



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 9IH0 / pdb_00009ih0
Title : Crystal structure of Vaspin with PolyP45
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Deposited on : 2025-02-20
Resolution : 2.26 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

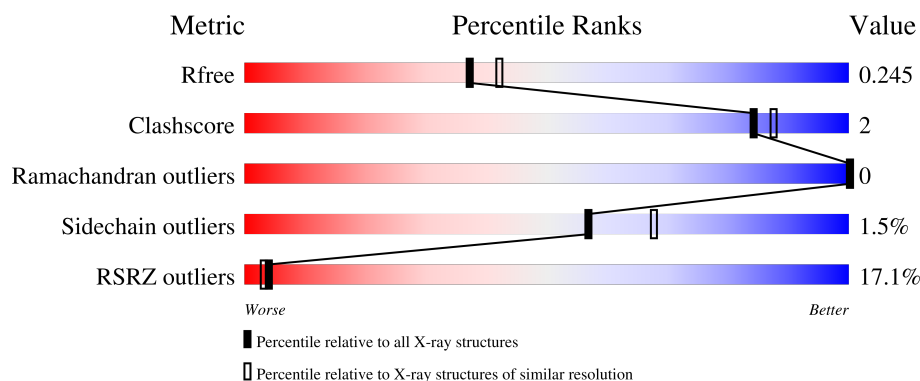
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.26 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	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	414	5% 84% 7% 10%
1	B	414	26% 82% 7% 11%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12350 atoms, of which 6196 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 Serpin A12.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	374	Total	C	H	N	O	S	0	2	0
			6135	1955	3102	514	550	14			
1	B	367	Total	C	H	N	O	S	0	4	0
			6114	1948	3094	515	544	13			

There are 42 discrepancies between the modelled and reference sequences:

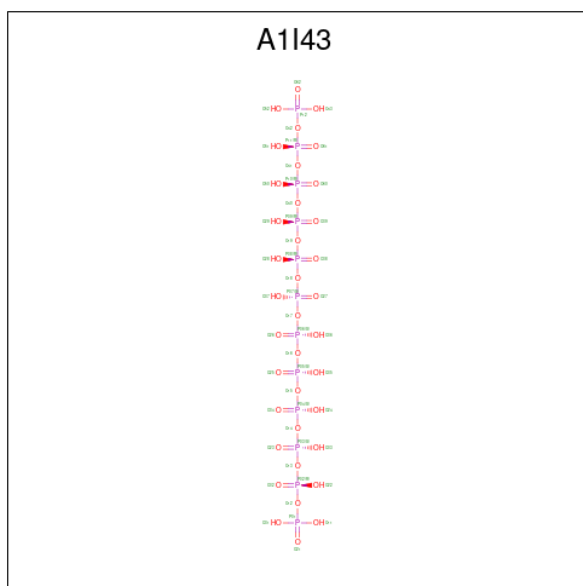
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP Q8IW75
A	2	HIS	-	expression tag	UNP Q8IW75
A	3	HIS	-	expression tag	UNP Q8IW75
A	4	HIS	-	expression tag	UNP Q8IW75
A	5	HIS	-	expression tag	UNP Q8IW75
A	6	HIS	-	expression tag	UNP Q8IW75
A	7	HIS	-	expression tag	UNP Q8IW75
A	8	HIS	-	expression tag	UNP Q8IW75
A	9	HIS	-	expression tag	UNP Q8IW75
A	10	HIS	-	expression tag	UNP Q8IW75
A	11	HIS	-	expression tag	UNP Q8IW75
A	12	SER	-	linker	UNP Q8IW75
A	13	SER	-	linker	UNP Q8IW75
A	14	GLY	-	linker	UNP Q8IW75
A	15	HIS	-	linker	UNP Q8IW75
A	16	ILE	-	linker	UNP Q8IW75
A	17	GLU	-	linker	UNP Q8IW75
A	18	GLY	-	linker	UNP Q8IW75
A	19	ARG	-	linker	UNP Q8IW75
A	20	HIS	-	linker	UNP Q8IW75
A	21	MET	-	linker	UNP Q8IW75
B	1	GLY	-	expression tag	UNP Q8IW75
B	2	HIS	-	expression tag	UNP Q8IW75
B	3	HIS	-	expression tag	UNP Q8IW75
B	4	HIS	-	expression tag	UNP Q8IW75

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Chain	Residue	Modelled	Actual	Comment	Reference
B	5	HIS	-	expression tag	UNP Q8IW75
B	6	HIS	-	expression tag	UNP Q8IW75
B	7	HIS	-	expression tag	UNP Q8IW75
B	8	HIS	-	expression tag	UNP Q8IW75
B	9	HIS	-	expression tag	UNP Q8IW75
B	10	HIS	-	expression tag	UNP Q8IW75
B	11	HIS	-	expression tag	UNP Q8IW75
B	12	SER	-	linker	UNP Q8IW75
B	13	SER	-	linker	UNP Q8IW75
B	14	GLY	-	linker	UNP Q8IW75
B	15	HIS	-	linker	UNP Q8IW75
B	16	ILE	-	linker	UNP Q8IW75
B	17	GLU	-	linker	UNP Q8IW75
B	18	GLY	-	linker	UNP Q8IW75
B	19	ARG	-	linker	UNP Q8IW75
B	20	HIS	-	linker	UNP Q8IW75
B	21	MET	-	linker	UNP Q8IW75

- Molecule 2 is dodecaphosphate (CCD ID: A1I43) (formula: $\text{H}_{14}\text{O}_{37}\text{P}_{12}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			49	37	12		

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



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	32	Total	O	0	1
			33	33		
4	B	12	Total	O	0	2
			14	14		

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	143.26Å 147.98Å 62.46Å 90.00° 104.95° 90.00°	Depositor
Resolution (Å)	35.37 – 2.26 35.37 – 2.26	Depositor EDS
% Data completeness (in resolution range)	69.2 (35.37-2.26) 69.1 (35.37-2.26)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.23 (at 2.27Å)	Xtriage
Refinement program	REFMAC 5.8.0419, PHENIX 1.21.2	Depositor
R, R_{free}	0.218 , 0.240 0.226 , 0.245	Depositor DCC
R_{free} test set	2059 reflections (3.51%)	wwPDB-VP
Wilson B-factor (Å ²)	53.7	Xtriage
Anisotropy	0.013	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 37.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12350	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.39% 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: A1I43, 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	0.18	0/3098	0.29	0/4168
1	B	0.15	0/3088	0.28	0/4151
All	All	0.16	0/6186	0.29	0/8319

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 [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	3033	3102	3101	13	0
1	B	3020	3094	3089	15	0
2	A	49	0	0	0	0
3	B	5	0	0	0	0
4	A	33	0	0	1	0
4	B	14	0	0	0	0
All	All	6154	6196	6190	28	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 (28) 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:50:ARG:NH2	1:A:289:VAL:HG21	2.12	0.64
1:A:306:VAL:HG12	1:A:308:VAL:HG23	1.80	0.61
1:B:308:VAL:HG22	1:B:386:ILE:HD13	1.84	0.59
1:A:308:VAL:HG22	1:A:386:ILE:HD13	1.85	0.59
1:B:306:VAL:HG12	1:B:308:VAL:HG23	1.85	0.57
1:A:181:ILE:HD12	1:A:207:TYR:CE1	2.40	0.56
1:A:70:ARG:NH2	4:A:601:HOH:O	2.41	0.54
1:B:271:ILE:HG22	1:B:273:ILE:CD1	2.38	0.53
1:A:271:ILE:HG22	1:A:273:ILE:CD1	2.38	0.53
1:B:306:VAL:CG1	1:B:308:VAL:HG23	2.41	0.50
1:A:306:VAL:CG1	1:A:308:VAL:HG23	2.41	0.50
1:B:365:THR:O	1:B:366:GLU:CB	2.61	0.48
1:B:255:LEU:HD13	1:B:283:LEU:HD12	1.96	0.48
1:A:399:ILE:O	1:A:400:PRO:C	2.57	0.47
1:A:287:LEU:HD11	1:A:292:PHE:CE1	2.49	0.47
1:B:365:THR:O	1:B:366:GLU:HB2	2.15	0.45
1:A:71:ASN:OD1	1:A:409:VAL:N	2.47	0.45
1:B:146:PRO:HB2	1:B:151:LEU:HD11	2.01	0.43
1:B:222:VAL:O	1:B:222:VAL:HG12	2.17	0.43
1:B:54:ASP:CG	1:B:289:VAL:HG11	2.43	0.43
1:B:82:ALA:HB1	1:B:204:LEU:HD21	2.00	0.43
1:B:273:ILE:HG21	1:B:283:LEU:HD21	1.99	0.43
1:B:132:LEU:HD23	1:B:133:SER:N	2.34	0.42
1:A:214:TRP:CE3	1:A:262:ILE:HG22	2.53	0.42
1:B:53:MET:HG2	1:B:402:VAL:HG23	2.02	0.42
1:A:139:PHE:CE2	1:A:177:ILE:HG23	2.55	0.41
1:B:123:LEU:O	1:B:124:THR:C	2.64	0.41
1:A:388:LYS:O	1:A:389:PRO:C	2.63	0.41

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	372/414 (90%)	358 (96%)	14 (4%)	0	100	100
1	B	367/414 (89%)	353 (96%)	14 (4%)	0	100	100
All	All	739/828 (89%)	711 (96%)	28 (4%)	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	336/369 (91%)	331 (98%)	5 (2%)	57	68
1	B	336/369 (91%)	330 (98%)	6 (2%)	51	63
All	All	672/738 (91%)	661 (98%)	11 (2%)	57	66

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	138	LEU
1	A	235	SER
1	A	321	LYS
1	A	344	HIS
1	A	351	GLU
1	B	148	ARG
1	B	161	GLU
1	B	211[A]	ARG
1	B	211[B]	ARG
1	B	258	THR
1	B	379	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	ASN
1	A	100	GLN

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Mol	Chain	Res	Type
1	A	117	HIS
1	A	265	GLN
1	A	335	HIS
1	B	100	GLN
1	B	117	HIS
1	B	128	GLN
1	B	142	GLN
1	B	216	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](#)

2 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	A1I43	A	501	-	46,48,48	1.00	0	62,83,83	0.86	0
3	SO4	B	501	-	4,4,4	0.75	0	6,6,6	0.10	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
2	A1I43	A	501	-	-	13/66/66/66	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

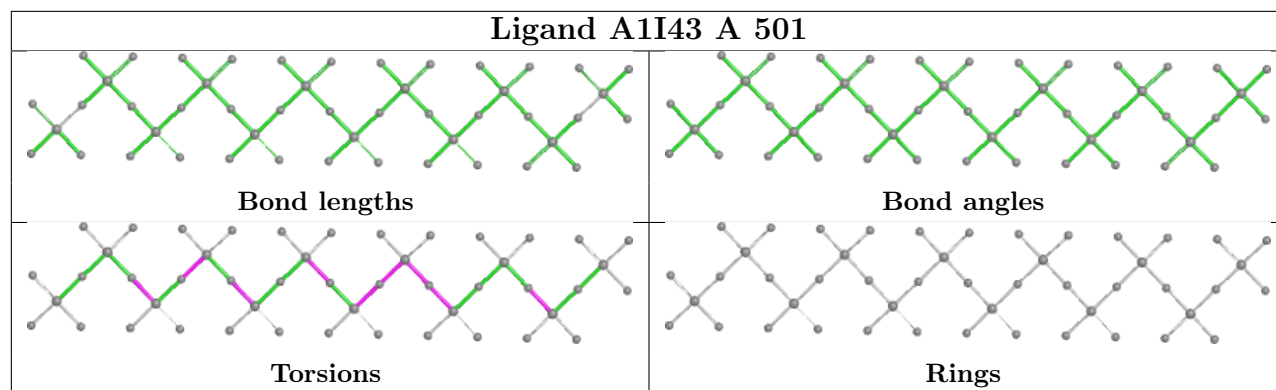
All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	A1I43	P11-O41-P10-O60
2	A	501	A1I43	P03-O13-P02-O32
2	A	501	A1I43	P06-O16-P05-O35
2	A	501	A1I43	P05-O16-P06-O36
2	A	501	A1I43	P05-O16-P06-O26
2	A	501	A1I43	P03-O13-P02-O22
2	A	501	A1I43	P04-O15-P05-O35
2	A	501	A1I43	P06-O16-P05-O25
2	A	501	A1I43	P06-O17-P07-O37
2	A	501	A1I43	P09-O19-P08-O28
2	A	501	A1I43	P05-O15-P04-O24
2	A	501	A1I43	P10-O40-P09-O29
2	A	501	A1I43	P04-O15-P05-O16

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.



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	374/414 (90%)	0.47	21 (5%)	30 28	24, 52, 81, 137	2 (0%)
1	B	367/414 (88%)	1.45	106 (28%)	1 1	35, 77, 131, 157	4 (1%)
All	All	741/828 (89%)	0.96	127 (17%)	4 3	24, 60, 125, 157	6 (0%)

All (127) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	36	VAL	6.4
1	A	368	ALA	5.9
1	B	218	PHE	5.9
1	A	285	LYS	5.3
1	B	378	MET	5.2
1	B	292	PHE	5.0
1	B	229	PHE	5.0
1	A	371	THR	5.0
1	A	372	GLY	4.9
1	B	382	LEU	4.9
1	B	399	ILE	4.9
1	B	242	PHE	4.7
1	B	250	GLY	4.7
1	B	381	PRO	4.6
1	B	247	TYR	4.5
1	B	232	LYS	4.5
1	B	308	VAL	4.5
1	B	384	VAL	4.4
1	B	216	HIS	4.4
1	B	228	PHE	4.3
1	B	386	ILE	4.3
1	B	246	ILE	4.3
1	A	378	MET	4.2
1	B	251	TYR	4.0

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Mol	Chain	Res	Type	RSRZ
1	B	237	LYS	3.9
1	A	367	GLY	3.9
1	B	239	PRO	3.9
1	B	363[A]	ARG	3.9
1	B	214	TRP	3.8
1	B	295	TRP	3.8
1	B	303	VAL	3.8
1	B	236	VAL	3.8
1	A	369	ALA	3.7
1	B	253	ASP	3.6
1	B	230	LEU	3.6
1	B	304	VAL	3.6
1	B	380	THR	3.6
1	B	140	ILE	3.6
1	B	289	VAL	3.6
1	B	306	VAL	3.6
1	B	383	VAL	3.6
1	B	151	LEU	3.5
1	B	297	THR	3.5
1	B	222	VAL	3.5
1	B	299	LEU	3.4
1	A	380	THR	3.4
1	B	249	VAL	3.4
1	B	267	ASN	3.4
1	B	238	VAL	3.3
1	B	234	SER	3.3
1	B	254	LYS	3.2
1	B	241	MET	3.2
1	B	255	LEU	3.1
1	B	123	LEU	3.1
1	B	393	LEU	3.1
1	B	398	LYS	3.1
1	B	263	PRO	3.1
1	B	260	LEU	3.1
1	B	412	ILE	3.0
1	B	126	LYS	3.0
1	B	244	SER	3.0
1	B	296	LYS	3.0
1	B	209[A]	PHE	2.9
1	B	145	GLN	2.9
1	A	336	GLY	2.8
1	A	370	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	400	PRO	2.8
1	B	411	PRO	2.8
1	B	215	LYS	2.7
1	B	305	ASP	2.7
1	B	361	ASP	2.7
1	B	225	GLU	2.7
1	B	365	THR	2.7
1	B	240	MET	2.7
1	B	265	GLN	2.7
1	B	70	ARG	2.6
1	A	37	GLN	2.5
1	B	310	ARG	2.5
1	B	259	ILE	2.5
1	B	298	LEU	2.5
1	B	279	LYS	2.5
1	B	300	SER	2.4
1	B	287	LEU	2.4
1	B	248	GLN	2.4
1	B	414	LYS	2.4
1	B	243	ARG	2.4
1	B	309	PRO	2.4
1	B	274	LEU	2.4
1	B	213	ARG	2.4
1	B	379	GLU	2.4
1	A	414	LYS	2.3
1	B	212	ALA	2.3
1	B	413	GLY	2.3
1	B	258	THR	2.3
1	B	121	HIS	2.3
1	B	37	GLN	2.3
1	B	104	PHE	2.3
1	B	106	LYS	2.3
1	B	366	GLU	2.2
1	B	293[A]	SER	2.2
1	B	301	ARG	2.2
1	A	344	HIS	2.2
1	A	398	LYS	2.2
1	B	307	SER	2.2
1	A	70	ARG	2.2
1	B	233	ASN	2.2
1	B	302	ARG	2.2
1	B	220	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	105	ARG	2.1
1	B	273	ILE	2.1
1	B	280	LEU	2.1
1	B	408	ILE	2.1
1	A	306	VAL	2.1
1	B	191	ASN	2.1
1	B	276	ASP	2.1
1	A	175	LYS	2.1
1	B	272	PHE	2.1
1	B	193	ILE	2.1
1	A	183	GLN	2.1
1	B	288	GLN	2.1
1	A	125	GLN	2.1
1	B	245	GLY	2.1
1	B	345	ARG	2.1
1	A	288	GLN	2.0
1	B	264	TYR	2.0
1	B	122	GLU	2.0
1	B	283	LEU	2.0

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.

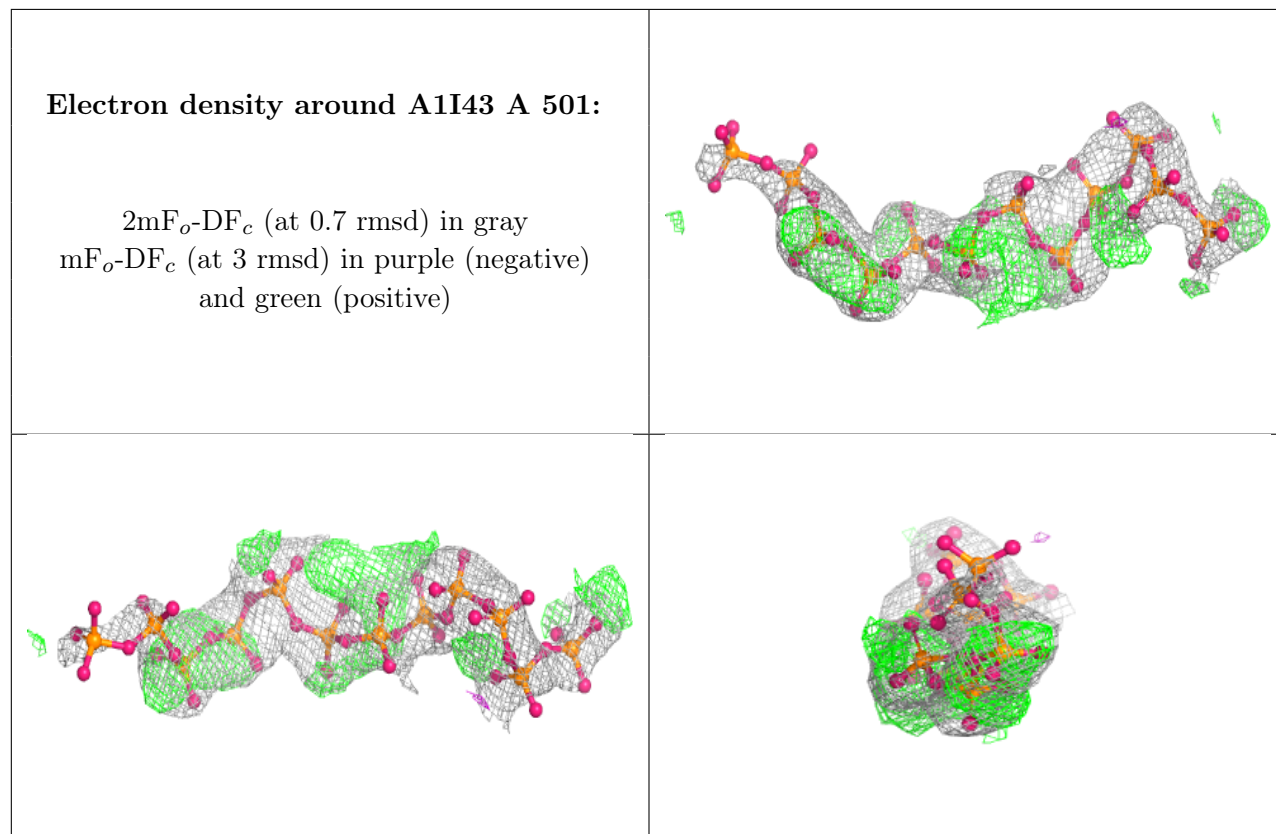
6.4 Ligands [i](#)

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($\text{\AA}^2$)	Q<0.9
3	SO4	B	501	5/5	0.72	0.12	74,76,82,109	0
2	A1I43	A	501	49/49	0.81	0.28	41,72,91,97	49

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.