



Full wwPDB X-ray Structure Validation Report ⓘ

May 6, 2025 – 10:11 pm BST

PDB ID : 8RJN / pdb_00008rjn
Title : Serial femtosecond X-ray structure of a fluorescence optimized bathy phytochrome PAiRFP2 derived from wild-type Agp2 in its Pfr state (I0b).
Authors : Sauthof, L.; Schmidt, A.; Szczepek, M.; Brewster, A.S.; Kern, J.F.; Scheerer, P.
Deposited on : 2023-12-21
Resolution : 2.20 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 Phenix2.0rc1
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

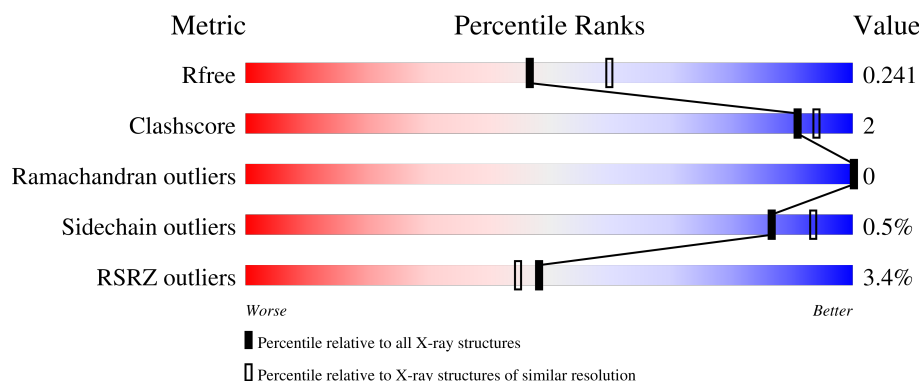
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

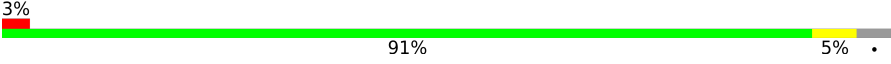
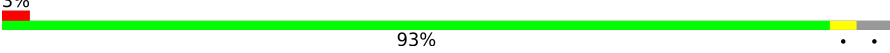
The reported resolution of this entry is 2.20 Å.

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	5791 (2.20-2.20)
Clashscore	180529	6634 (2.20-2.20)
Ramachandran outliers	177936	6560 (2.20-2.20)
Sidechain outliers	177891	6561 (2.20-2.20)
RSRZ outliers	164620	5791 (2.20-2.20)

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	509	
1	B	509	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7828 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 histidine kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	491	Total	C	N	O	S	0	3	0
			3753	2381	660	690	22			
1	B	490	Total	C	N	O	S	0	2	0
			3758	2385	662	691	20			

There are 56 discrepancies between the modelled and reference sequences:

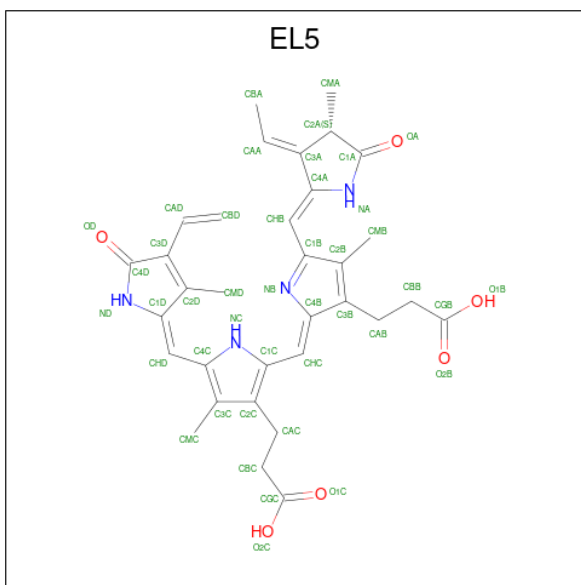
Chain	Residue	Modelled	Actual	Comment	Reference
A	69	ARG	LYS	engineered mutation	UNP A9CI81
A	83	LYS	ARG	engineered mutation	UNP A9CI81
A	120	ASP	GLY	engineered mutation	UNP A9CI81
A	123	THR	ALA	engineered mutation	UNP A9CI81
A	163	LEU	MET	engineered mutation	UNP A9CI81
A	168	GLU	GLN	engineered mutation	UNP A9CI81
A	220	PRO	ARG	engineered mutation	UNP A9CI81
A	243	ASN	SER	engineered mutation	UNP A9CI81
A	244	PHE	VAL	engineered mutation	UNP A9CI81
A	269	ASP	GLY	engineered mutation	UNP A9CI81
A	276	VAL	ALA	engineered mutation	UNP A9CI81
A	280	CYS	TYR	engineered mutation	UNP A9CI81
A	294	ALA	GLU	engineered mutation	UNP A9CI81
A	303	PHE	HIS	engineered mutation	UNP A9CI81
A	333	ARG	HIS	engineered mutation	UNP A9CI81
A	336	LEU	ILE	engineered mutation	UNP A9CI81
A	349	ARG	ASP	engineered mutation	UNP A9CI81
A	351	ILE	MET	engineered mutation	UNP A9CI81
A	386	VAL	ALA	engineered mutation	UNP A9CI81
A	409	ASP	GLY	engineered mutation	UNP A9CI81
A	419	ILE	LEU	engineered mutation	UNP A9CI81
A	469	SER	THR	engineered mutation	UNP A9CI81
A	487	THR	ALA	engineered mutation	UNP A9CI81
A	494	GLY	GLU	engineered mutation	UNP A9CI81
A	506	LEU	-	expression tag	UNP A9CI81

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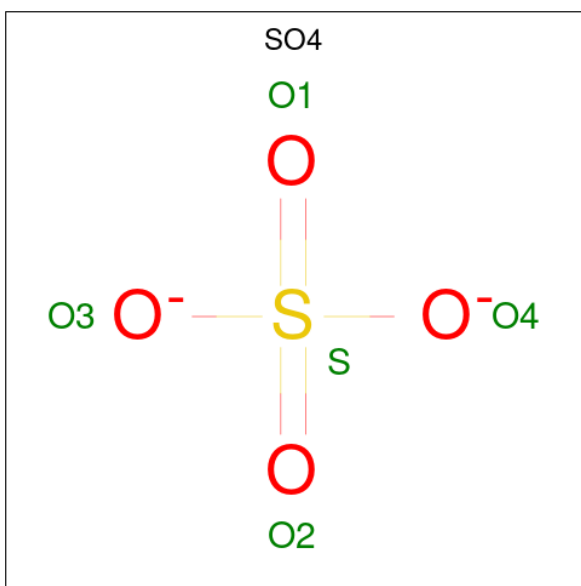
Chain	Residue	Modelled	Actual	Comment	Reference
A	507	GLU	-	expression tag	UNP A9CI81
A	508	TYR	-	expression tag	UNP A9CI81
A	509	LYS	-	expression tag	UNP A9CI81
B	69	ARG	LYS	engineered mutation	UNP A9CI81
B	83	LYS	ARG	engineered mutation	UNP A9CI81
B	120	ASP	GLY	engineered mutation	UNP A9CI81
B	123	THR	ALA	engineered mutation	UNP A9CI81
B	163	LEU	MET	engineered mutation	UNP A9CI81
B	168	GLU	GLN	engineered mutation	UNP A9CI81
B	220	PRO	ARG	engineered mutation	UNP A9CI81
B	243	ASN	SER	engineered mutation	UNP A9CI81
B	244	PHE	VAL	engineered mutation	UNP A9CI81
B	269	ASP	GLY	engineered mutation	UNP A9CI81
B	276	VAL	ALA	engineered mutation	UNP A9CI81
B	280	CYS	TYR	engineered mutation	UNP A9CI81
B	294	ALA	GLU	engineered mutation	UNP A9CI81
B	303	PHE	HIS	engineered mutation	UNP A9CI81
B	333	ARG	HIS	engineered mutation	UNP A9CI81
B	336	LEU	ILE	engineered mutation	UNP A9CI81
B	349	ARG	ASP	engineered mutation	UNP A9CI81
B	351	ILE	MET	engineered mutation	UNP A9CI81
B	386	VAL	ALA	engineered mutation	UNP A9CI81
B	409	ASP	GLY	engineered mutation	UNP A9CI81
B	419	ILE	LEU	engineered mutation	UNP A9CI81
B	469	SER	THR	engineered mutation	UNP A9CI81
B	487	THR	ALA	engineered mutation	UNP A9CI81
B	494	GLY	GLU	engineered mutation	UNP A9CI81
B	506	LEU	-	expression tag	UNP A9CI81
B	507	GLU	-	expression tag	UNP A9CI81
B	508	TYR	-	expression tag	UNP A9CI81
B	509	LYS	-	expression tag	UNP A9CI81

- Molecule 2 is 3-[(2Z)-2-({3-(2-carboxyethyl)-5-[(E)-(4-ethenyl-3-methyl-5-oxo-1,5-dihydro-2H-pyrrol-2-ylidene)methyl]-4-methyl-1H-pyrrol-2-yl}methylidene)-5-{(Z)-[(3E,4S)-3-ethylidene-4-methyl-5-oxopyrrolidin-2-ylidene]methyl}-4-methyl-2H-pyrrol-3-yl]propanoic acid (CCD ID: EL5) (formula: C₃₃H₃₆N₄O₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 43	C 33	N 4	O 6	0	0
2	B	1	Total 43	C 33	N 4	O 6	0	0

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 5	O 4	S 1	0	0
3	B	1	Total 5	O 4	S 1	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	S	0	0
			5	4	1		

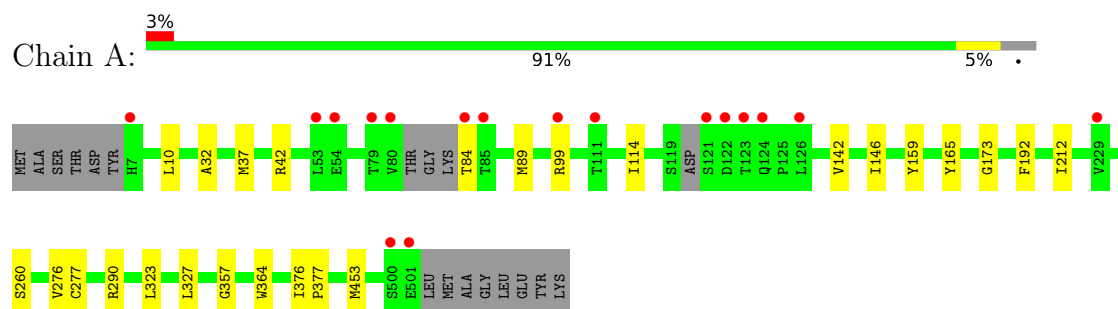
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	115	Total	O	0	0
			115	115		
4	B	101	Total	O	0	0
			101	101		

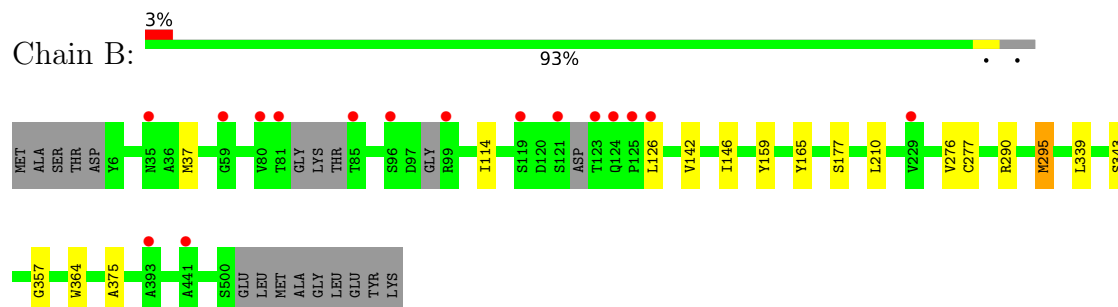
3 Residue-property plots [i](#)

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: histidine kinase



- Molecule 1: histidine kinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, α , β , γ	184.19Å 184.19Å 181.63Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	92.27 – 2.20 92.27 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (92.27-2.20) 100.0 (92.27-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.41 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0267, PHENIX 1.20.1-4487	Depositor
R, R_{free}	0.213 , 0.241 0.221 , 0.241	Depositor DCC
R_{free} test set	90005 reflections (2.17%)	wwPDB-VP
Wilson B-factor (Å ²)	48.4	Xtriage
Anisotropy	0.070	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 62.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7828	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.68% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EL5, SO4

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	1.04	0/3849	1.40	0/5241
1	B	1.04	0/3848	1.40	2/5239 (0.0%)
All	All	1.04	0/7697	1.40	2/10480 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	375	ALA	CA-C-N	5.19	124.48	120.33
1	B	375	ALA	C-N-CA	5.19	124.48	120.33

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3753	0	3644	14	0
1	B	3758	0	3656	10	0
2	A	43	0	0	0	0
2	B	43	0	0	0	0
3	A	5	0	0	0	0
3	B	10	0	0	0	0
4	A	115	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	101	0	0	0	0
All	All	7828	0	7300	24	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 2.

All (24) 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:357:GLY:HA3	1:A:364:TRP:CH2	2.41	0.55
1:B:357:GLY:HA3	1:B:364:TRP:CH2	2.43	0.54
1:B:165:TYR:CE2	1:B:276:VAL:HG21	2.43	0.52
1:B:142:VAL:HG12	1:B:146:ILE:HD12	1.95	0.49
1:B:210:LEU:HD11	1:B:290:ARG:O	2.14	0.47
1:B:37:MET:HE3	1:B:114:ILE:HD11	1.97	0.47
1:A:159:TYR:CG	1:A:277:CYS:HB3	2.51	0.45
1:A:142:VAL:HG12	1:A:146:ILE:HD12	2.00	0.44
1:B:339:LEU:O	1:B:343:SER:OG	2.26	0.44
1:A:37[A]:MET:HE3	1:A:114:ILE:HD11	2.00	0.43
1:A:173:GLY:HA3	1:A:192:PHE:CZ	2.54	0.43
1:B:159:TYR:CG	1:B:277:CYS:HB3	2.53	0.43
1:A:10:LEU:HG	1:A:453:MET:HG3	2.00	0.43
1:A:32:ALA:HB3	1:A:42:ARG:HB2	2.00	0.42
1:B:165:TYR:HE2	1:B:276:VAL:HG21	1.83	0.42
1:B:126:LEU:HD11	1:B:295:MET:HE1	2.02	0.42
1:A:323:LEU:O	1:A:327:LEU:HG	2.20	0.41
1:A:165:TYR:CE2	1:A:276:VAL:HG21	2.55	0.41
1:A:165:TYR:HE2	1:A:276:VAL:HG21	1.86	0.41
1:A:260:SER:HA	1:A:277:CYS:O	2.21	0.41
1:A:376:ILE:N	1:A:377:PRO:CD	2.84	0.40
1:B:146:ILE:CG2	1:B:177:SER:HB2	2.51	0.40
1:A:37[A]:MET:HE2	1:A:37[A]:MET:HB3	1.80	0.40
1:A:212:ILE:HD11	1:A:290:ARG:HD2	2.04	0.40

There are no symmetry-related clashes.

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	488/509 (96%)	482 (99%)	6 (1%)	0	100	100
1	B	484/509 (95%)	472 (98%)	12 (2%)	0	100	100
All	All	972/1018 (96%)	954 (98%)	18 (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	390/426 (92%)	387 (99%)	3 (1%)	79	88
1	B	393/426 (92%)	392 (100%)	1 (0%)	91	96
All	All	783/852 (92%)	779 (100%)	4 (0%)	86	93

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	84	THR
1	A	89	MET
1	A	99	ARG
1	B	295	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	HIS
1	A	499	HIS
1	B	76	ASN
1	B	243	ASN
1	B	367	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](#)

5 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	EL5	A	601	1	42,46,46	2.86	12 (28%)	47,67,67	1.44	7 (14%)
3	SO4	B	602	-	4,4,4	0.39	0	6,6,6	0.05	0
3	SO4	B	603	-	4,4,4	0.39	0	6,6,6	0.05	0
3	SO4	A	602	-	4,4,4	0.38	0	6,6,6	0.04	0
2	EL5	B	601	1	42,46,46	2.87	12 (28%)	47,67,67	1.55	7 (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	EL5	A	601	1	-	5/26/74/74	0/4/4/4
2	EL5	B	601	1	-	6/26/74/74	0/4/4/4

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	EL5	C2A-C1A	-10.73	1.38	1.51
2	A	601	EL5	C2A-C1A	-10.67	1.38	1.51
2	B	601	EL5	C2A-C3A	-9.79	1.38	1.51
2	A	601	EL5	C2A-C3A	-9.79	1.38	1.51
2	A	601	EL5	CHC-C4B	5.25	1.39	1.35
2	B	601	EL5	CHC-C4B	5.10	1.39	1.35
2	B	601	EL5	CBA-CAA	-4.17	1.33	1.49
2	A	601	EL5	C4B-C3B	-4.02	1.39	1.45
2	B	601	EL5	C4B-C3B	-3.99	1.39	1.45
2	A	601	EL5	CBA-CAA	-3.96	1.34	1.49
2	A	601	EL5	C4A-C3A	-3.06	1.39	1.45
2	A	601	EL5	CAA-C3A	3.06	1.41	1.33
2	B	601	EL5	C4A-C3A	-3.03	1.39	1.45
2	A	601	EL5	C1B-C2B	-2.97	1.39	1.45
2	B	601	EL5	C1B-C2B	-2.94	1.39	1.45
2	B	601	EL5	CAA-C3A	2.85	1.41	1.33
2	A	601	EL5	C3D-C4D	-2.82	1.39	1.47
2	B	601	EL5	C3D-C4D	-2.82	1.39	1.47
2	B	601	EL5	C1D-C2D	-2.81	1.40	1.45
2	A	601	EL5	C1D-C2D	-2.78	1.40	1.45
2	B	601	EL5	CHD-C1D	2.75	1.40	1.34
2	A	601	EL5	CHD-C1D	2.60	1.39	1.34
2	B	601	EL5	CAD-C3D	-2.23	1.41	1.47
2	A	601	EL5	CAD-C3D	-2.12	1.41	1.47

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	EL5	CMD-C2D-C1D	4.35	129.60	124.17
2	A	601	EL5	CMD-C2D-C1D	4.13	129.32	124.17
2	B	601	EL5	CHC-C4B-NB	-3.87	123.46	128.83
2	B	601	EL5	CHD-C1D-C2D	3.81	134.49	126.97
2	A	601	EL5	CHD-C1D-C2D	3.70	134.27	126.97
2	A	601	EL5	CHC-C4B-NB	-3.52	123.95	128.83
2	A	601	EL5	CHD-C1D-ND	-3.46	118.79	130.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	EL5	CHD-C1D-ND	-3.42	118.91	130.40
2	B	601	EL5	C2A-C3A-C4A	-3.37	104.12	107.81
2	A	601	EL5	C2A-C3A-C4A	-2.82	104.72	107.81
2	B	601	EL5	OA-C1A-C2A	2.54	128.74	126.28
2	B	601	EL5	CMD-C2D-C3D	-2.45	122.29	128.30
2	A	601	EL5	OA-C1A-C2A	2.25	128.46	126.28
2	A	601	EL5	CMD-C2D-C3D	-2.23	122.85	128.30

There are no chirality outliers.

All (11) torsion outliers are listed below:

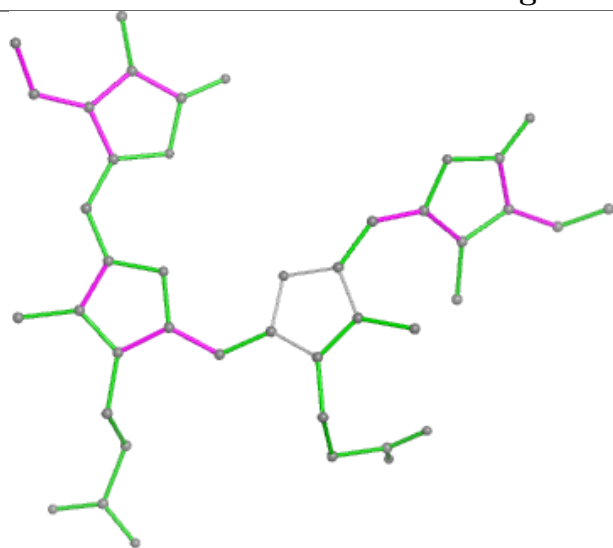
Mol	Chain	Res	Type	Atoms
2	A	601	EL5	C2C-C1C-CHC-C4B
2	A	601	EL5	C2D-C1D-CHD-C4C
2	A	601	EL5	ND-C1D-CHD-C4C
2	B	601	EL5	C2C-C1C-CHC-C4B
2	B	601	EL5	C2D-C1D-CHD-C4C
2	B	601	EL5	ND-C1D-CHD-C4C
2	B	601	EL5	C4A-C3A-CAA-CBA
2	A	601	EL5	CAB-CBB-CGB-O1B
2	A	601	EL5	CAB-CBB-CGB-O2B
2	B	601	EL5	CAB-CBB-CGB-O1B
2	B	601	EL5	CAB-CBB-CGB-O2B

There are no ring outliers.

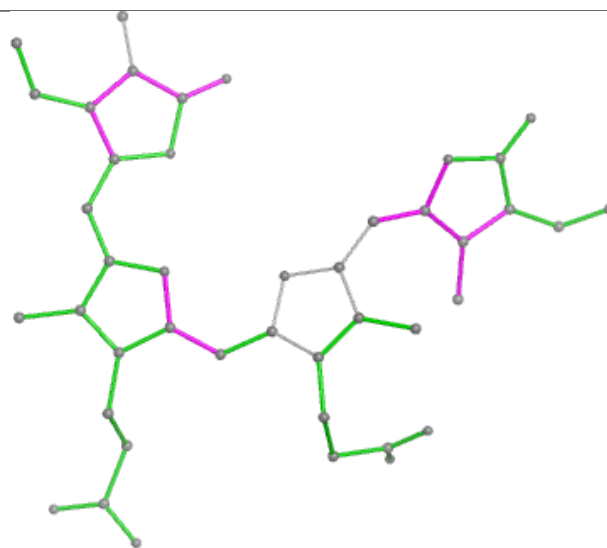
No monomer is involved in short contacts.

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.

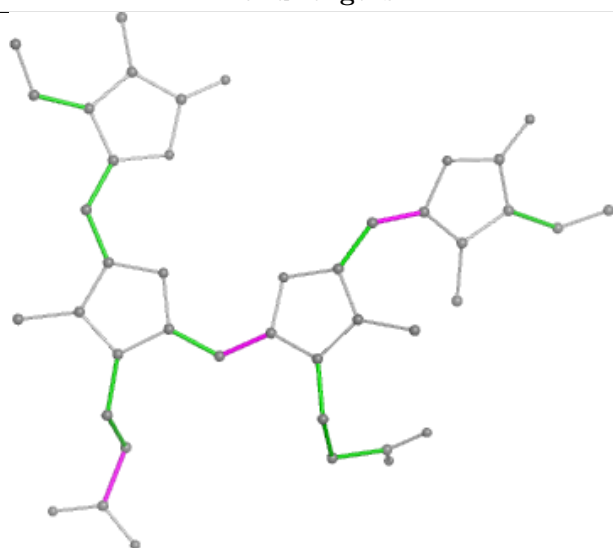
Ligand EL5 A 601



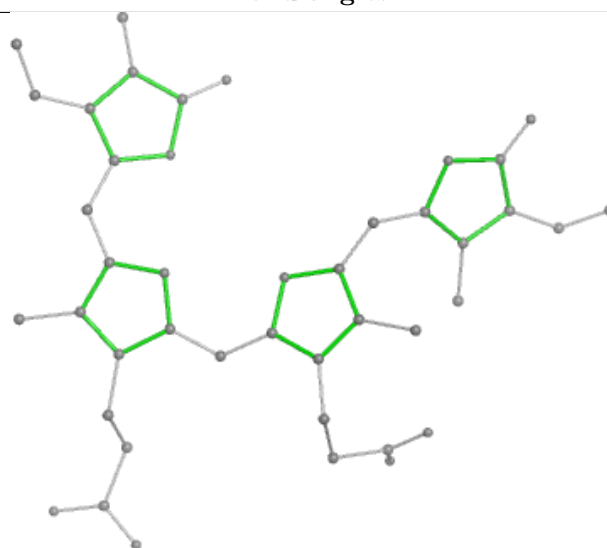
Bond lengths



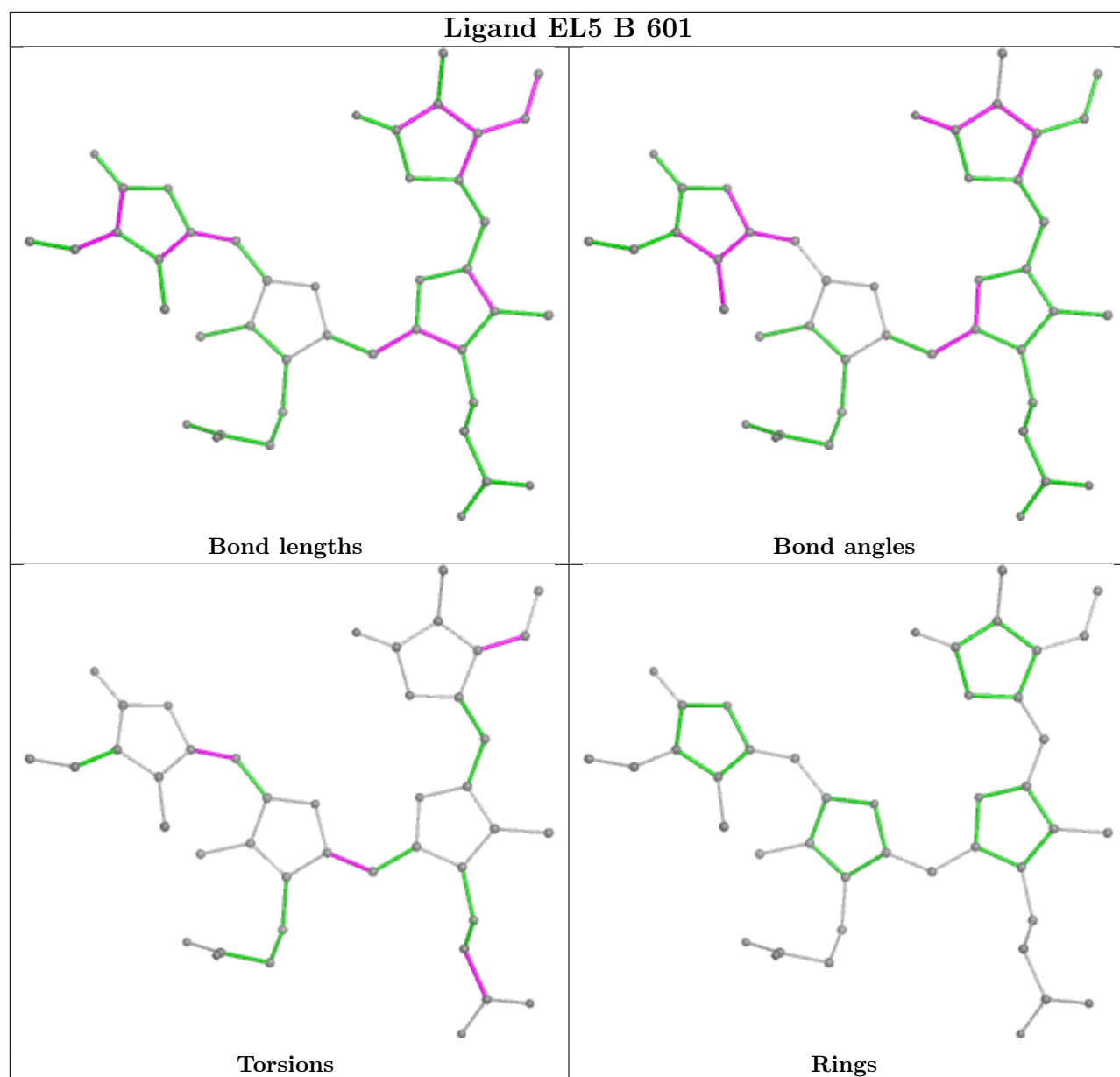
Bond angles



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	491/509 (96%)	0.30	17 (3%)	47	44	27, 59, 97, 127	6 (1%)
1	B	490/509 (96%)	0.35	16 (3%)	49	46	31, 59, 94, 129	2 (0%)
All	All	981/1018 (96%)	0.32	33 (3%)	48	45	27, 59, 97, 129	8 (0%)

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	126	LEU	5.7
1	A	500	SER	4.6
1	B	125	PRO	4.3
1	B	126	LEU	4.2
1	B	80	VAL	3.6
1	B	123	THR	3.5
1	A	124	GLN	3.3
1	B	229	VAL	3.3
1	A	121	SER	3.2
1	A	85	THR	3.1
1	B	85	THR	2.9
1	A	123	THR	2.8
1	B	441	ALA	2.7
1	A	84	THR	2.7
1	B	119	SER	2.7
1	A	122	ASP	2.7
1	A	79	THR	2.6
1	B	81	THR	2.6
1	B	96	SER	2.6
1	A	53	LEU	2.5
1	A	80	VAL	2.5
1	A	501	GLU	2.5
1	B	59	GLY	2.4
1	B	99	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	99	ARG	2.3
1	A	229	VAL	2.3
1	B	124	GLN	2.3
1	A	111	THR	2.3
1	A	7	HIS	2.2
1	B	393	ALA	2.2
1	B	35	ASN	2.1
1	A	54	GLU	2.1
1	B	121	SER	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

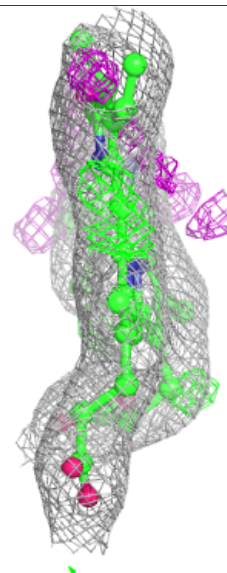
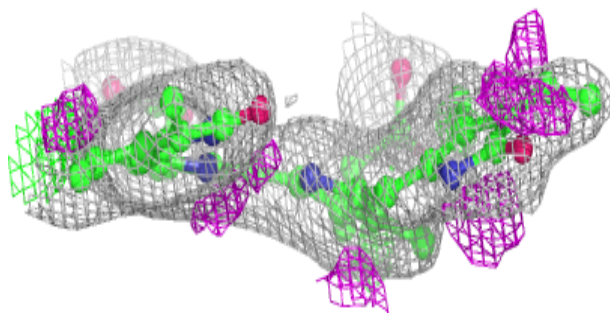
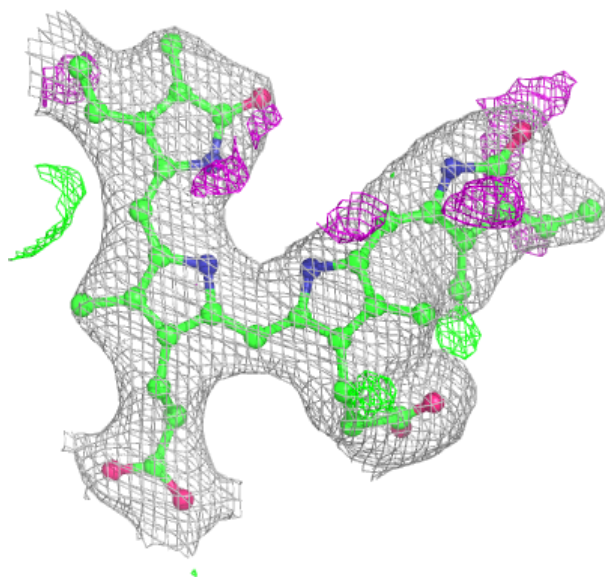
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	SO4	B	602	5/5	0.74	0.12	154,155,155,155	5
3	SO4	A	602	5/5	0.80	0.08	113,113,113,114	5
3	SO4	B	603	5/5	0.87	0.14	106,106,108,108	5
2	EL5	A	601	43/43	0.93	0.12	51,57,60,63	0
2	EL5	B	601	43/43	0.94	0.11	49,54,57,58	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.

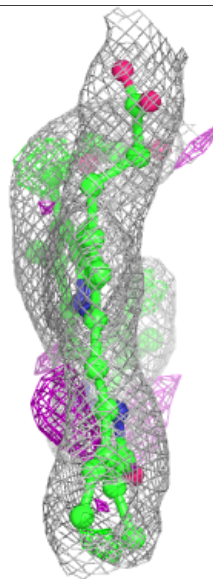
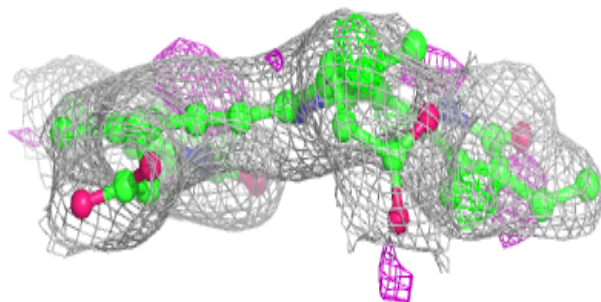
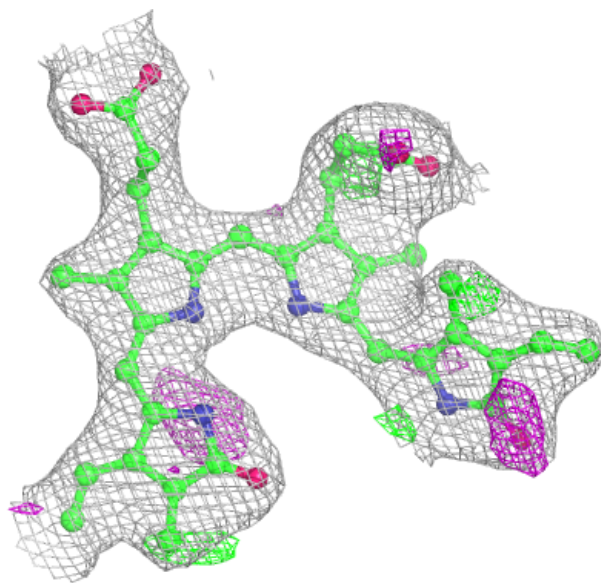
Electron density around EL5 A 601:

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



Electron density around EL5 B 601:

$2mF_o-DF_c$ (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.