



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 02:47 PM GMT

PDB ID : 3JWQ
Title : Crystal structure of chimeric PDE5/PDE6 catalytic domain complexed with sildenafil
Authors : Barren, B.; Gakhar, L.; Muradov, H.; Boyd, K.K.; Ramaswamy, S.; Artemyev, N.O.
Deposited on : 2009-09-18
Resolution : 2.87 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

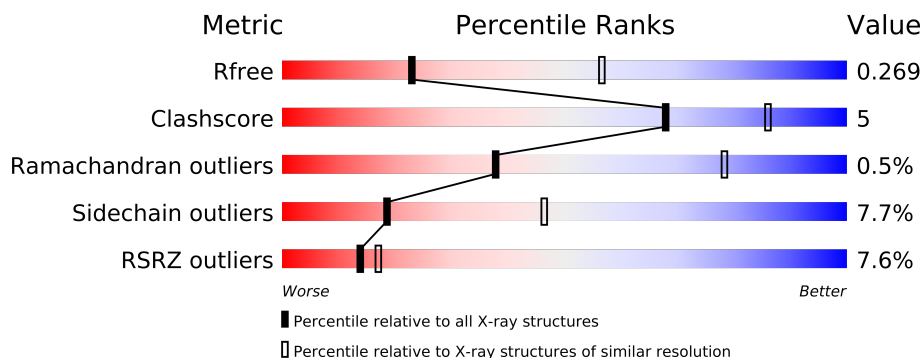
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.87 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}	66092	1360 (2.90-2.86)
Clashscore	79885	1696 (2.90-2.86)
Ramachandran outliers	78287	1647 (2.90-2.86)
Sidechain outliers	78261	1650 (2.90-2.86)
RSRZ outliers	66119	1362 (2.90-2.86)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	330	
1	B	330	
1	C	330	
1	D	330	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	ZN	D	899	-	X
3	MG	A	900	-	X
3	MG	C	900	-	X
3	MG	D	900	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
4	VIA	B	901	-	X
4	VIA	C	901	-	X
4	VIA	D	901	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10723 atoms, of which 0 are hydrogen and 0 are deuterium.

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 cGMP-specific 3',5'-cyclic phosphodiesterase catalytic domain, Cone cGMP-specific 3',5'-cyclic phosphodiesterase subunit alpha chimera.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	324	Total	C	N	O	S	0	0	0
			2638	1681	459	480	18			
1	B	324	Total	C	N	O	S	0	0	0
			2638	1681	459	480	18			
1	C	327	Total	C	N	O	S	0	0	0
			2665	1697	464	485	19			
1	D	323	Total	C	N	O	S	0	0	0
			2629	1676	458	477	18			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	531	GLY	-	EXPRESSION TAG	UNP O76074
A	532	SER	-	EXPRESSION TAG	UNP O76074
A	533	HIS	-	EXPRESSION TAG	UNP O76074
A	534	MET	-	EXPRESSION TAG	UNP O76074
B	531	GLY	-	EXPRESSION TAG	UNP O76074
B	532	SER	-	EXPRESSION TAG	UNP O76074
B	533	HIS	-	EXPRESSION TAG	UNP O76074
B	534	MET	-	EXPRESSION TAG	UNP O76074
C	531	GLY	-	EXPRESSION TAG	UNP O76074
C	532	SER	-	EXPRESSION TAG	UNP O76074
C	533	HIS	-	EXPRESSION TAG	UNP O76074
C	534	MET	-	EXPRESSION TAG	UNP O76074
D	531	GLY	-	EXPRESSION TAG	UNP O76074
D	532	SER	-	EXPRESSION TAG	UNP O76074
D	533	HIS	-	EXPRESSION TAG	UNP O76074
D	534	MET	-	EXPRESSION TAG	UNP O76074

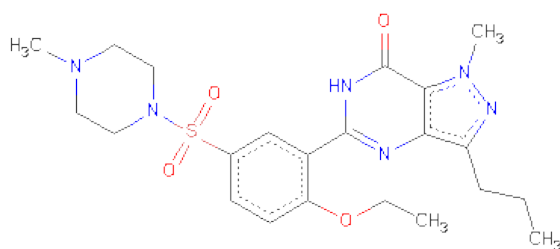
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Zn 1 1	0	0
2	A	1	Total Zn 1 1	0	0
2	D	1	Total Zn 1 1	0	0
2	C	1	Total Zn 1 1	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Mg 1 1	0	0
3	A	1	Total Mg 1 1	0	0
3	D	1	Total Mg 1 1	0	0
3	C	1	Total Mg 1 1	0	0

- Molecule 4 is 5-{2-ETHOXY-5-[(4-METHYLPIPERAZIN-1-YL)SULFONYL]PHENYL}-1-METHYL-3-PROPYL-1H,6H,7H-PYRAZOLO[4,3-D]PYRIMIDIN-7-ONE (three-letter code: VIA) (formula: C₂₂H₃₀N₆O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O S 33 22 6 4 1	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	S	0	0
			33	22	6	4	1		
4	C	1	Total	C	N	O	S	0	0
			33	22	6	4	1		
4	D	1	Total	C	N	O	S	0	0
			33	22	6	4	1		

- Molecule 5 is water.

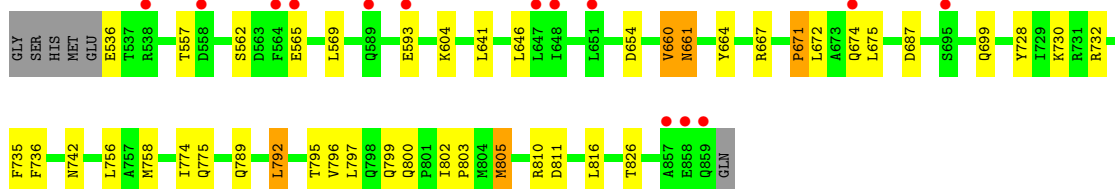
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	6	Total	O	0	0
			6	6		
5	B	3	Total	O	0	0
			3	3		
5	C	3	Total	O	0	0
			3	3		
5	D	1	Total	O	0	0
			1	1		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

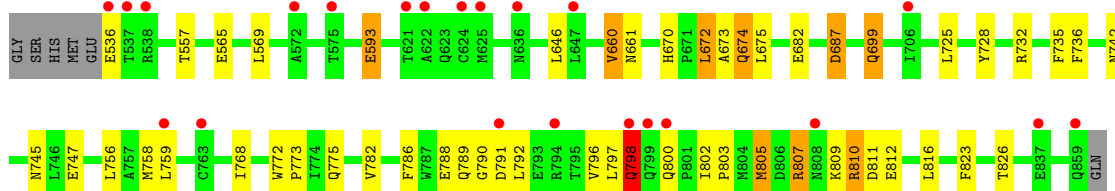
- Molecule 1: cGMP-specific 3',5'-cyclic phosphodiesterase catalytic domain, Cone cGMP-specific 3',5'-cyclic phosphodiesterase subunit alpha chimera

Chain A: 



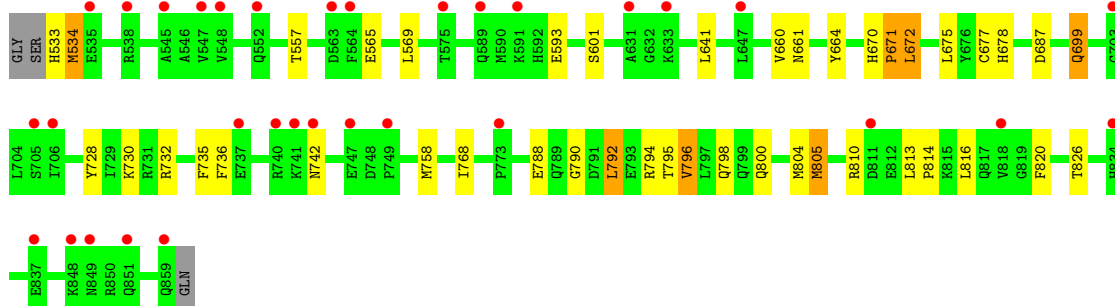
- Molecule 1: cGMP-specific 3',5'-cyclic phosphodiesterase catalytic domain, Cone cGMP-specific 3',5'-cyclic phosphodiesterase subunit alpha chimera

Chain B: 



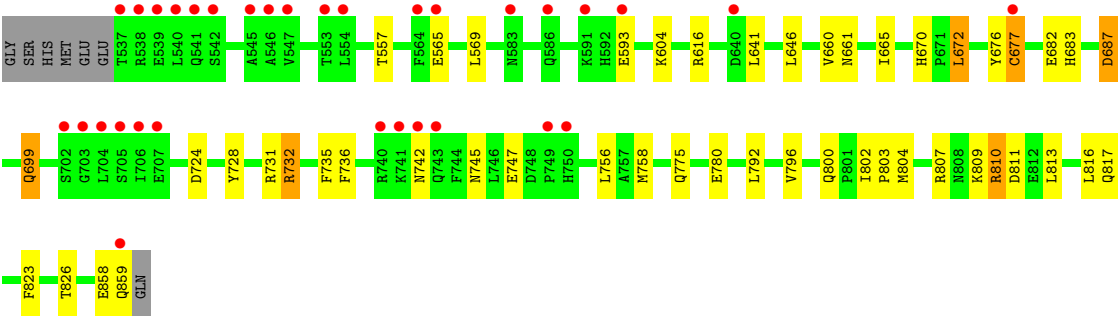
- Molecule 1: cGMP-specific 3',5'-cyclic phosphodiesterase catalytic domain, Cone cGMP-specific 3',5'-cyclic phosphodiesterase subunit alpha chimera

Chain C: 



- Molecule 1: cGMP-specific 3',5'-cyclic phosphodiesterase catalytic domain, Cone cGMP-specific 3',5'-cyclic phosphodiesterase subunit alpha chimera

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	75.73Å 109.83Å 199.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	23.08 – 2.87 23.08 – 2.87	Depositor EDS
% Data completeness (in resolution range)	86.7 (23.08-2.87) 86.8 (23.08-2.87)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 2.89Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.223 , 0.275 0.219 , 0.269	Depositor DCC
R_{free} test set	1655 reflections (5.18%)	DCC
Wilson B-factor (Å ²)	60.3	Xtriage
Anisotropy	0.148	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , -1.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Outliers	0 of 33596 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	10723	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.06% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, VIA, MG

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	0.79	0/2692	0.76	2/3640 (0.1%)
1	B	0.74	2/2692 (0.1%)	0.76	1/3640 (0.0%)
1	C	0.66	0/2720	0.72	1/3677 (0.0%)
1	D	0.67	1/2683 (0.0%)	0.71	2/3628 (0.1%)
All	All	0.72	3/10787 (0.0%)	0.74	6/14585 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	780	GLU	CG-CD	5.40	1.60	1.51
1	B	682	GLU	CG-CD	5.12	1.59	1.51
1	B	593	GLU	CG-CD	5.02	1.59	1.51

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	661	ASN	CB-CA-C	-7.37	95.66	110.40
1	D	661	ASN	CB-CA-C	-7.29	95.83	110.40
1	C	661	ASN	CB-CA-C	-6.96	96.47	110.40
1	A	661	ASN	CB-CA-C	-5.63	99.14	110.40
1	D	661	ASN	N-CA-C	5.42	125.62	111.00
1	A	654	ASP	CB-CG-OD1	5.07	122.86	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2638	0	2644	32	0
1	B	2638	0	2644	29	0
1	C	2665	0	2666	27	0
1	D	2629	0	2638	28	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	33	0	30	0	0
4	B	33	0	30	4	0
4	C	33	0	30	6	0
4	D	33	0	30	5	0
5	A	6	0	0	0	0
5	B	3	0	0	0	0
5	C	3	0	0	0	0
5	D	1	0	0	0	0
All	All	10723	0	10712	105	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

All (105) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:660:VAL:CG2	1:B:789:GLN:HG3	1.96	0.96
1:D:670:HIS:CE1	1:D:672:LEU:HD22	2.12	0.85
1:D:810:ARG:HG3	1:D:810:ARG:HH11	1.43	0.83
1:B:660:VAL:HG22	1:B:789:GLN:HG3	1.59	0.83
1:A:800:GLN:HG3	1:D:803:PRO:HD2	1.59	0.83
1:A:796:VAL:HG23	1:A:797:LEU:HG	1.59	0.82
4:D:901:VIA:H192	4:D:901:VIA:H8	1.63	0.78

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:792:LEU:O	1:A:796:VAL:HG22	1.85	0.76
1:C:813:LEU:HB3	1:C:814:PRO:HD3	1.71	0.73
1:A:796:VAL:CG2	1:A:797:LEU:HG	2.20	0.71
1:A:730:LYS:NZ	1:B:687:ASP:OD2	2.25	0.70
1:B:660:VAL:HG23	1:B:789:GLN:HG3	1.73	0.68
1:C:804:MET:HE1	4:C:901:VIA:H191	1.77	0.66
1:C:820:PHE:HD1	4:C:901:VIA:O11	1.79	0.66
1:C:820:PHE:CD1	4:C:901:VIA:H8	2.31	0.66
4:B:901:VIA:H192	1:C:795:THR:HA	1.79	0.64
1:A:660:VAL:CG2	1:A:789:GLN:HG3	2.28	0.63
1:A:730:LYS:CE	1:B:687:ASP:OD2	2.47	0.62
1:B:646:LEU:HD11	1:B:756:LEU:HD22	1.83	0.61
1:A:660:VAL:HG23	1:A:789:GLN:HG3	1.83	0.60
1:C:533:HIS:O	1:C:534:MET:CB	2.50	0.60
1:B:660:VAL:HG22	1:B:789:GLN:CG	2.31	0.59
1:C:820:PHE:CD1	4:C:901:VIA:C8	2.85	0.59
4:B:901:VIA:H311	4:B:901:VIA:O27	2.03	0.58
4:B:901:VIA:H152	4:B:901:VIA:H8	1.85	0.58
1:C:533:HIS:O	1:C:534:MET:HB2	2.03	0.57
1:B:735:PHE:CD2	1:B:758:MET:HG3	2.40	0.57
1:B:810:ARG:O	1:B:812:GLU:N	2.38	0.57
1:D:810:ARG:HG3	1:D:810:ARG:NH1	2.10	0.57
1:D:670:HIS:CE1	1:D:672:LEU:CD2	2.88	0.55
1:A:735:PHE:CD2	1:A:758:MET:HG3	2.41	0.55
1:C:804:MET:HE1	4:C:901:VIA:C19	2.36	0.55
1:A:646:LEU:HD11	1:A:756:LEU:HD22	1.88	0.55
1:D:728:TYR:CZ	1:D:732:ARG:HD3	2.42	0.54
1:C:678:HIS:HD2	1:D:677:CYS:SG	2.30	0.54
1:B:732:ARG:HD2	1:B:736:PHE:CE1	2.42	0.54
1:B:803:PRO:HD2	1:C:800:GLN:CG	2.38	0.54
1:A:800:GLN:CG	1:D:802:ILE:HB	2.38	0.53
1:B:728:TYR:CZ	1:B:732:ARG:HD3	2.43	0.52
1:C:670:HIS:ND1	1:C:672:LEU:HB2	2.23	0.52
1:A:730:LYS:HD2	1:B:675:LEU:HD21	1.91	0.52
1:A:796:VAL:HG23	1:A:797:LEU:CG	2.35	0.52
1:C:728:TYR:CZ	1:C:732:ARG:HD3	2.44	0.52
1:D:732:ARG:HD2	1:D:736:PHE:CE1	2.45	0.52
1:D:735:PHE:CD2	1:D:758:MET:HG3	2.45	0.51
1:C:735:PHE:CD2	1:C:758:MET:HG3	2.46	0.51
1:D:804:MET:HE1	4:D:901:VIA:H152	1.92	0.51
1:B:803:PRO:HD2	1:C:800:GLN:HG3	1.92	0.50
1:B:802:ILE:HB	1:C:800:GLN:HG2	1.94	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:786:PHE:O	1:B:805:MET:HG3	2.10	0.50
1:A:796:VAL:CG2	1:A:797:LEU:N	2.75	0.49
1:C:732:ARG:HD2	1:C:736:PHE:CE1	2.47	0.49
1:A:800:GLN:HG2	1:D:802:ILE:HB	1.94	0.49
1:B:823:PHE:HZ	1:C:792:LEU:HD13	1.77	0.48
1:A:792:LEU:HD13	1:D:823:PHE:HZ	1.79	0.48
1:A:796:VAL:HG23	1:A:797:LEU:N	2.28	0.47
1:B:791:ASP:OD2	1:B:807:ARG:NH1	2.48	0.47
1:A:671:PRO:O	1:A:674:GLN:HG2	2.14	0.47
1:C:790:GLY:HA3	1:C:805:MET:O	2.13	0.47
4:D:901:VIA:H192	4:D:901:VIA:C8	2.40	0.46
1:A:664:TYR:CE2	1:A:796:VAL:HG21	2.50	0.46
1:D:745:ASN:HD21	1:D:747:GLU:HB2	1.80	0.46
1:A:730:LYS:HE3	1:B:687:ASP:OD2	2.16	0.46
1:A:604:LYS:HE2	1:A:604:LYS:HB3	1.71	0.45
1:A:789:GLN:HB3	1:A:805:MET:HE2	1.99	0.45
1:B:797:LEU:O	1:B:798:GLN:C	2.56	0.45
1:D:670:HIS:HE1	1:D:672:LEU:HD22	1.78	0.45
1:A:728:TYR:CZ	1:A:732:ARG:HD3	2.52	0.44
1:A:796:VAL:HG23	1:A:797:LEU:CD2	2.46	0.44
1:C:670:HIS:CD2	1:C:671:PRO:HD2	2.53	0.44
1:B:782:VAL:CG1	4:B:901:VIA:H21	2.48	0.44
1:D:731:ARG:O	1:D:732:ARG:C	2.55	0.43
1:D:616:ARG:HA	1:D:616:ARG:HD3	1.81	0.43
1:B:790:GLY:HA3	1:B:805:MET:O	2.18	0.43
1:D:682:GLU:HG2	1:D:724:ASP:HB2	2.00	0.43
1:A:732:ARG:HD2	1:A:736:PHE:CE1	2.54	0.43
1:C:699:GLN:H	1:C:699:GLN:HG2	1.59	0.43
1:C:794:ARG:O	1:C:798:GLN:HA	2.19	0.43
1:D:699:GLN:H	1:D:699:GLN:HG2	1.57	0.43
1:D:817:GLN:OE1	4:D:901:VIA:O3	2.37	0.43
1:C:813:LEU:HB3	1:C:814:PRO:CD	2.45	0.43
1:A:660:VAL:HG22	1:A:789:GLN:HG3	2.00	0.43
1:B:670:HIS:ND1	1:B:672:LEU:HB2	2.34	0.42
1:B:768:ILE:HG13	1:B:768:ILE:O	2.20	0.42
1:A:800:GLN:CG	1:D:803:PRO:HD2	2.39	0.42
1:C:664:TYR:CE2	1:C:792:LEU:HB3	2.54	0.42
1:B:670:HIS:CE1	1:B:672:LEU:HD22	2.55	0.42
1:A:562:SER:HB2	1:A:774:ILE:HD11	2.02	0.42
1:D:858:GLU:O	1:D:859:GLN:HB2	2.20	0.41
1:C:796:VAL:O	1:C:796:VAL:CG2	2.67	0.41
1:B:699:GLN:HG2	1:B:699:GLN:H	1.54	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:536:GLU:C	1:A:536:GLU:OE1	2.58	0.41
4:C:901:VIA:H21	4:C:901:VIA:H5	1.93	0.41
1:B:745:ASN:HD21	1:B:747:GLU:HB2	1.85	0.41
1:B:673:ALA:HB3	1:B:674:GLN:HE21	1.86	0.41
1:D:604:LYS:HB3	1:D:604:LYS:HE2	1.76	0.41
1:A:800:GLN:HG3	1:D:802:ILE:HB	2.02	0.41
1:B:772:TRP:O	1:B:773:PRO:C	2.58	0.41
1:A:802:ILE:O	1:A:803:PRO:C	2.59	0.41
1:C:730:LYS:HE3	1:D:687:ASP:OD2	2.21	0.41
1:D:676:TYR:CD1	1:D:683:HIS:HB3	2.56	0.41
1:A:664:TYR:CE2	1:A:792:LEU:HB3	2.56	0.41
1:D:817:GLN:OE1	4:D:901:VIA:C4	2.69	0.40
1:C:768:ILE:O	1:C:768:ILE:HG13	2.22	0.40
1:D:646:LEU:HD11	1:D:756:LEU:HD22	2.03	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	322/330 (98%)	307 (95%)	15 (5%)	0	100	100
1	B	322/330 (98%)	308 (96%)	11 (3%)	3 (1%)	25	64
1	C	325/330 (98%)	310 (95%)	14 (4%)	1 (0%)	50	85
1	D	321/330 (97%)	307 (96%)	12 (4%)	2 (1%)	33	75
All	All	1290/1320 (98%)	1232 (96%)	52 (4%)	6 (0%)	38	78

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	811	ASP
1	C	534	MET
1	D	732	ARG
1	B	798	GLN

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Mol	Chain	Res	Type
1	B	810	ARG
1	D	677	CYS

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	290/295 (98%)	267 (92%)	23 (8%)	18	45
1	B	290/295 (98%)	266 (92%)	24 (8%)	16	42
1	C	293/295 (99%)	272 (93%)	21 (7%)	21	50
1	D	289/295 (98%)	267 (92%)	22 (8%)	19	47
All	All	1162/1180 (98%)	1072 (92%)	90 (8%)	18	46

All (90) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	557	THR
1	A	565	GLU
1	A	569	LEU
1	A	593	GLU
1	A	641	LEU
1	A	660	VAL
1	A	661	ASN
1	A	667	ARG
1	A	671	PRO
1	A	672	LEU
1	A	675	LEU
1	A	687	ASP
1	A	699	GLN
1	A	742	ASN
1	A	775	GLN
1	A	792	LEU
1	A	795	THR
1	A	799	GLN
1	A	805	MET
1	A	810	ARG

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Mol	Chain	Res	Type
1	A	811	ASP
1	A	816	LEU
1	A	826	THR
1	B	536	GLU
1	B	557	THR
1	B	565	GLU
1	B	569	LEU
1	B	593	GLU
1	B	660	VAL
1	B	672	LEU
1	B	674	GLN
1	B	687	ASP
1	B	699	GLN
1	B	725	LEU
1	B	742	ASN
1	B	759	LEU
1	B	775	GLN
1	B	788	GLU
1	B	792	LEU
1	B	796	VAL
1	B	798	GLN
1	B	800	GLN
1	B	805	MET
1	B	807	ARG
1	B	809	LYS
1	B	816	LEU
1	B	826	THR
1	C	557	THR
1	C	565	GLU
1	C	569	LEU
1	C	593	GLU
1	C	601	SER
1	C	641	LEU
1	C	660	VAL
1	C	671	PRO
1	C	672	LEU
1	C	675	LEU
1	C	677	CYS
1	C	687	ASP
1	C	699	GLN
1	C	742	ASN
1	C	788	GLU

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Mol	Chain	Res	Type
1	C	792	LEU
1	C	796	VAL
1	C	805	MET
1	C	810	ARG
1	C	816	LEU
1	C	826	THR
1	D	557	THR
1	D	565	GLU
1	D	569	LEU
1	D	593	GLU
1	D	641	LEU
1	D	660	VAL
1	D	665	ILE
1	D	672	LEU
1	D	687	ASP
1	D	699	GLN
1	D	742	ASN
1	D	775	GLN
1	D	792	LEU
1	D	796	VAL
1	D	800	GLN
1	D	807	ARG
1	D	809	LYS
1	D	810	ARG
1	D	811	ASP
1	D	813	LEU
1	D	816	LEU
1	D	826	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	541	GLN
1	A	586	GLN
1	A	661	ASN
1	A	678	HIS
1	A	742	ASN
1	A	745	ASN
1	B	541	GLN
1	B	586	GLN
1	B	661	ASN
1	B	666	GLN

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Mol	Chain	Res	Type
1	B	674	GLN
1	B	678	HIS
1	B	742	ASN
1	B	745	ASN
1	C	541	GLN
1	C	586	GLN
1	C	666	GLN
1	C	678	HIS
1	C	742	ASN
1	C	745	ASN
1	C	798	GLN
1	D	541	GLN
1	D	586	GLN
1	D	661	ASN
1	D	666	GLN
1	D	742	ASN
1	D	745	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 for Mogul analysis.

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
4	VIA	A	901	-	36,36,36	2.99	8 (22%)	49,53,53	2.88	18 (36%)
4	VIA	B	901	-	36,36,36	3.22	9 (25%)	49,53,53	2.34	15 (30%)
4	VIA	C	901	-	36,36,36	3.25	8 (22%)	49,53,53	2.81	13 (26%)
4	VIA	D	901	-	36,36,36	3.03	9 (25%)	49,53,53	2.29	19 (38%)

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	VIA	A	901	-	-	0/22/32/32	0/2/4/4
4	VIA	B	901	-	-	0/22/32/32	0/2/4/4
4	VIA	C	901	-	-	0/22/32/32	0/2/4/4
4	VIA	D	901	-	-	0/22/32/32	1/2/4/4

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	901	VIA	C9-C21	-10.19	1.38	1.49
4	C	901	VIA	N29-N28	-10.08	1.24	1.37
4	C	901	VIA	C9-C21	-9.85	1.38	1.49
4	A	901	VIA	N29-N28	-9.85	1.24	1.37
4	D	901	VIA	N29-N28	-9.77	1.24	1.37
4	B	901	VIA	N29-N28	-9.63	1.24	1.37
4	D	901	VIA	C9-C21	-9.31	1.39	1.49
4	A	901	VIA	C9-C21	-8.49	1.40	1.49
4	C	901	VIA	S10-N14	7.99	1.75	1.63
4	A	901	VIA	O12-S10	6.87	1.52	1.43
4	A	901	VIA	O11-S10	6.79	1.52	1.43
4	B	901	VIA	O11-S10	6.35	1.51	1.43
4	D	901	VIA	O12-S10	5.87	1.51	1.43
4	B	901	VIA	S10-N14	5.83	1.72	1.63
4	D	901	VIA	S10-N14	5.66	1.72	1.63
4	D	901	VIA	O11-S10	5.49	1.50	1.43
4	B	901	VIA	O12-S10	5.24	1.50	1.43
4	C	901	VIA	O11-S10	5.21	1.50	1.43
4	B	901	VIA	C21-N22	5.14	1.43	1.34
4	C	901	VIA	O12-S10	4.67	1.49	1.43
4	D	901	VIA	C21-N22	4.26	1.42	1.34
4	C	901	VIA	C21-N22	4.15	1.42	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	901	VIA	C31-N28	3.90	1.52	1.46
4	C	901	VIA	C15-N14	3.70	1.52	1.47
4	A	901	VIA	C21-N22	3.58	1.41	1.34
4	B	901	VIA	C24-N28	-3.13	1.32	1.37
4	B	901	VIA	C7-S10	-3.06	1.71	1.76
4	D	901	VIA	C21-N26	2.71	1.37	1.32
4	C	901	VIA	C23-N22	2.66	1.41	1.37
4	A	901	VIA	C15-N14	2.52	1.50	1.47
4	D	901	VIA	C31-N28	2.27	1.50	1.46
4	D	901	VIA	C23-N22	2.23	1.41	1.37
4	B	901	VIA	C8-C9	-2.07	1.36	1.39
4	A	901	VIA	S10-N14	2.00	1.66	1.63

All (65) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	901	VIA	C16-C15-N14	10.10	117.01	109.02
4	A	901	VIA	O12-S10-N14	8.28	115.15	106.71
4	A	901	VIA	C16-C15-N14	7.86	115.24	109.02
4	A	901	VIA	O12-S10-O11	-7.20	106.53	119.38
4	B	901	VIA	O11-S10-N14	6.98	113.82	106.71
4	D	901	VIA	C30-N29-N28	6.87	110.41	104.48
4	C	901	VIA	C30-N29-N28	6.74	110.29	104.48
4	C	901	VIA	C16-N17-C18	6.60	118.75	109.54
4	B	901	VIA	C30-N29-N28	6.27	109.89	104.48
4	A	901	VIA	C30-N29-N28	6.06	109.70	104.48
4	C	901	VIA	C7-S10-N14	5.91	114.79	107.29
4	C	901	VIA	O12-S10-O11	-5.90	108.86	119.38
4	D	901	VIA	C7-S10-N14	5.64	114.46	107.29
4	A	901	VIA	C15-N14-S10	-5.60	106.82	117.00
4	B	901	VIA	C31-N28-N29	4.90	126.20	120.78
4	B	901	VIA	O12-S10-O11	-4.77	110.87	119.38
4	D	901	VIA	C15-C16-N17	-4.68	105.66	110.82
4	A	901	VIA	C19-N14-S10	-4.62	108.60	117.00
4	C	901	VIA	O12-S10-N14	4.53	111.33	106.71
4	A	901	VIA	C18-C19-N14	3.98	112.17	109.02
4	C	901	VIA	C15-N14-S10	-3.88	109.94	117.00
4	A	901	VIA	C21-N26-C25	3.86	120.49	116.33
4	D	901	VIA	C21-N26-C25	3.80	120.42	116.33
4	B	901	VIA	O3-C4-C9	3.46	121.02	116.09
4	D	901	VIA	C16-C15-N14	-3.42	106.31	109.02
4	C	901	VIA	C19-C18-N17	3.38	114.55	110.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	901	VIA	C7-S10-N14	3.35	111.55	107.29
4	D	901	VIA	O12-S10-N14	3.28	110.06	106.71
4	B	901	VIA	C21-N26-C25	3.24	119.82	116.33
4	A	901	VIA	C31-N28-N29	3.23	124.36	120.78
4	D	901	VIA	O12-S10-O11	-3.15	113.76	119.38
4	D	901	VIA	C24-C25-N26	-3.12	120.11	125.85
4	D	901	VIA	C30-C25-N26	3.07	135.39	125.50
4	D	901	VIA	O3-C4-C9	2.99	120.35	116.09
4	B	901	VIA	C8-C7-S10	-2.97	115.80	119.43
4	C	901	VIA	C15-C16-N17	2.96	114.09	110.82
4	A	901	VIA	C30-C25-N26	2.96	135.03	125.50
4	C	901	VIA	C21-N26-C25	2.93	119.49	116.33
4	A	901	VIA	C24-C25-N26	-2.92	120.46	125.85
4	C	901	VIA	C6-C7-S10	2.88	123.00	119.80
4	A	901	VIA	C8-C7-S10	2.82	122.87	119.43
4	D	901	VIA	C31-N28-N29	2.81	123.89	120.78
4	A	901	VIA	N22-C21-N26	-2.65	119.80	122.70
4	D	901	VIA	C18-C19-N14	2.63	111.10	109.02
4	A	901	VIA	C9-C21-N26	2.63	123.32	117.87
4	B	901	VIA	C15-C16-N17	-2.57	107.98	110.82
4	B	901	VIA	O12-S10-N14	2.57	109.33	106.71
4	B	901	VIA	C30-C25-N26	2.57	133.76	125.50
4	B	901	VIA	O12-S10-C7	2.55	111.33	107.94
4	D	901	VIA	O11-S10-C7	-2.53	104.58	107.94
4	B	901	VIA	C24-C25-N26	-2.52	121.22	125.85
4	C	901	VIA	C18-C19-N14	2.47	110.98	109.02
4	D	901	VIA	C19-C18-N17	2.47	113.55	110.82
4	B	901	VIA	C9-C21-N22	2.45	122.26	118.06
4	A	901	VIA	O11-S10-C7	2.35	111.06	107.94
4	C	901	VIA	C8-C9-C4	2.32	120.66	118.17
4	D	901	VIA	C8-C9-C4	2.31	120.65	118.17
4	B	901	VIA	C31-N28-C24	-2.28	121.51	125.00
4	A	901	VIA	C6-C7-S10	-2.26	117.29	119.80
4	D	901	VIA	C23-C24-C25	2.22	121.52	119.92
4	D	901	VIA	C30-C25-C24	-2.17	104.48	109.16
4	A	901	VIA	C30-C25-C24	-2.16	104.50	109.16
4	B	901	VIA	C6-C7-S10	2.15	122.19	119.80
4	D	901	VIA	C15-N14-C19	-2.13	109.53	112.16
4	D	901	VIA	C33-C32-C30	-2.01	107.41	115.48

There are no chirality outliers.

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	901	VIA	C15-C16-C18-C19-N14-N17

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	324/330 (98%)	0.33	14 (4%)	34 41	14, 22, 32, 43	0
1	B	324/330 (98%)	0.45	22 (6%)	17 21	14, 22, 32, 43	0
1	C	327/330 (99%)	0.41	32 (9%)	8 10	14, 22, 32, 43	0
1	D	323/330 (97%)	0.37	32 (9%)	8 10	14, 22, 32, 43	0
All	All	1298/1320 (98%)	0.39	100 (7%)	14 16	14, 22, 32, 43	0

All (100) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	798	GLN	5.4
1	D	706	ILE	4.5
1	D	538	ARG	4.3
1	C	547	VAL	4.2
1	C	631	ALA	4.1
1	A	538	ARG	4.1
1	A	859	GLN	4.0
1	D	740	ARG	3.8
1	B	537	THR	3.8
1	D	677	CYS	3.5
1	C	747	GLU	3.5
1	C	703	GLY	3.5
1	D	705	SER	3.5
1	C	740	ARG	3.4
1	D	564	PHE	3.3
1	B	538	ARG	3.3
1	B	636	ASN	3.3
1	D	547	VAL	3.3
1	D	539	GLU	3.2
1	B	763	CYS	3.2
1	B	536	GLU	3.2

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Mol	Chain	Res	Type	RSRZ
1	C	859	GLN	3.1
1	C	548	VAL	3.1
1	A	674	GLN	3.1
1	C	705	SER	3.1
1	D	545	ALA	3.1
1	C	837	GLU	3.1
1	D	749	PRO	3.0
1	C	575	THR	3.0
1	C	552	GLN	3.0
1	A	647	LEU	3.0
1	C	851	GLN	3.0
1	C	591	LYS	2.9
1	D	702	SER	2.9
1	D	565	GLU	2.9
1	D	707	GLU	2.9
1	C	706	ILE	2.9
1	A	651	LEU	2.9
1	B	759	LEU	2.8
1	C	589	GLN	2.8
1	C	538	ARG	2.8
1	C	564	PHE	2.7
1	C	737	GLU	2.7
1	D	541	GLN	2.7
1	D	704	LEU	2.7
1	B	647	LEU	2.6
1	D	750	HIS	2.6
1	A	589	GLN	2.6
1	D	586	GLN	2.6
1	B	624	CYS	2.6
1	D	554	LEU	2.6
1	D	546	ALA	2.6
1	C	742	ASN	2.6
1	B	706	ILE	2.5
1	D	743	GLN	2.5
1	B	625	MET	2.5
1	B	622	ALA	2.4
1	A	593	GLU	2.4
1	C	545	ALA	2.4
1	A	648	ILE	2.4
1	A	857	ALA	2.4
1	B	575	THR	2.4
1	B	791	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	811	ASP	2.4
1	D	591	LYS	2.4
1	A	565	GLU	2.4
1	D	742	ASN	2.4
1	C	749	PRO	2.4
1	D	542	SER	2.3
1	A	695	SER	2.3
1	C	741	LYS	2.3
1	D	540	LEU	2.3
1	C	834	HIS	2.3
1	B	621	THR	2.3
1	B	859	GLN	2.3
1	C	633	LYS	2.3
1	A	564	PHE	2.3
1	C	773	PRO	2.3
1	B	799	GLN	2.3
1	D	859	GLN	2.2
1	D	537	THR	2.2
1	A	558	ASP	2.2
1	C	647	LEU	2.2
1	C	535	GLU	2.2
1	D	593	GLU	2.2
1	C	563	ASP	2.2
1	D	703	GLY	2.2
1	C	848	LYS	2.2
1	A	858	GLU	2.2
1	B	808	ASN	2.1
1	B	794	ARG	2.1
1	D	640	ASP	2.1
1	D	553	THR	2.1
1	D	583	ASN	2.1
1	B	837	GLU	2.1
1	D	741	LYS	2.1
1	C	849	ASN	2.0
1	C	818	VAL	2.0
1	B	800	GLN	2.0
1	B	572	ALA	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	MG	D	900	1/1	0.56	9.51	54,54,54,54	0
3	MG	C	900	1/1	0.35	7.83	28,28,28,28	0
3	MG	A	900	1/1	0.38	7.70	17,17,17,17	0
4	VIA	B	901	33/33	0.42	6.74	47,52,64,66	0
4	VIA	D	901	33/33	0.37	5.29	42,48,56,59	0
2	ZN	D	899	1/1	0.22	3.96	42,42,42,42	0
4	VIA	C	901	33/33	0.34	3.09	61,65,78,79	0
3	MG	B	900	1/1	0.26	1.98	29,29,29,29	0
4	VIA	A	901	33/33	0.27	1.43	36,40,60,62	0
2	ZN	C	899	1/1	0.21	1.24	50,50,50,50	0
2	ZN	A	899	1/1	0.24	0.89	28,28,28,28	0
2	ZN	B	899	1/1	0.21	0.17	34,34,34,34	0

6.5 Other polymers ⓘ

There are no such residues in this entry.