



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:14 AM UTC

PDB ID : 7BVX / pdb_00007bvx
Title : Crystal structure of C-terminal fragment of pilus adhesin SpaC from Lactobacillus rhamnosus GG-Iodide soaked
Authors : Kant, A.; Palva, A.; von Ossowski, I.; Krishnan, V.
Deposited on : 2020-04-12
Resolution : 3.36 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
Xtriage (Phenix)	:	2.0
EDS	:	3.0
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

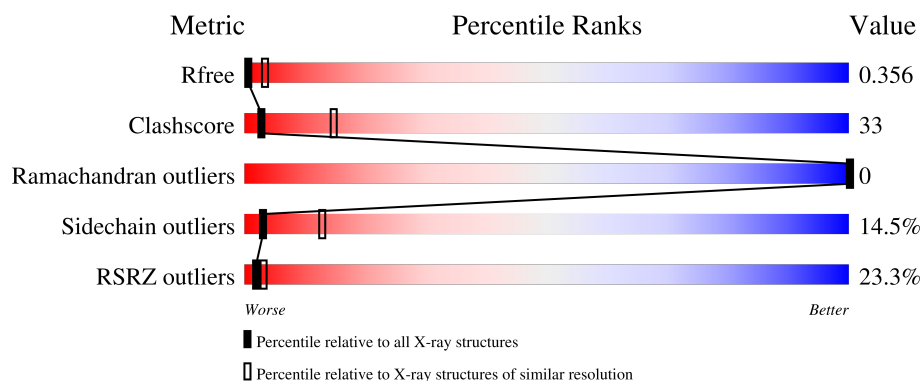
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.36 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	1099 (3.40-3.32)
Clashscore	190562	1116 (3.40-3.32)
Ramachandran outliers	187476	1101 (3.40-3.32)
Sidechain outliers	187428	1101 (3.40-3.32)
RSRZ outliers	180081	1099 (3.40-3.32)

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	292	21% 51% 33% 5% 12%

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
2	IOD	A	904	-	-	X	-

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1680 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 Pilus assembly protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	258	Total	C	N	O	S	0	0	0
			1674	1031	293	349	1			

There are 29 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	573	MET	-	initiating methionine	UNP A0A1Y0DVK9
A	574	GLY	-	expression tag	UNP A0A1Y0DVK9
A	575	SER	-	expression tag	UNP A0A1Y0DVK9
A	576	SER	-	expression tag	UNP A0A1Y0DVK9
A	577	HIS	-	expression tag	UNP A0A1Y0DVK9
A	578	HIS	-	expression tag	UNP A0A1Y0DVK9
A	579	HIS	-	expression tag	UNP A0A1Y0DVK9
A	580	HIS	-	expression tag	UNP A0A1Y0DVK9
A	581	HIS	-	expression tag	UNP A0A1Y0DVK9
A	582	HIS	-	expression tag	UNP A0A1Y0DVK9
A	583	SER	-	expression tag	UNP A0A1Y0DVK9
A	584	SER	-	expression tag	UNP A0A1Y0DVK9
A	585	GLY	-	expression tag	UNP A0A1Y0DVK9
A	586	LEU	-	expression tag	UNP A0A1Y0DVK9
A	587	VAL	-	expression tag	UNP A0A1Y0DVK9
A	588	PRO	-	expression tag	UNP A0A1Y0DVK9
A	589	ARG	-	expression tag	UNP A0A1Y0DVK9
A	590	GLY	-	expression tag	UNP A0A1Y0DVK9
A	591	SER	-	expression tag	UNP A0A1Y0DVK9
A	592	HIS	-	expression tag	UNP A0A1Y0DVK9
A	593	MET	-	expression tag	UNP A0A1Y0DVK9
A	857	LEU	-	expression tag	UNP A0A1Y0DVK9
A	858	GLU	-	expression tag	UNP A0A1Y0DVK9
A	859	HIS	-	expression tag	UNP A0A1Y0DVK9
A	860	HIS	-	expression tag	UNP A0A1Y0DVK9
A	861	HIS	-	expression tag	UNP A0A1Y0DVK9
A	862	HIS	-	expression tag	UNP A0A1Y0DVK9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	863	HIS	-	expression tag	UNP A0A1Y0DVK9
A	864	HIS	-	expression tag	UNP A0A1Y0DVK9

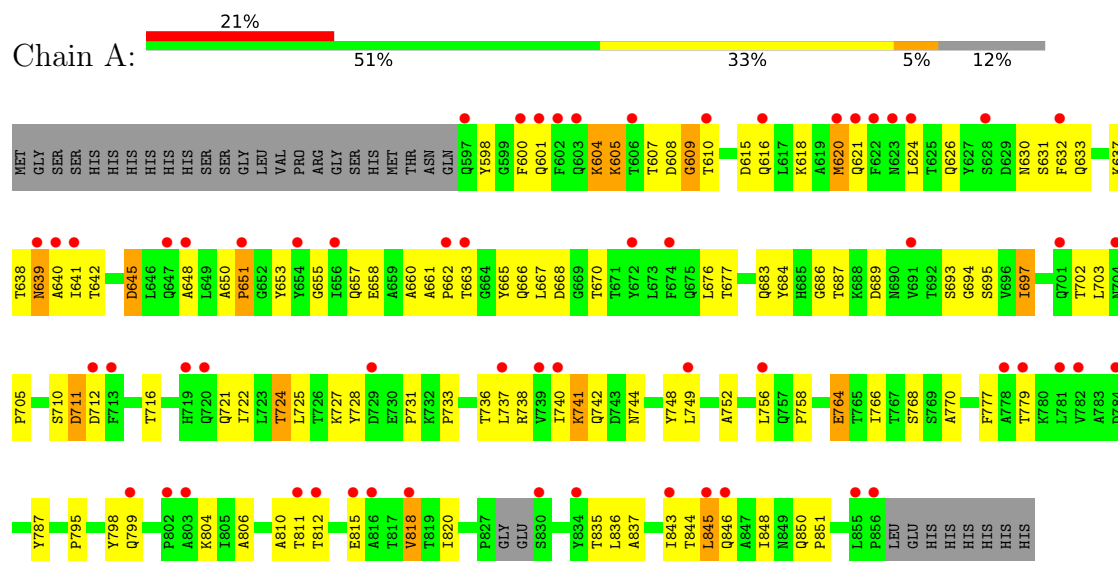
- Molecule 2 is IODIDE ION (CCD ID: IOD) (formula: I) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	6	Total I 6 6	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: Pilus assembly protein



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	60.05Å 114.92Å 122.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	57.46 – 3.36 57.46 – 3.36	Depositor EDS
% Data completeness (in resolution range)	99.9 (57.46-3.36) 99.9 (57.46-3.36)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.42 (at 3.33Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.305 , 0.346 0.304 , 0.356	Depositor DCC
R_{free} test set	295 reflections (4.65%)	wwPDB-VP
Wilson B-factor (Å ²)	149.6	Xtriage
Anisotropy	0.221	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 202.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	1680	wwPDB-VP
Average B, all atoms (Å ²)	145.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.34% 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: IOD

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	1.16	0/1701	1.60	7/2338 (0.3%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	725	LEU	CA-C-O	-6.33	113.69	120.46
1	A	665	TYR	CB-CA-C	6.09	119.53	109.72
1	A	609	GLY	N-CA-C	-5.41	108.25	115.40
1	A	651	PRO	CA-C-O	-5.31	114.94	121.31
1	A	711	ASP	CA-C-O	-5.21	115.66	121.81
1	A	811	THR	CA-C-N	5.16	127.50	120.54
1	A	811	THR	C-N-CA	5.16	127.50	120.54

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	1674	0	1362	100	0
2	A	6	0	0	4	0
All	All	1680	0	1362	100	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 33.

All (100) 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:666:GLN:HB3	2:A:904:IOD:I	2.25	1.07
1:A:632:PHE:HE1	1:A:653:TYR:HB3	1.28	0.96
1:A:742:GLN:O	1:A:848:ILE:HA	1.68	0.94
1:A:607:THR:OG1	1:A:731:PRO:HD3	1.67	0.93
1:A:601:GLN:HB2	1:A:724:THR:HG23	1.53	0.90
1:A:632:PHE:CE1	1:A:653:TYR:HB3	2.10	0.86
1:A:630:ASN:HB3	1:A:653:TYR:CE1	2.12	0.84
1:A:806:ALA:O	1:A:818:VAL:HA	1.76	0.83
1:A:804:LYS:O	1:A:820:ILE:HA	1.86	0.76
1:A:620:MET:HG3	1:A:662:PRO:HD3	1.65	0.75
1:A:835:THR:O	1:A:845:LEU:HA	1.89	0.73
1:A:601:GLN:HB2	1:A:724:THR:CG2	2.18	0.72
1:A:605:LYS:HB3	1:A:728:TYR:CD1	2.27	0.70
1:A:850:GLN:OE1	1:A:850:GLN:HA	1.91	0.70
1:A:607:THR:HG1	1:A:731:PRO:HD3	1.56	0.69
1:A:604:LYS:HG3	1:A:620:MET:SD	2.33	0.68
1:A:758:PRO:HB3	1:A:787:TYR:CE1	2.29	0.67
1:A:741:LYS:HG2	1:A:752:ALA:HB3	1.77	0.67
1:A:721:GLN:O	1:A:721:GLN:HG2	1.94	0.66
1:A:683:GLN:O	1:A:697:ILE:HD12	1.96	0.64
1:A:615:ASP:CB	2:A:907:IOD:I	3.16	0.64
1:A:741:LYS:HG2	1:A:752:ALA:CB	2.28	0.64
1:A:650:ALA:HB1	1:A:651:PRO:HD2	1.80	0.63
1:A:810:ALA:H	1:A:815:GLU:CB	2.11	0.63
1:A:601:GLN:CB	1:A:724:THR:CG2	2.77	0.62
1:A:721:GLN:N	1:A:721:GLN:OE1	2.31	0.60
1:A:616:GLN:C	1:A:618:LYS:H	2.10	0.60
1:A:848:ILE:O	1:A:848:ILE:HD12	2.01	0.59
1:A:600:PHE:CG	1:A:601:GLN:N	2.69	0.59
1:A:836:LEU:HA	1:A:845:LEU:HD23	1.83	0.59
1:A:615:ASP:O	1:A:618:LYS:CB	2.51	0.58
1:A:624:LEU:HD12	1:A:655:GLY:O	2.03	0.58
1:A:703:LEU:HD12	1:A:712:ASP:CA	2.34	0.58
1:A:639:ASN:ND2	1:A:640:ALA:O	2.35	0.57
1:A:621:GLN:N	1:A:660:ALA:O	2.34	0.57
1:A:608:ASP:CB	1:A:731:PRO:HG3	2.35	0.56
1:A:799:GLN:N	1:A:850:GLN:O	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:626:GLN:HG3	1:A:626:GLN:O	2.05	0.56
1:A:684:TYR:HB2	1:A:697:ILE:HD11	1.88	0.56
1:A:684:TYR:HB2	1:A:697:ILE:CD1	2.37	0.55
1:A:722:ILE:HG22	1:A:722:ILE:O	2.05	0.55
1:A:604:LYS:HD3	1:A:727:LYS:O	2.08	0.54
1:A:639:ASN:ND2	1:A:639:ASN:C	2.66	0.54
1:A:733:PRO:HG2	1:A:812:THR:O	2.09	0.53
1:A:837:ALA:HB3	1:A:844:THR:HG22	1.91	0.53
1:A:631:SER:HB2	1:A:633:GLN:HG3	1.91	0.53
1:A:657:GLN:HG2	1:A:658:GLU:N	2.24	0.53
1:A:697:ILE:HG22	1:A:697:ILE:O	2.09	0.52
1:A:620:MET:HA	1:A:660:ALA:O	2.10	0.52
1:A:798:TYR:HA	1:A:850:GLN:O	2.10	0.51
1:A:607:THR:OG1	1:A:731:PRO:CD	2.49	0.51
1:A:620:MET:HG3	1:A:662:PRO:CD	2.38	0.51
1:A:616:GLN:C	1:A:618:LYS:N	2.67	0.50
1:A:764:GLU:OE1	1:A:777:PHE:HB3	2.11	0.50
1:A:600:PHE:CD2	1:A:601:GLN:N	2.79	0.50
1:A:637:LYS:HA	2:A:903:IOD:I	2.81	0.50
1:A:661:ALA:HB1	1:A:662:PRO:HD2	1.94	0.49
1:A:806:ALA:O	1:A:818:VAL:HG23	2.12	0.49
1:A:668:ASP:C	1:A:670:THR:H	2.20	0.49
1:A:744:ASN:OD1	1:A:851:PRO:HG3	2.12	0.49
1:A:616:GLN:HA	1:A:662:PRO:HB3	1.95	0.49
1:A:806:ALA:O	1:A:818:VAL:CA	2.55	0.48
1:A:850:GLN:OE1	1:A:851:PRO:HD3	2.13	0.48
1:A:608:ASP:CB	1:A:731:PRO:CG	2.91	0.48
1:A:740:ILE:HB	1:A:846:GLN:HG3	1.94	0.48
1:A:684:TYR:OH	1:A:686:GLY:HA2	2.14	0.48
1:A:601:GLN:HB3	1:A:724:THR:HG22	1.95	0.47
1:A:642:THR:OG1	1:A:645:ASP:HB2	2.13	0.47
1:A:687:THR:HG23	1:A:689:ASP:HB2	1.96	0.47
1:A:630:ASN:HA	1:A:653:TYR:CD1	2.49	0.47
1:A:705:PRO:HB3	1:A:710:SER:CB	2.44	0.47
1:A:601:GLN:CB	1:A:724:THR:HG22	2.44	0.47
1:A:741:LYS:HD2	1:A:741:LYS:HA	1.69	0.47
1:A:684:TYR:O	1:A:694:GLY:HA2	2.16	0.46
1:A:703:LEU:HB2	1:A:711:ASP:C	2.41	0.46
1:A:608:ASP:C	1:A:610:THR:H	2.23	0.45
1:A:605:LYS:HB3	1:A:728:TYR:CE1	2.51	0.44
1:A:598:TYR:CE2	1:A:721:GLN:HB2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:741:LYS:HB2	1:A:768:SER:OG	2.17	0.44
1:A:748:TYR:HB3	1:A:770:ALA:HA	2.00	0.44
1:A:738:ARG:O	1:A:844:THR:HA	2.18	0.44
1:A:658:GLU:OE2	1:A:667:LEU:HA	2.17	0.44
1:A:703:LEU:HB2	1:A:711:ASP:O	2.18	0.43
1:A:666:GLN:CB	2:A:904:IOD:I	3.17	0.43
1:A:737:LEU:HD12	1:A:843:ILE:O	2.19	0.43
1:A:607:THR:C	1:A:609:GLY:H	2.26	0.42
1:A:598:TYR:O	1:A:648:ALA:HA	2.20	0.42
1:A:738:ARG:HH21	1:A:844:THR:HG21	1.84	0.42
1:A:756:LEU:HB2	1:A:777:PHE:CD2	2.54	0.42
1:A:779:THR:O	1:A:779:THR:OG1	2.29	0.42
1:A:749:LEU:HD12	1:A:749:LEU:HA	1.91	0.41
1:A:607:THR:C	1:A:609:GLY:N	2.78	0.41
1:A:766:ILE:HG12	1:A:777:PHE:CE2	2.56	0.41
1:A:703:LEU:HD12	1:A:712:ASP:HA	2.01	0.41
1:A:737:LEU:HA	1:A:843:ILE:O	2.20	0.41
1:A:850:GLN:OE1	1:A:851:PRO:CD	2.69	0.41
1:A:752:ALA:HB2	1:A:795:PRO:HB3	2.02	0.41
1:A:676:LEU:HD12	1:A:677:THR:H	1.86	0.40
1:A:616:GLN:O	1:A:620:MET:HB2	2.22	0.40
1:A:684:TYR:CZ	1:A:686:GLY:HA2	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	254/292 (87%)	232 (91%)	22 (9%)	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	131/240 (55%)	112 (86%)	19 (14%)	3 13

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	604	LYS
1	A	605	LYS
1	A	620	MET
1	A	638	THR
1	A	639	ASN
1	A	641	ILE
1	A	645	ASP
1	A	663	THR
1	A	693	SER
1	A	695	SER
1	A	697	ILE
1	A	702	THR
1	A	716	THR
1	A	724	THR
1	A	736	THR
1	A	741	LYS
1	A	764	GLU
1	A	818	VAL
1	A	845	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	742	GLN

5.3.3 RNA ⓘ

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](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	258/292 (88%)	1.20	60 (23%) 2 3	94, 148, 197, 225	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	845	LEU	6.1
1	A	672	TYR	6.0
1	A	739	VAL	5.7
1	A	623	ASN	5.6
1	A	778	ALA	5.3
1	A	621	GLN	4.8
1	A	737	LEU	4.6
1	A	600	PHE	4.5
1	A	597	GLN	4.2
1	A	601	GLN	3.7
1	A	674	PHE	3.7
1	A	834	TYR	3.6
1	A	641	ILE	3.6
1	A	602	PHE	3.4
1	A	719	HIS	3.4
1	A	756	LEU	3.3
1	A	647	GLN	3.3
1	A	749	LEU	3.3
1	A	812	THR	3.3
1	A	624	LEU	3.2
1	A	640	ALA	3.2
1	A	802	PRO	2.9
1	A	799	GLN	2.9
1	A	632	PHE	2.8
1	A	713	PHE	2.8
1	A	855	LEU	2.8
1	A	662	PRO	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	843	ILE	2.7
1	A	720	GLN	2.6
1	A	701	GLN	2.6
1	A	704	ASN	2.6
1	A	846	GLN	2.6
1	A	654	TYR	2.6
1	A	639	ASN	2.6
1	A	779	THR	2.4
1	A	616	GLN	2.4
1	A	606	THR	2.4
1	A	610	THR	2.4
1	A	663	THR	2.4
1	A	691	VAL	2.4
1	A	729	ASP	2.4
1	A	784	ASP	2.3
1	A	603	GLN	2.3
1	A	628	SER	2.3
1	A	740	ILE	2.3
1	A	712	ASP	2.3
1	A	856	PRO	2.3
1	A	816	ALA	2.3
1	A	811	THR	2.3
1	A	815	GLU	2.3
1	A	782	VAL	2.2
1	A	620	MET	2.1
1	A	622	PHE	2.1
1	A	781	LEU	2.1
1	A	830	SER	2.1
1	A	818	VAL	2.1
1	A	648	ALA	2.0
1	A	656	ILE	2.0
1	A	803	ALA	2.0
1	A	651	PRO	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

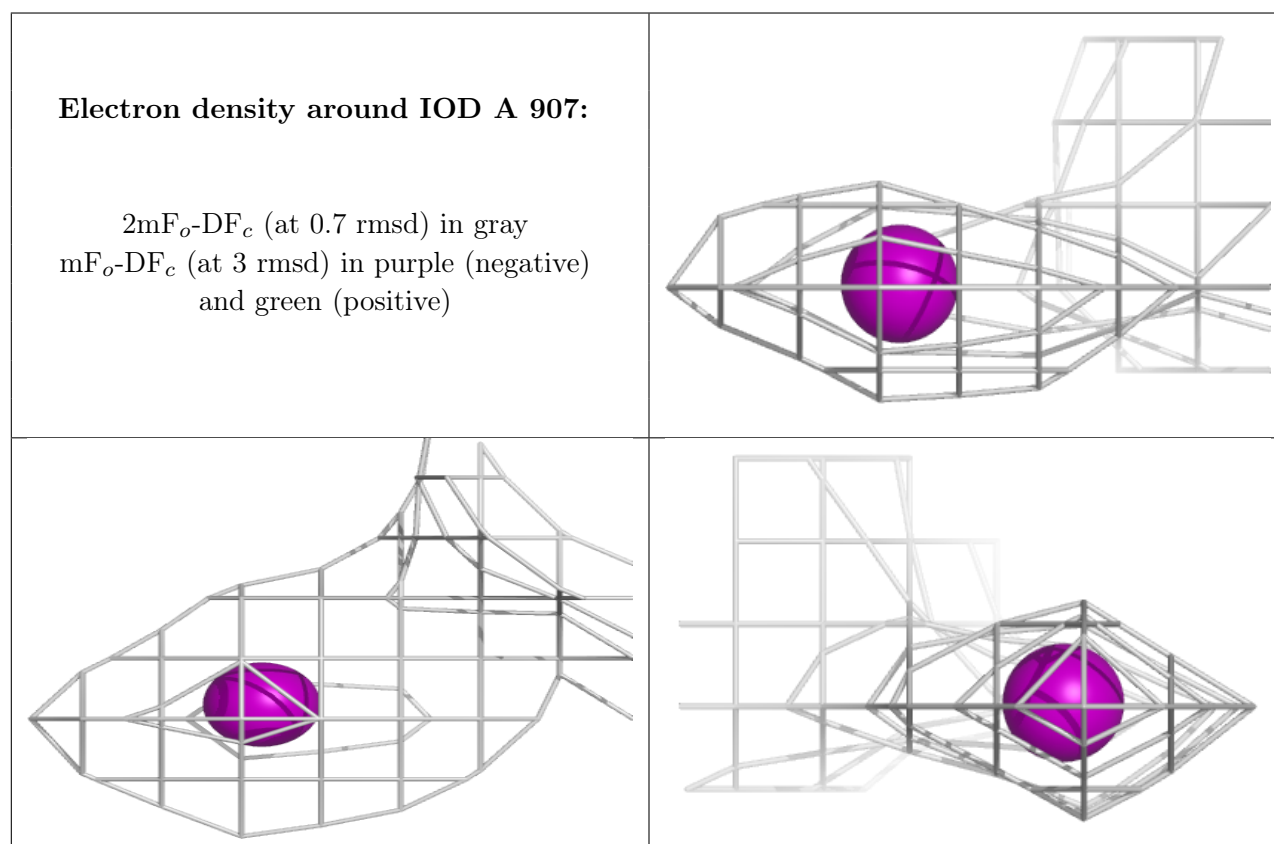
There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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

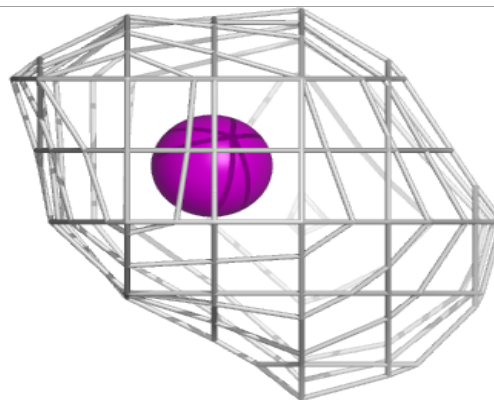
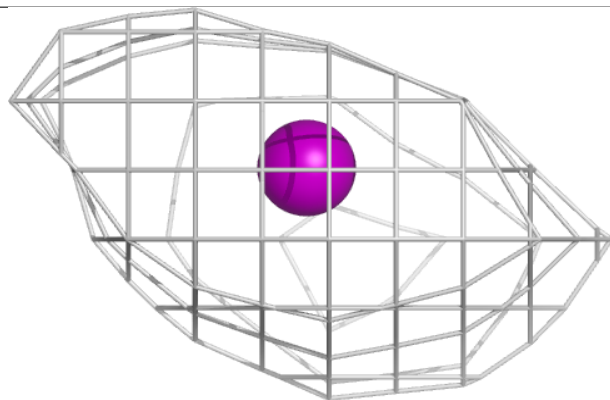
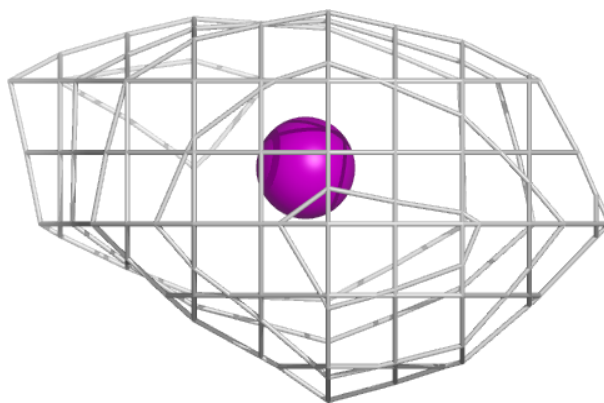
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	IOD	A	907	1/1	0.69	0.21	129,129,129,129	1
2	IOD	A	906	1/1	0.81	0.17	135,135,135,135	1
2	IOD	A	902	1/1	0.83	0.21	131,131,131,131	1
2	IOD	A	903	1/1	0.91	0.13	124,124,124,124	1
2	IOD	A	901	1/1	0.93	0.29	123,123,123,123	0
2	IOD	A	904	1/1	0.94	0.12	143,143,143,143	1

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.



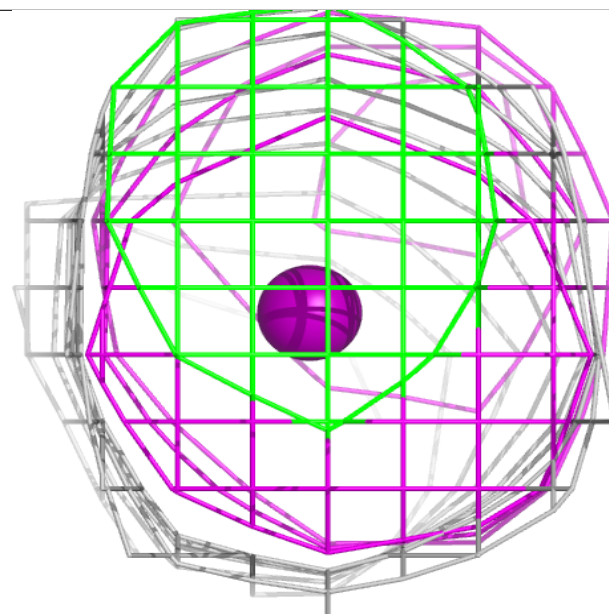
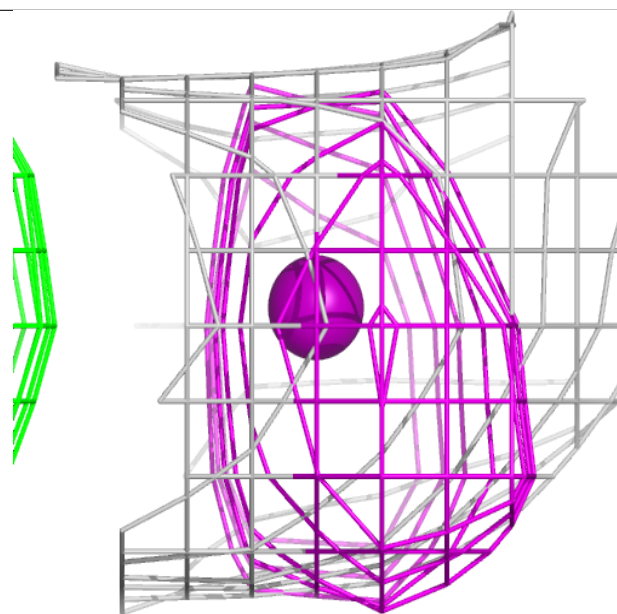
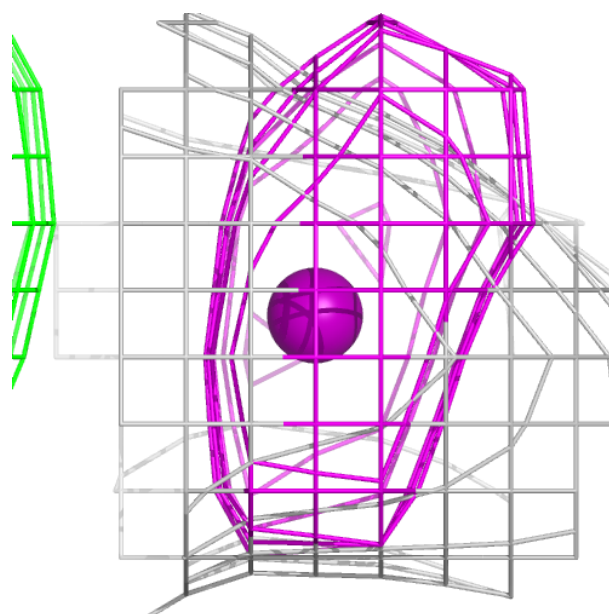
Electron density around IOD A 906:

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



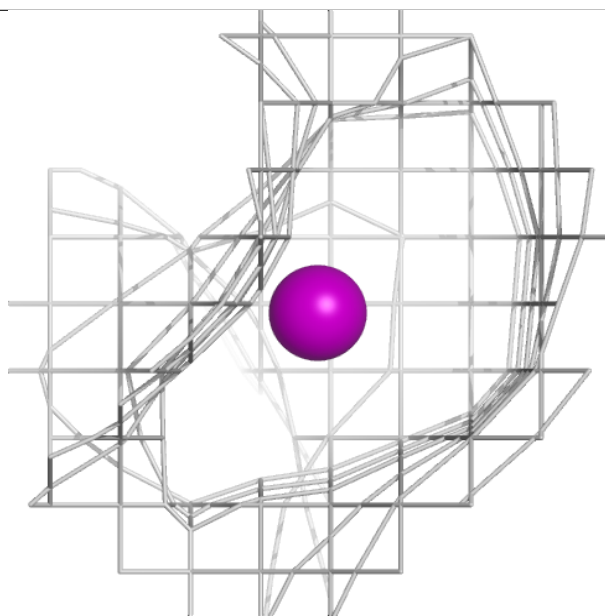
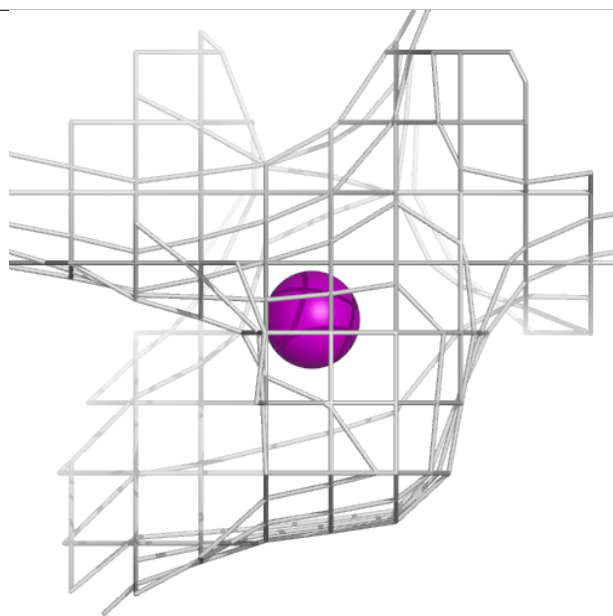
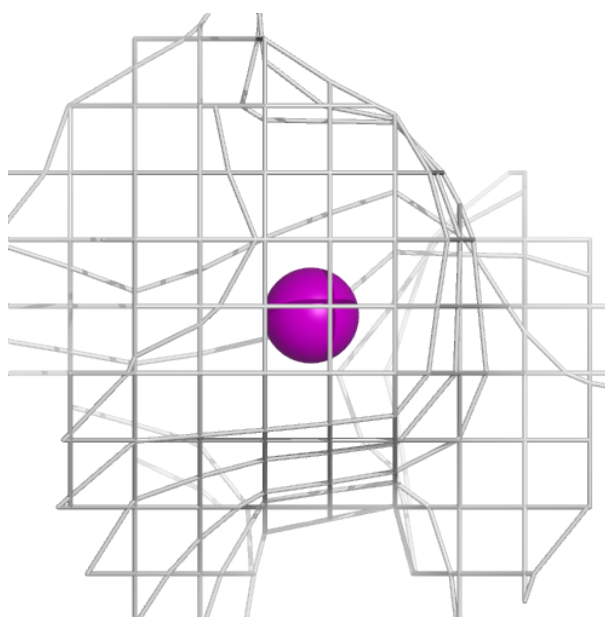
Electron density around IOD A 902:

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



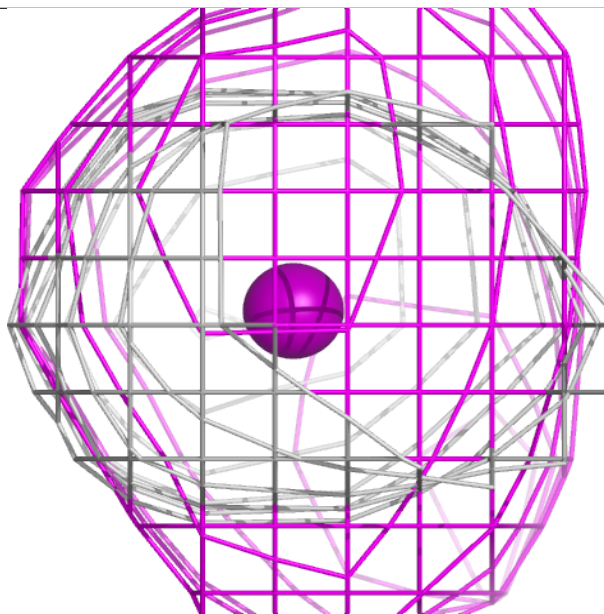
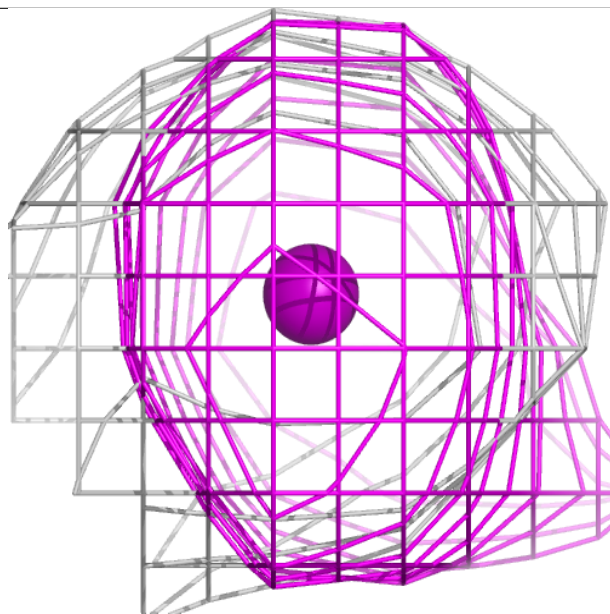
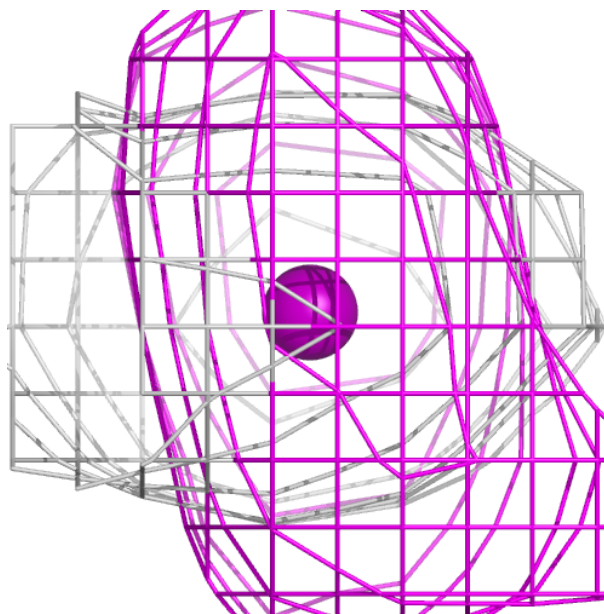
Electron density around IOD A 903:

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



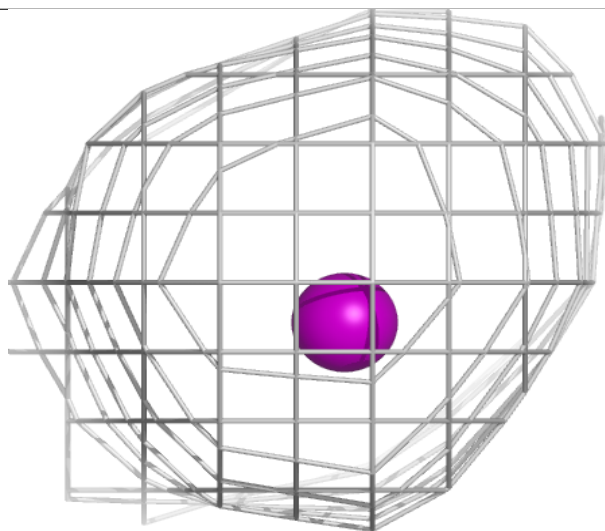
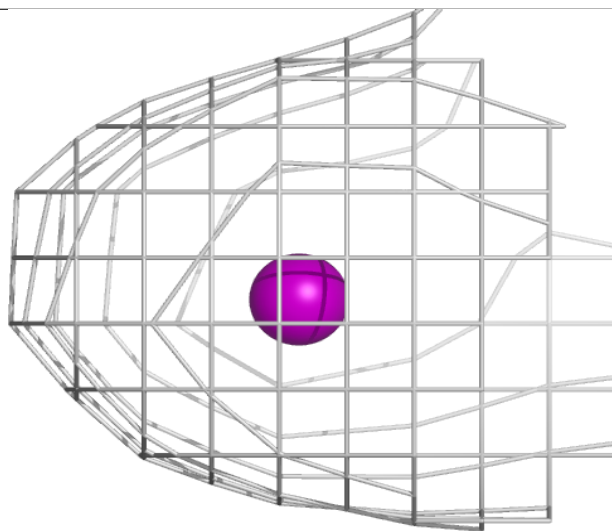
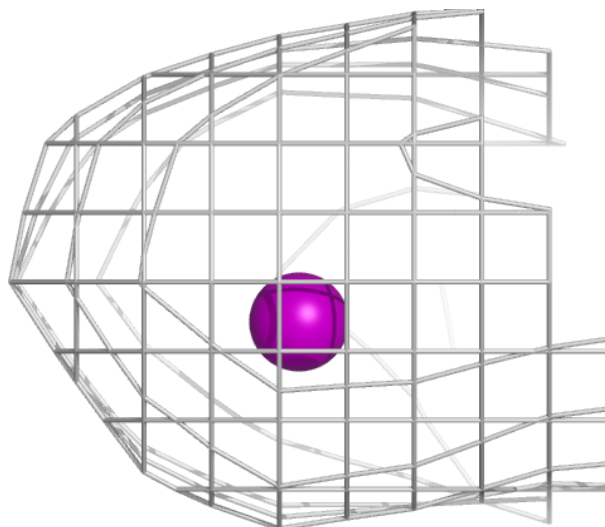
Electron density around IOD A 901:

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



Electron density around IOD A 904:

$2mF_o-DF_c$ (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.