



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:21 PM UTC

PDB ID : 6BZG / pdb_00006bzg
Title : Structure of *S. cerevisiae* Zip2:Spo16 complex, P212121 form
Authors : Arora, K.; Corbett, K.D.
Deposited on : 2017-12-23
Resolution : 2.13 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

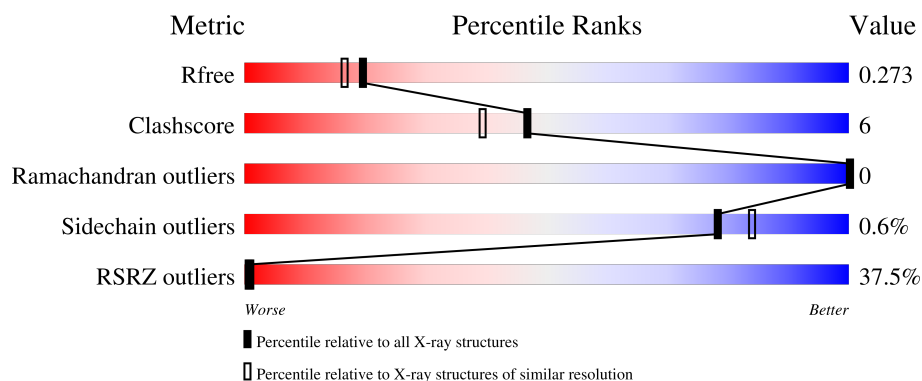
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.13 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}	180053	3689 (2.16-2.12)
Clashscore	190562	3812 (2.16-2.12)
Ramachandran outliers	187476	3773 (2.16-2.12)
Sidechain outliers	187428	3772 (2.16-2.12)
RSRZ outliers	180081	3691 (2.16-2.12)

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	B	206	27% 82% 14% .
2	A	197	45% 79% 17% .

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3322 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 Protein ZIP2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	198	Total	C	N	O	S	0	0	0
			1659	1084	267	299	9			

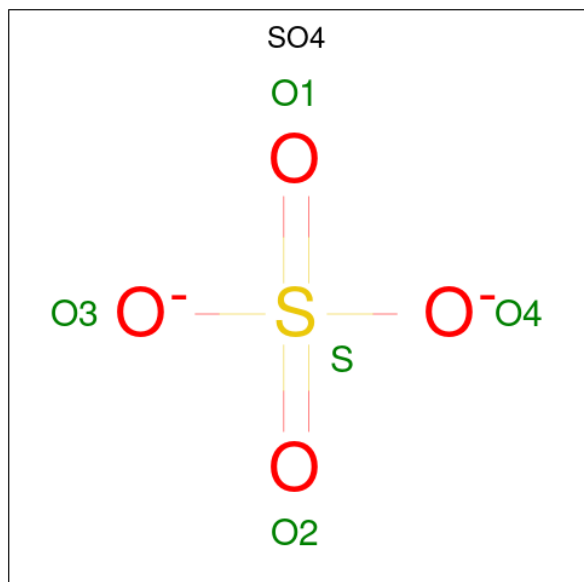
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	641	ALA	LYS	engineered mutation	UNP P53061
B	642	ALA	GLU	engineered mutation	UNP P53061
B	643	ALA	LYS	engineered mutation	UNP P53061

- Molecule 2 is a protein called Sporulation-specific protein 16.

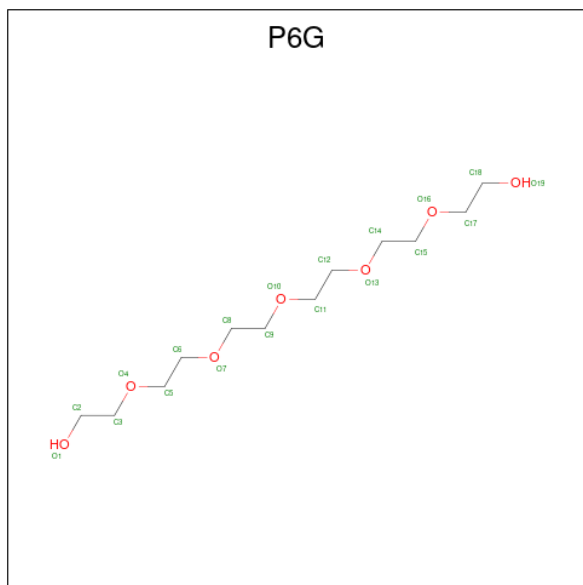
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	189	Total	C	N	O	S	0	0	0
			1560	1003	259	295	3			

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 4 is HEXAETHYLENE GLYCOL (CCD ID: P6G) (formula: $C_{12}H_{26}O_7$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 19 12 7	0	0

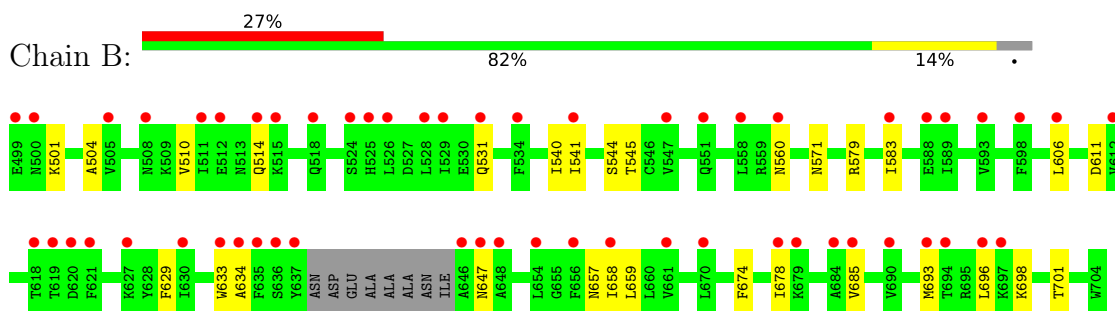
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	48	Total O 48 48	0	0
5	A	26	Total O 26 26	0	0

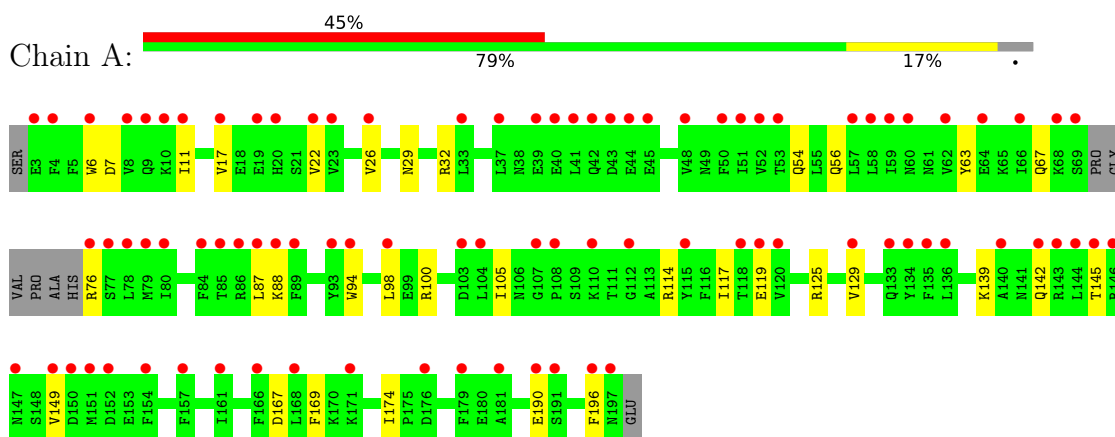
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Protein ZIP2



- Molecule 2: Sporulation-specific protein 16



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	50.25Å 96.21Å 101.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	69.81 – 2.13 69.81 – 2.13	Depositor EDS
% Data completeness (in resolution range)	98.4 (69.81-2.13) 99.3 (69.81-2.13)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.21	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 2.12Å)	Xtriage
Refinement program	PHENIX (1.11.1 _2575: ???)	Depositor
R, R_{free}	0.249 , 0.270 0.254 , 0.273	Depositor DCC
R_{free} test set	1464 reflections (5.22%)	wwPDB-VP
Wilson B-factor (Å ²)	50.5	Xtriage
Anisotropy	0.162	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 41.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	3322	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.08% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, P6G

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	B	0.10	0/1693	0.26	0/2282
2	A	0.09	0/1587	0.25	0/2145
All	All	0.09	0/3280	0.26	0/4427

There are no bond length outliers.

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	B	1659	0	1667	20	0
2	A	1560	0	1546	21	0
3	A	5	0	0	0	0
3	B	5	0	0	1	0
4	A	19	0	26	2	0
5	A	26	0	0	1	0
5	B	48	0	0	1	0
All	All	3322	0	3239	37	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 6.

All (37) 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)
2:A:7:ASP:HB2	2:A:29:ASN:HB3	1.75	0.68
1:B:571:ASN:HB3	2:A:145:THR:HG21	1.78	0.65
1:B:647:ASN:ND2	2:A:167:ASP:OD2	2.34	0.59
1:B:611:ASP:OD1	2:A:114:ARG:NH2	2.35	0.58
2:A:100:ARG:HG2	4:A:202:P6G:H61	1.87	0.57
2:A:11:ILE:HG22	2:A:26:VAL:HG13	1.87	0.56
1:B:540:ILE:HG22	1:B:659:LEU:HD12	1.90	0.53
1:B:606:LEU:HD23	2:A:17:VAL:HG11	1.90	0.53
1:B:685:VAL:HG13	1:B:693:MET:HE3	1.91	0.52
1:B:541:ILE:HD13	1:B:629:PHE:HB3	1.90	0.52
1:B:501:LYS:NZ	5:B:904:HOH:O	2.43	0.51
2:A:139:LYS:HD3	2:A:142:GLN:HE21	1.75	0.51
2:A:98:LEU:HD22	2:A:117:ILE:HG13	1.94	0.50
1:B:545:THR:OG1	1:B:579:ARG:NH1	2.46	0.49
2:A:17:VAL:HG22	2:A:129:VAL:HG21	1.95	0.49
1:B:501:LYS:HD3	1:B:634:ALA:HB3	1.94	0.48
1:B:678:ILE:HG12	2:A:190:GLU:HG3	1.96	0.47
2:A:119:GLU:O	2:A:125:ARG:NH2	2.49	0.46
1:B:531:GLN:HB2	1:B:658:ILE:HD12	1.98	0.45
1:B:504:ALA:HB3	1:B:540:ILE:HB	1.99	0.45
1:B:531:GLN:HE22	1:B:657:ASN:HA	1.83	0.44
2:A:169:PHE:HA	2:A:174:ILE:HD12	1.99	0.44
1:B:560:ASN:ND2	3:B:801:SO4:O1	2.51	0.43
2:A:6:TRP:C	2:A:32:ARG:HH21	2.27	0.42
2:A:56:GLN:HA	2:A:105:ILE:HD11	2.00	0.42
1:B:583:ILE:HD11	1:B:629:PHE:HE2	1.85	0.42
2:A:22:VAL:HG23	2:A:76:ARG:HD2	2.01	0.42
2:A:174:ILE:HD11	2:A:196:PHE:CE1	2.55	0.42
1:B:541:ILE:HG21	1:B:633:TRP:HB2	2.01	0.41
1:B:698:LYS:HA	1:B:701:THR:HG22	2.01	0.41
4:A:202:P6G:H182	4:A:202:P6G:H52	2.03	0.41
1:B:510:VAL:O	1:B:514:GLN:HG3	2.21	0.40
2:A:87:LEU:HD22	2:A:94:TRP:CD1	2.56	0.40
2:A:63:TYR:O	2:A:67:GLN:HG3	2.21	0.40
2:A:88:LYS:NZ	5:A:303:HOH:O	2.42	0.40
2:A:6:TRP:NE1	2:A:54:GLN:HB3	2.36	0.40
1:B:674:PHE:CE1	1:B:696:LEU:HD11	2.57	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	B	194/206 (94%)	189 (97%)	5 (3%)	0	100	100
2	A	185/197 (94%)	183 (99%)	2 (1%)	0	100	100
All	All	379/403 (94%)	372 (98%)	7 (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	B	186/191 (97%)	185 (100%)	1 (0%)	81	86
2	A	177/185 (96%)	176 (99%)	1 (1%)	78	84
All	All	363/376 (96%)	361 (99%)	2 (1%)	78	84

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	544	SER
2	A	149	VAL

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

Mol	Chain	Res	Type
1	B	523	ASN

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Mol	Chain	Res	Type
1	B	557	GLN
2	A	36	GLN
2	A	67	GLN
2	A	83	ASN

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](#)

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	$\# Z > 2$
3	SO4	A	201	-	4,4,4	0.23	0	6,6,6	0.07	0
3	SO4	B	801	-	4,4,4	0.24	0	6,6,6	0.07	0
4	P6G	A	202	-	18,18,18	0.55	0	17,17,17	0.21	0

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	P6G	A	202	-	-	7/16/16/16	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

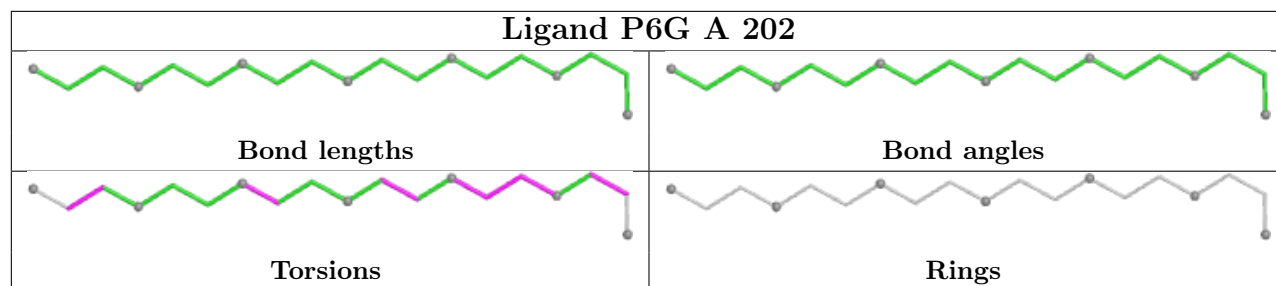
Mol	Chain	Res	Type	Atoms
4	A	202	P6G	O4-C5-C6-O7
4	A	202	P6G	O7-C8-C9-O10
4	A	202	P6G	C5-C6-O7-C8
4	A	202	P6G	O16-C17-C18-O19
4	A	202	P6G	C6-C5-O4-C3
4	A	202	P6G	O1-C2-C3-O4
4	A	202	P6G	C11-C12-O13-C14

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	801	SO4	1	0
4	A	202	P6G	2	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.



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	B	198/206 (96%)	1.60	56 (28%)  	37, 56, 90, 135	0
2	A	189/197 (95%)	2.02	89 (47%)  	44, 70, 115, 142	0
All	All	387/403 (96%)	1.80	145 (37%)  	37, 64, 105, 142	0

All (145) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	534	PHE	5.8
2	A	145	THR	5.7
1	B	635	PHE	5.6
1	B	646	ALA	5.2
2	A	11	ILE	5.1
2	A	93	TYR	4.8
1	B	528	LEU	4.8
1	B	505	VAL	4.4
1	B	633	TRP	4.3
1	B	637	TYR	4.3
2	A	104	LEU	4.1
2	A	89	PHE	4.1
2	A	146	ARG	4.1
2	A	144	LEU	4.1
1	B	541	ILE	4.1
2	A	68	LYS	3.9
2	A	41	LEU	3.9
1	B	526	LEU	3.8
2	A	40	GLU	3.7
1	B	583	ILE	3.7
2	A	42	GLN	3.6
2	A	37	LEU	3.6
2	A	151	MET	3.5
2	A	94	TRP	3.5

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Mol	Chain	Res	Type	RSRZ
2	A	53	THR	3.5
2	A	57	LEU	3.5
1	B	558	LEU	3.5
2	A	133	GLN	3.5
2	A	135	PHE	3.4
2	A	45	GLU	3.3
2	A	44	GLU	3.3
2	A	77	SER	3.2
2	A	98	LEU	3.2
1	B	499	GLU	3.2
2	A	26	VAL	3.2
1	B	696	LEU	3.2
1	B	621	PHE	3.2
2	A	79	MET	3.2
2	A	196	PHE	3.1
1	B	518	GLN	3.1
1	B	693	MET	3.1
1	B	619	THR	3.1
2	A	143	ARG	3.1
1	B	531	GLN	3.1
2	A	107	GLY	3.1
1	B	636	SER	3.1
1	B	551	GLN	3.1
2	A	20	HIS	3.0
2	A	134	TYR	3.0
2	A	147	ASN	3.0
1	B	524	SER	2.9
1	B	593	VAL	2.9
1	B	658	ILE	2.9
1	B	525	HIS	2.9
2	A	76	ARG	2.9
1	B	620	ASP	2.9
2	A	171	LYS	2.9
2	A	140	ALA	2.9
2	A	22	VAL	2.8
2	A	191	SER	2.8
1	B	529	ILE	2.8
2	A	51	ILE	2.8
2	A	119	GLU	2.7
2	A	115	TYR	2.7
2	A	10	LYS	2.7
2	A	86	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
2	A	166	PHE	2.7
2	A	39	GLU	2.7
2	A	69	SER	2.7
2	A	33	LEU	2.6
2	A	120	VAL	2.6
1	B	508	ASN	2.6
1	B	606	LEU	2.6
2	A	88	LYS	2.6
2	A	66	ILE	2.6
2	A	129	VAL	2.6
2	A	150	ASP	2.6
1	B	500	ASN	2.5
1	B	511	ILE	2.5
1	B	627	LYS	2.5
2	A	110	LYS	2.5
1	B	648	ALA	2.5
2	A	157	PHE	2.5
2	A	19	GLU	2.5
1	B	618	THR	2.5
1	B	515	LYS	2.5
1	B	656	PHE	2.5
1	B	589	ILE	2.5
1	B	612	VAL	2.4
2	A	52	VAL	2.4
2	A	152	ASP	2.4
1	B	598	PHE	2.4
2	A	154	PHE	2.4
1	B	670	LEU	2.4
1	B	512	GLU	2.4
2	A	179	PHE	2.4
2	A	6	TRP	2.4
1	B	661	VAL	2.3
1	B	634	ALA	2.3
2	A	4	PHE	2.3
2	A	17	VAL	2.3
1	B	588	GLU	2.3
2	A	50	PHE	2.3
2	A	62	VAL	2.3
2	A	103	ASP	2.3
2	A	176	ASP	2.3
1	B	647	ASN	2.2
2	A	197	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
2	A	9	GLN	2.2
2	A	43	ASP	2.2
2	A	136	LEU	2.2
1	B	679	LYS	2.2
1	B	678	ILE	2.2
2	A	80	ILE	2.2
2	A	84	PHE	2.2
2	A	149	VAL	2.2
2	A	78	LEU	2.2
1	B	697	LYS	2.2
2	A	59	ILE	2.1
2	A	190	GLU	2.1
1	B	685	VAL	2.1
2	A	23	VAL	2.1
2	A	168	LEU	2.1
2	A	85	THR	2.1
1	B	514	GLN	2.1
2	A	161	ILE	2.1
1	B	690	VAL	2.1
2	A	58	LEU	2.1
1	B	560	ASN	2.1
1	B	630	ILE	2.1
1	B	547	VAL	2.1
2	A	181	ALA	2.1
2	A	3	GLU	2.1
2	A	142	GLN	2.1
2	A	108	PRO	2.1
2	A	8	VAL	2.1
2	A	118	THR	2.0
2	A	48	VAL	2.0
2	A	64	GLU	2.0
1	B	684	ALA	2.0
2	A	60	ASN	2.0
1	B	654	LEU	2.0
2	A	87	LEU	2.0
1	B	694	THR	2.0
2	A	112	GLY	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 [i](#)

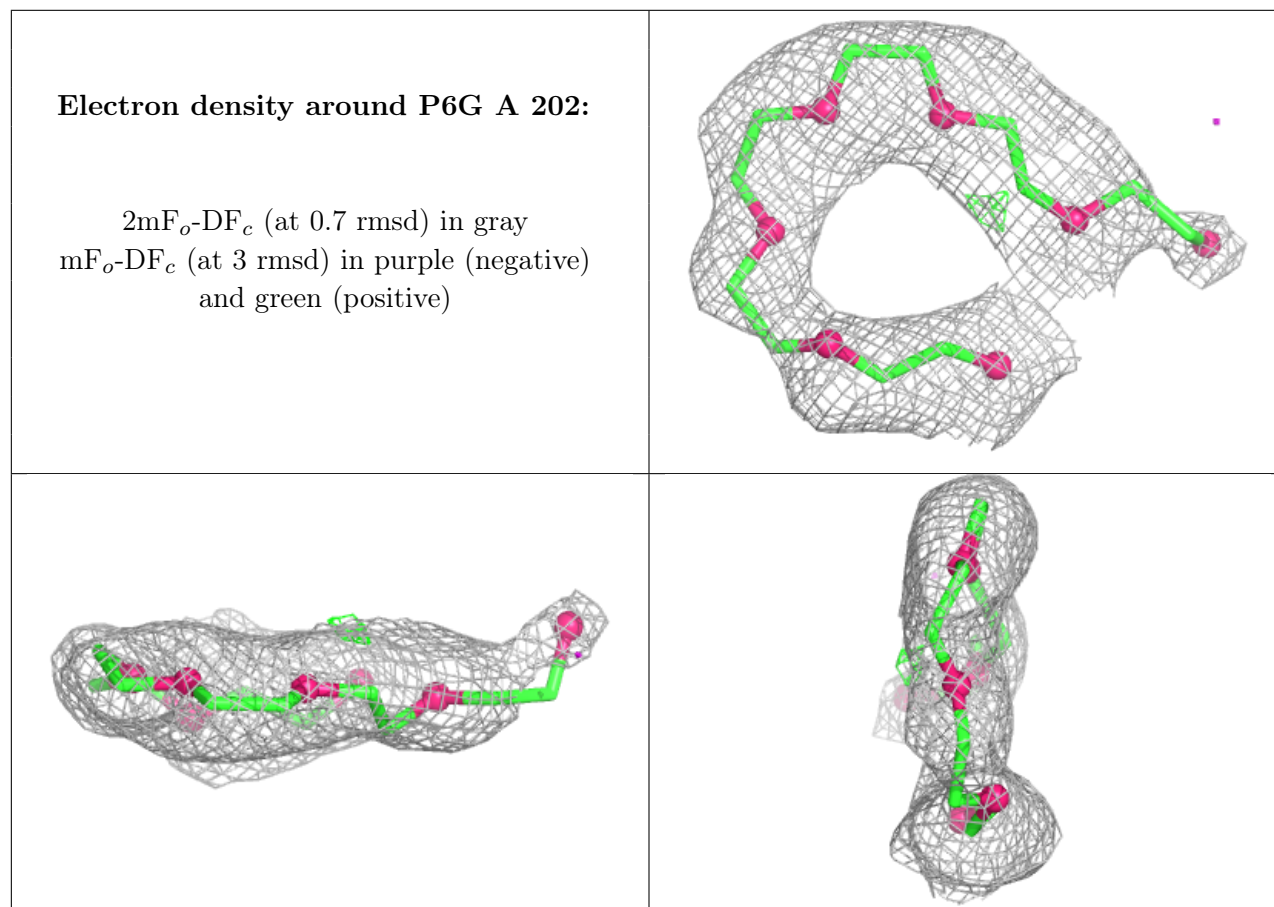
There are no oligosaccharides in this entry.

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($\text{\AA}^2$)	Q<0.9
3	SO4	A	201	5/5	0.53	0.16	140,141,142,142	0
3	SO4	B	801	5/5	0.77	0.15	111,113,115,116	0
4	P6G	A	202	19/19	0.79	0.21	58,82,92,93	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.