124.08
4	A	481	RGS	CA'-C'-N4'	-2.21	111.78	116.54
3	A	479	FAD	C5X-C9A-N10	2.19	119.95	117.97
3	A	479	FAD	C9A-C5X-N5	-2.14	120.19	122.45
3	A	479	FAD	O5'-P-O1P	-2.11	100.58	108.94
4	A	481	RGS	CA'-N'-C5'	-2.01	116.65	121.68

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	481	RGS	C6-C5-N-CA
4	A	481	RGS	CA'-CB'-SG'-SG
4	A	481	RGS	C'-CA'-CB'-SG'
4	A	481	RGS	N2'-C2'-C3'-C4'
4	A	481	RGS	C3'-C4'-N4'-C'
4	A	481	RGS	O5-C5-N-CA
3	A	479	FAD	PA-O3P-P-O5'
4	A	481	RGS	N2-C2-C3-C4
3	A	479	FAD	P-O3P-PA-O2A
4	A	481	RGS	N'-CA'-CB'-SG'
4	A	481	RGS	C5-C6-C7-O7B
4	A	481	RGS	C-CA-N-C5
4	A	481	RGS	C1'-C2'-C3'-C4'
4	A	481	RGS	C-CA-CB-SG
4	A	481	RGS	CB-SG-SG'-CB'
3	A	479	FAD	P-O3P-PA-O1A
4	A	481	RGS	C5-C6-C7-O7A

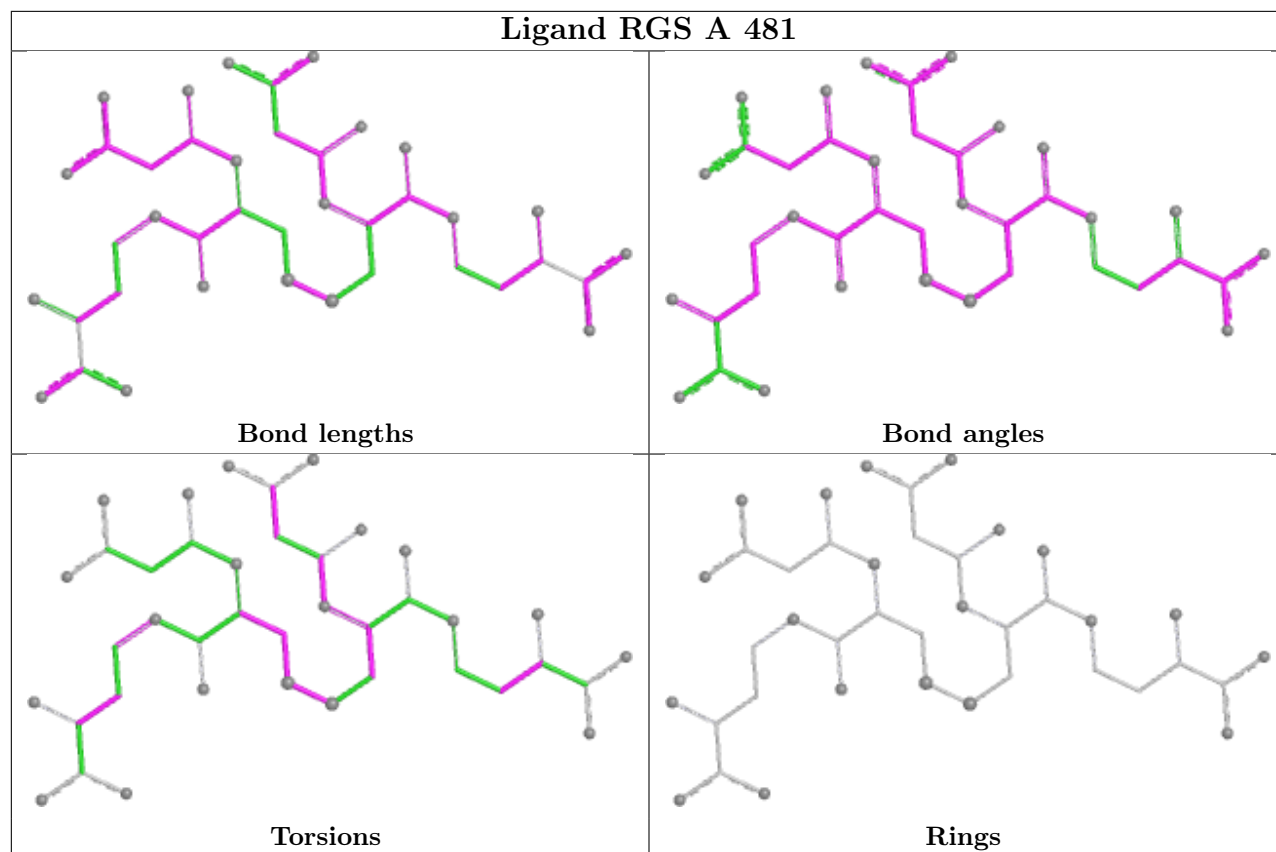
There are no ring outliers.

1 monomer is involved in 6 short contacts:

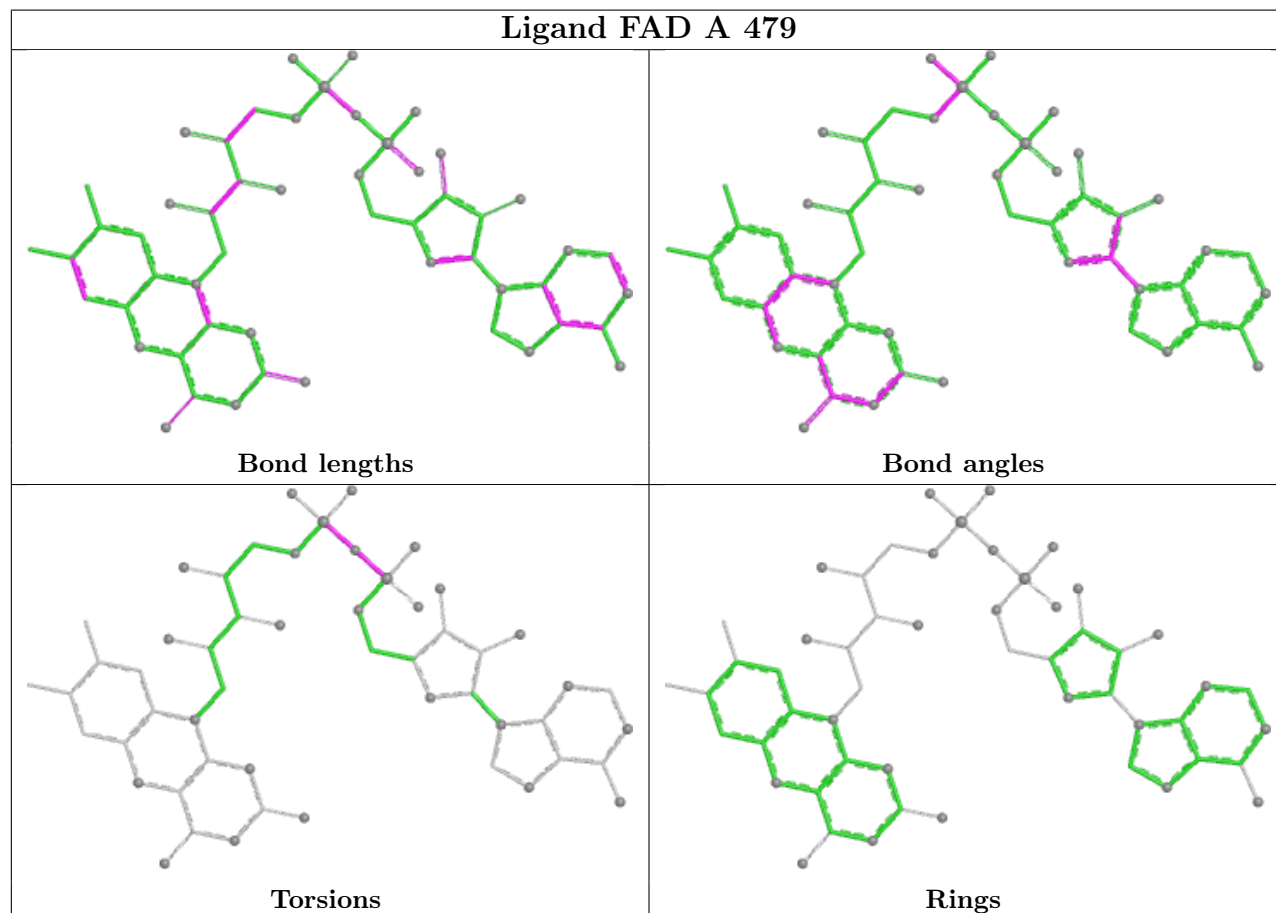
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	481	RGS	6	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand RGS A 481



Ligand FAD A 479



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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	461/478 (96%)	-0.90	0 100 100	9, 18, 38, 56	0

There are no RSRZ outliers to report.

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

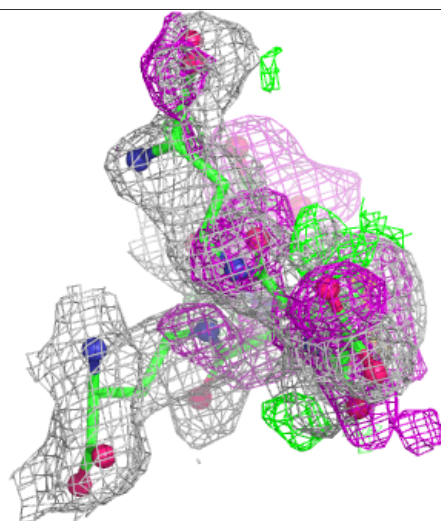
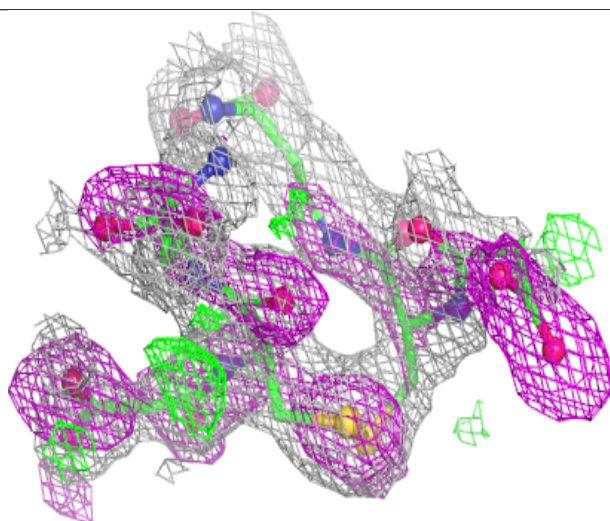
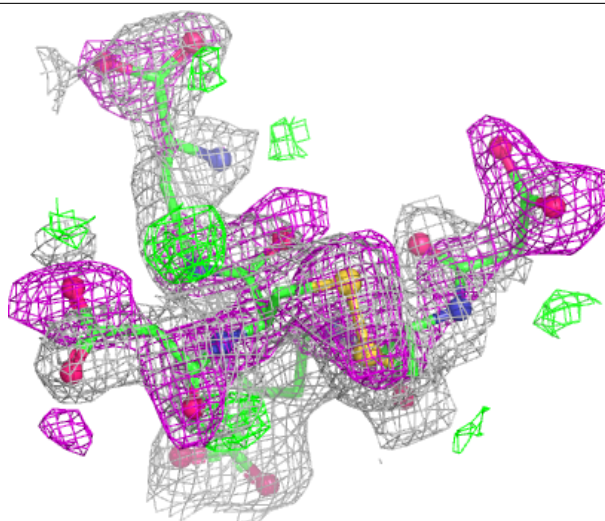
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

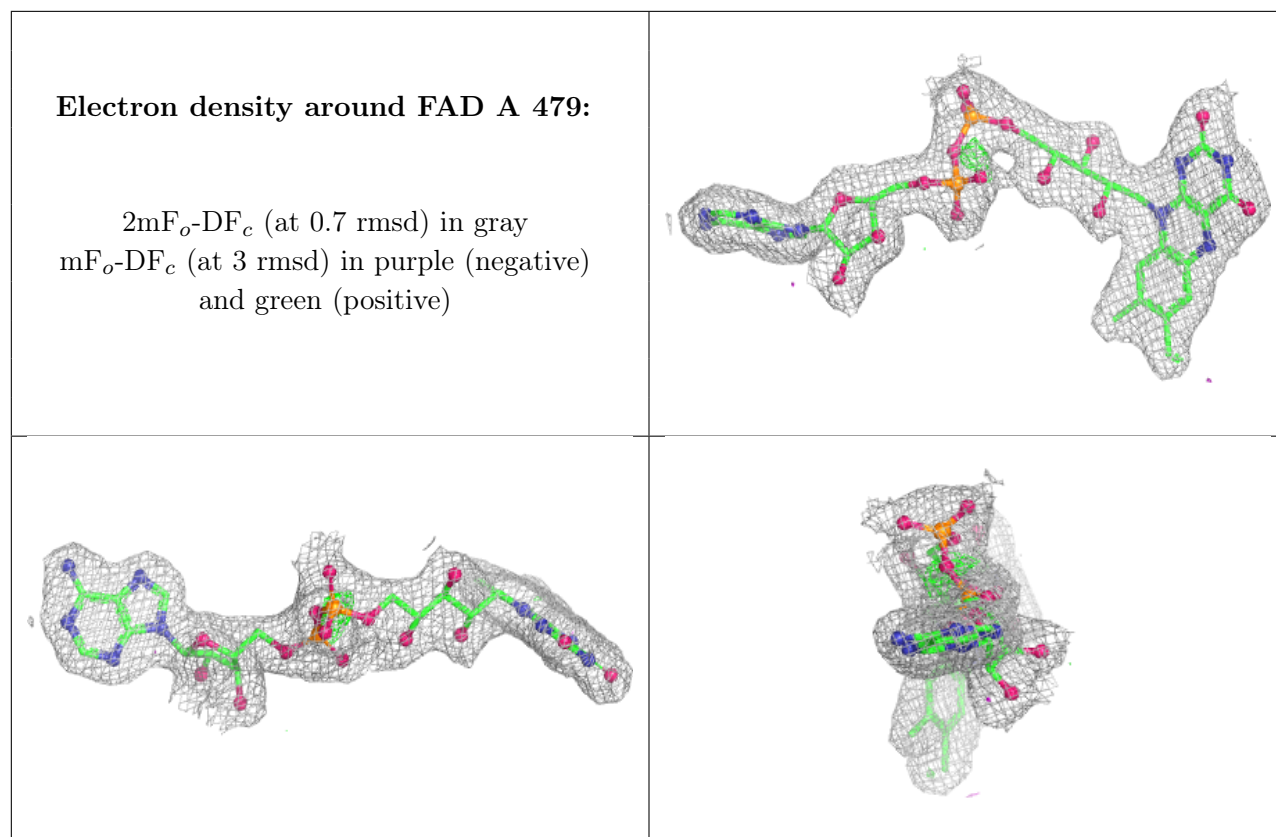
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	RGS	A	481	40/40	0.81	0.12	15,26,43,43	0
2	PO4	A	480	5/5	0.96	0.16	33,37,38,40	5
3	FAD	A	479	53/53	0.98	0.04	5,10,16,20	0

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 RGS A 481:

$2mF_o-DF_c$ (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.