WORLDWIDE PDB

PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report ⓘ

Aug 8, 2020 – 05:06 AM BST

PDB ID	:	1RPT
Title	:	CRYSTAL STRUCTURES OF RAT ACID PHOSPHATASE COMPLEXED WITH THE TRANSITIONS STATE ANALOGS VANADATE AND MOLYBDATE: IMPLICATIONS FOR THE REACTION MECHANISM
Authors	:	Lindqvist, Y.; Schneider, G.
Deposited on	:	1993-11-29
Resolution	:	3.00 Å(reported)

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

|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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.
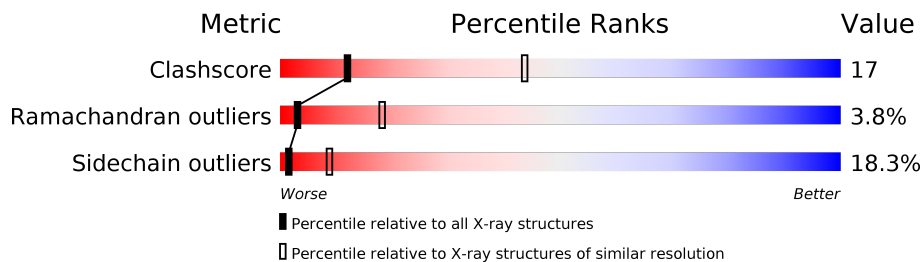
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)

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 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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	342	44% 37% 15% •
2	B	3	33% 67%

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
4	VO4	A	343	-	-	X	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2852 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 PROSTATIC ACID PHOSPHATASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	342	2794	1793	468	517	16	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	97	ASN	ILE	conflict	UNP P20646
A	191	LEU	PHE	conflict	UNP P20646
A	192	PRO	ARG	conflict	UNP P20646
A	257	HIS	TYR	conflict	UNP P20646
A	269	ASP	GLU	conflict	UNP P20646
A	270	VAL	LEU	conflict	UNP P20646
A	293	HIS	THR	conflict	UNP P20646

- Molecule 2 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	3	39	22	2	15	0	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is VANADATE ION (three-letter code: VO4) (formula: O_4V).
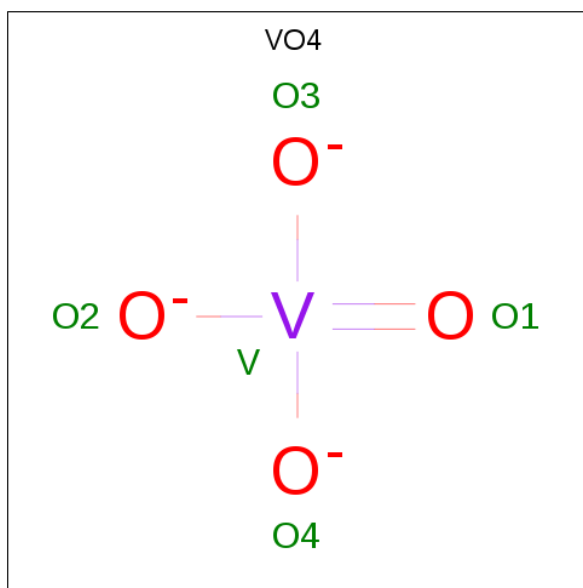
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	V	0	0
			5	4	1		

3 Residue-property plots ⓘ

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. 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. 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.

Note EDS was not executed.

• Molecule 1: PROSTATIC ACID PHOSPHATASE

Chain A:
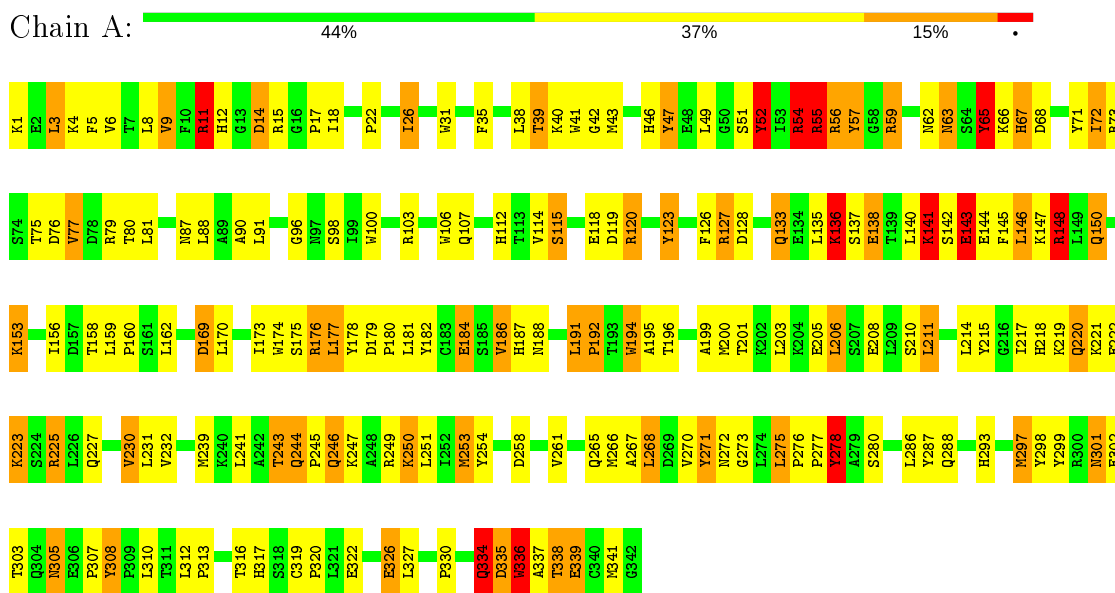
• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:

Full wwPDB X-ray Structure Validation Report

4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	89.40Å 89.40Å 152.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	(Not available) – 3.00	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-3.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.215 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2852	wwPDB-VP
Average B, all atoms (Å^2)	16.0	wwPDB-VP

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: VO4, BMA, NAG

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	1.26	5/2873 (0.2%)	2.10	108/3898 (2.8%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	6

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	31	TRP	CG-CD2	-5.73	1.33	1.43
1	A	127	ARG	NE-CZ	5.71	1.40	1.33
1	A	59	ARG	CZ-NH1	5.50	1.40	1.33
1	A	51	SER	CA-CB	-5.41	1.44	1.52
1	A	31	TRP	CD1-NE1	-5.11	1.29	1.38

All (108) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	127	ARG	NE-CZ-NH1	15.47	128.03	120.30
1	A	47	TYR	CB-CG-CD1	-14.15	112.51	121.00
1	A	55	ARG	NE-CZ-NH1	13.38	126.99	120.30
1	A	31	TRP	CD1-CG-CD2	11.89	115.81	106.30
1	A	103	ARG	NE-CZ-NH1	11.15	125.87	120.30
1	A	54	ARG	NE-CZ-NH1	10.66	125.63	120.30
1	A	194	TRP	CD1-CG-CD2	10.57	114.75	106.30
1	A	59	ARG	NE-CZ-NH2	-10.01	115.30	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	41	TRP	CD1-CG-CD2	9.49	113.89	106.30
1	A	41	TRP	CG-CD2-CE3	9.45	142.41	133.90
1	A	194	TRP	CE2-CD2-CG	-8.82	100.24	107.30
1	A	31	TRP	CE2-CD2-CG	-8.71	100.33	107.30
1	A	57	TYR	CB-CG-CD2	-8.12	116.13	121.00
1	A	59	ARG	NE-CZ-NH1	7.96	124.28	120.30
1	A	55	ARG	NE-CZ-NH2	-7.82	116.39	120.30
1	A	253	MET	CG-SD-CE	-7.70	87.88	100.20
1	A	41	TRP	CE2-CD2-CG	-7.68	101.16	107.30
1	A	120	ARG	NE-CZ-NH2	-7.62	116.49	120.30
1	A	336	TRP	CD1-CG-CD2	7.61	112.39	106.30
1	A	192	PRO	CA-C-N	-7.59	100.50	117.20
1	A	31	TRP	CG-CD1-NE1	-7.37	102.73	110.10
1	A	41	TRP	CB-CG-CD1	-7.36	117.43	127.00
1	A	136	LYS	CA-CB-CG	7.31	129.49	113.40
1	A	194	TRP	CG-CD2-CE3	7.25	140.42	133.90
1	A	230	VAL	CA-CB-CG1	-7.24	100.04	110.90
1	A	184	GLU	CA-CB-CG	7.22	129.28	113.40
1	A	150	GLN	CA-CB-CG	-7.18	97.61	113.40
1	A	301	ASN	CA-C-N	7.17	132.97	117.20
1	A	243	THR	CA-CB-CG2	-7.12	102.43	112.40
1	A	336	TRP	CG-CD2-CE3	7.04	140.23	133.90
1	A	107	GLN	CA-CB-CG	6.97	128.74	113.40
1	A	194	TRP	CB-CG-CD1	-6.97	117.94	127.00
1	A	6	VAL	CA-CB-CG2	-6.91	100.53	110.90
1	A	76	ASP	CB-CG-OD2	-6.85	112.14	118.30
1	A	176	ARG	CB-CG-CD	6.83	129.35	111.60
1	A	71	TYR	CB-CG-CD1	-6.82	116.91	121.00
1	A	250	LYS	CB-CG-CD	-6.82	93.88	111.60
1	A	100	TRP	CE2-CD2-CG	-6.80	101.86	107.30
1	A	112	HIS	CA-C-N	6.75	132.05	117.20
1	A	336	TRP	CE2-CD2-CG	-6.61	102.01	107.30
1	A	100	TRP	CD1-CG-CD2	6.60	111.58	106.30
1	A	278	TYR	CB-CG-CD1	6.52	124.91	121.00
1	A	194	TRP	CG-CD1-NE1	-6.52	103.58	110.10
1	A	138	GLU	CA-CB-CG	6.43	127.56	113.40
1	A	186	VAL	CG1-CB-CG2	-6.34	100.75	110.90
1	A	46	HIS	CA-CB-CG	-6.34	102.83	113.60
1	A	65	TYR	O-C-N	-6.29	112.64	122.70
1	A	206	LEU	CA-CB-CG	6.28	129.74	115.30
1	A	67	HIS	N-CA-C	6.27	127.94	111.00
1	A	57	TYR	CG-CD1-CE1	-6.26	116.30	121.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	41	TRP	CG-CD1-NE1	-6.25	103.85	110.10
1	A	11	ARG	NE-CZ-NH1	6.24	123.42	120.30
1	A	106	TRP	CD1-CG-CD2	6.24	111.29	106.30
1	A	123	TYR	CB-CG-CD2	-6.24	117.26	121.00
1	A	308	TYR	CB-CG-CD2	-6.17	117.30	121.00
1	A	47	TYR	CG-CD2-CE2	-6.10	116.42	121.30
1	A	253	MET	N-CA-CB	-6.05	99.71	110.60
1	A	208	GLU	CA-CB-CG	6.00	126.61	113.40
1	A	8	LEU	CA-C-N	5.99	130.38	117.20
1	A	141	LYS	CB-CG-CD	5.97	127.12	111.60
1	A	100	TRP	CG-CD2-CE3	5.92	139.23	133.90
1	A	103	ARG	NE-CZ-NH2	-5.86	117.37	120.30
1	A	336	TRP	CG-CD1-NE1	-5.85	104.25	110.10
1	A	278	TYR	CA-CB-CG	5.79	124.40	113.40
1	A	4	LYS	O-C-N	-5.78	113.45	122.70
1	A	107	GLN	CA-C-N	5.77	133.26	117.10
1	A	147	LYS	CA-CB-CG	5.77	126.10	113.40
1	A	106	TRP	CE2-CD2-CG	-5.76	102.69	107.30
1	A	4	LYS	CA-C-N	5.73	129.81	117.20
1	A	52	TYR	CA-C-N	5.73	129.81	117.20
1	A	186	VAL	CA-CB-CG2	-5.72	102.32	110.90
1	A	191	LEU	CA-CB-CG	5.65	128.30	115.30
1	A	178	TYR	CB-CG-CD2	-5.64	117.62	121.00
1	A	57	TYR	CD1-CG-CD2	5.63	124.09	117.90
1	A	100	TRP	CB-CG-CD1	-5.56	119.77	127.00
1	A	336	TRP	CB-CG-CD1	-5.54	119.80	127.00
1	A	174	TRP	CA-CB-CG	5.53	124.21	113.70
1	A	186	VAL	CA-CB-CG1	5.50	119.16	110.90
1	A	305	ASN	CA-CB-CG	-5.49	101.32	113.40
1	A	196	THR	CA-CB-CG2	-5.47	104.75	112.40
1	A	76	ASP	N-CA-CB	-5.45	100.78	110.60
1	A	26	ILE	CA-CB-CG1	-5.40	100.73	111.00
1	A	268	LEU	CA-CB-CG	5.40	127.72	115.30
1	A	123	TYR	CD1-CG-CD2	5.36	123.80	117.90
1	A	31	TRP	CB-CG-CD2	-5.34	119.66	126.60
1	A	47	TYR	CB-CG-CD2	5.32	124.19	121.00
1	A	334	GLN	CA-CB-CG	-5.30	101.74	113.40
1	A	174	TRP	CE2-CD2-CG	-5.30	103.06	107.30
1	A	127	ARG	NH1-CZ-NH2	-5.30	113.57	119.40
1	A	220	GLN	CA-C-N	5.29	128.85	117.20
1	A	39	THR	CB-CA-C	-5.29	97.33	111.60
1	A	254	TYR	CA-C-N	5.28	128.81	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1	LYS	CA-CB-CG	5.26	124.98	113.40
1	A	225	ARG	CB-CG-CD	-5.26	97.93	111.60
1	A	268	LEU	N-CA-CB	-5.26	99.89	110.40
1	A	145	PHE	CA-CB-CG	-5.25	101.30	113.90
1	A	14	ASP	CB-CG-OD1	5.24	123.01	118.30
1	A	338	THR	CA-CB-CG2	-5.20	105.12	112.40
1	A	179	ASP	CA-C-N	5.19	131.63	117.10
1	A	147	LYS	N-CA-CB	-5.16	101.31	110.60
1	A	297	MET	CG-SD-CE	5.15	108.44	100.20
1	A	271	TYR	CB-CG-CD1	5.12	124.07	121.00
1	A	148	ARG	NE-CZ-NH1	-5.09	117.75	120.30
1	A	195	ALA	CA-C-N	-5.08	106.02	117.20
1	A	65	TYR	CA-C-N	5.08	128.37	117.20
1	A	267	ALA	CA-C-N	-5.06	106.07	117.20
1	A	43	MET	N-CA-C	-5.04	97.40	111.00
1	A	147	LYS	CB-CA-C	5.00	120.41	110.40

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	128	ASP	Mainchain
1	A	182	TYR	Sidechain
1	A	278	TYR	Sidechain
1	A	298	TYR	Sidechain
1	A	52	TYR	Sidechain
1	A	65	TYR	Sidechain

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	2794	0	2736	94	0
2	B	39	0	34	2	0
3	A	14	0	13	2	0
4	A	5	0	0	4	0
All	All	2852	0	2783	97	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 17.

All (97) 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:266:MET:SD	1:A:271:TYR:HD2	1.95	0.89
1:A:55:ARG:HG2	1:A:55:ARG:HH11	1.44	0.81
1:A:338:THR:HA	1:A:341:MET:SD	2.19	0.81
1:A:258:ASP:HB2	1:A:276:PRO:HG2	1.68	0.76
1:A:211:LEU:HD23	1:A:275:LEU:HD23	1.71	0.71
1:A:54:ARG:HH22	1:A:63:ASN:HB3	1.57	0.69
1:A:126:PHE:CE2	1:A:230:VAL:HG21	2.28	0.69
1:A:135:LEU:HD22	1:A:219:LYS:HD3	1.75	0.69
1:A:266:MET:SD	1:A:271:TYR:CD2	2.84	0.67
1:A:312:LEU:HD12	1:A:313:PRO:HD2	1.76	0.67
1:A:327:LEU:O	1:A:330:PRO:HD2	1.95	0.66
4:A:343:VO4:V	4:A:343:VO4:O2	1.53	0.66
1:A:72:ILE:HG12	1:A:88:LEU:HD11	1.78	0.65
1:A:180:PRO:O	1:A:184:GLU:HG2	1.97	0.64
1:A:66:LYS:CE	3:A:347:NAG:H81	2.29	0.62
1:A:66:LYS:HE2	3:A:347:NAG:H81	1.80	0.62
1:A:239:MET:SD	1:A:286:LEU:HD13	2.40	0.62
1:A:322:GLU:O	1:A:326:GLU:HB2	2.01	0.61
1:A:203:LEU:HA	1:A:206:LEU:HD12	1.82	0.61
1:A:144:GLU:O	1:A:148:ARG:HB2	2.02	0.59
1:A:270:VAL:HG11	1:A:310:LEU:HB3	1.85	0.59
1:A:169:ASP:O	1:A:173:ILE:HG12	2.04	0.58
1:A:191:LEU:HB2	1:A:192:PRO:HD2	1.86	0.58
1:A:79:ARG:NH1	4:A:343:VO4:O2	2.36	0.57
1:A:334:GLN:HA	1:A:334:GLN:OE1	2.04	0.56
1:A:186:VAL:HG12	1:A:187:HIS:ND1	2.20	0.56
1:A:55:ARG:HG2	1:A:55:ARG:NH1	2.17	0.56
1:A:159:LEU:HA	1:A:162:LEU:HD12	1.87	0.56
1:A:218:HIS:NE2	1:A:219:LYS:HD2	2.22	0.55
1:A:126:PHE:HE2	1:A:230:VAL:HG21	1.72	0.54
1:A:214:LEU:O	1:A:223:LYS:HE2	2.07	0.54
1:A:144:GLU:HB3	1:A:148:ARG:HH21	1.72	0.54
1:A:258:ASP:CB	1:A:276:PRO:HG2	2.36	0.53
1:A:243:THR:HG22	1:A:293:HIS:CD2	2.43	0.53
1:A:17:PRO:HD2	1:A:35:PHE:CD1	2.44	0.53
1:A:244:GLN:HB2	1:A:245:PRO:HD2	1.90	0.53
1:A:215:TYR:HB2	1:A:266:MET:HG3	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:335:ASP:O	1:A:339:GLU:HB2	2.09	0.52
1:A:5:PHE:HE2	1:A:239:MET:HG2	1.75	0.52
1:A:319:CYS:SG	1:A:320:PRO:HD2	2.50	0.51
1:A:261:VAL:O	1:A:265:GLN:HG3	2.11	0.51
1:A:133:GLN:HA	1:A:136:LYS:HG3	1.92	0.50
1:A:288:GLN:OE1	1:A:293:HIS:NE2	2.44	0.50
1:A:47:TYR:CE1	1:A:90:ALA:HB2	2.47	0.50
1:A:218:HIS:O	1:A:219:LYS:HB2	2.11	0.50
1:A:12:HIS:HE1	1:A:15:ARG:HE	1.60	0.50
1:A:191:LEU:H	1:A:191:LEU:HD23	1.77	0.50
1:A:14:ASP:H	1:A:42:GLY:HA2	1.76	0.50
1:A:225:ARG:NH2	1:A:334:GLN:H	2.10	0.50
2:B:2:NAG:H2	2:B:2:NAG:O6	2.12	0.50
1:A:170:LEU:HB3	1:A:210:SER:HB3	1.93	0.49
1:A:177:LEU:HD22	1:A:181:LEU:HD11	1.94	0.49
1:A:12:HIS:NE2	4:A:343:VO4:O2	2.46	0.48
1:A:297:MET:O	1:A:317:HIS:HE1	1.97	0.48
1:A:114:VAL:HG12	1:A:115:SER:N	2.29	0.48
1:A:54:ARG:NH1	1:A:54:ARG:HG3	2.27	0.48
1:A:14:ASP:HA	1:A:278:TYR:CD2	2.49	0.47
1:A:251:LEU:CD2	1:A:253:MET:HB2	2.44	0.47
1:A:52:TYR:OH	1:A:307:PRO:HG3	2.14	0.47
1:A:162:LEU:HD13	1:A:194:TRP:CE3	2.50	0.46
1:A:17:PRO:HD2	1:A:35:PHE:HD1	1.81	0.46
1:A:159:LEU:HD23	1:A:162:LEU:HD12	1.97	0.46
1:A:162:LEU:HD22	1:A:194:TRP:CG	2.51	0.46
1:A:126:PHE:HD2	1:A:336:TRP:CZ2	2.33	0.46
1:A:301:ASN:OD1	1:A:302:GLU:N	2.49	0.46
1:A:138:GLU:O	1:A:142:SER:HB3	2.17	0.45
1:A:146:LEU:O	1:A:150:GLN:NE2	2.50	0.45
1:A:312:LEU:HD21	1:A:327:LEU:HD12	1.97	0.45
1:A:66:LYS:O	1:A:68:ASP:N	2.48	0.45
1:A:299:TYR:N	1:A:308:TYR:O	2.50	0.45
1:A:137:SER:O	1:A:141:LYS:HE2	2.17	0.45
1:A:77:VAL:HG23	1:A:80:THR:OG1	2.17	0.44
1:A:187:HIS:O	1:A:188:ASN:HB3	2.17	0.44
1:A:156:ILE:O	1:A:160:PRO:HD3	2.17	0.44
4:A:343:VO4:O3	4:A:343:VO4:O2	2.36	0.44
1:A:75:THR:HG21	1:A:123:TYR:HD1	1.83	0.44
1:A:65:TYR:O	1:A:65:TYR:CG	2.71	0.43
1:A:47:TYR:CZ	1:A:90:ALA:HB2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:LEU:HA	1:A:287:TYR:HA	2.00	0.43
1:A:201:THR:O	1:A:205:GLU:HG3	2.18	0.42
1:A:56:ARG:HD3	1:A:57:TYR:CZ	2.54	0.42
1:A:277:PRO:HD2	1:A:280:SER:HB3	2.00	0.42
1:A:302:GLU:HG3	2:B:1:NAG:H82	2.02	0.42
1:A:186:VAL:HG12	1:A:187:HIS:CE1	2.54	0.42
1:A:227:GLN:O	1:A:230:VAL:HG23	2.20	0.42
1:A:143:GLU:OE1	1:A:144:GLU:HG2	2.20	0.41
1:A:162:LEU:HD22	1:A:194:TRP:CD1	2.55	0.41
1:A:11:ARG:NH1	1:A:278:TYR:HD1	2.18	0.41
1:A:177:LEU:HD22	1:A:181:LEU:CD1	2.51	0.41
1:A:232:VAL:HG22	1:A:268:LEU:HD13	2.01	0.41
1:A:246:GLN:NE2	1:A:247:LYS:H	2.19	0.41
1:A:211:LEU:HD23	1:A:275:LEU:CD2	2.45	0.41
1:A:9:VAL:HG22	1:A:9:VAL:O	2.20	0.41
1:A:14:ASP:HA	1:A:278:TYR:CE2	2.56	0.41
1:A:199:ALA:O	1:A:203:LEU:N	2.54	0.41
1:A:138:GLU:HB2	1:A:218:HIS:NE2	2.36	0.41
1:A:177:LEU:HD21	1:A:194:TRP:HH2	1.86	0.41

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	340/342 (99%)	283 (83%)	44 (13%)	13 (4%)	3 18

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	67	HIS
1	A	127	ARG

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Mol	Chain	Res	Type
1	A	337	ALA
1	A	62	ASN
1	A	143	GLU
1	A	217	ILE
1	A	220	GLN
1	A	272	ASN
1	A	153	LYS
1	A	96	GLY
1	A	221	LYS
1	A	336	TRP
1	A	273	GLY

5.3.2   Protein sidechains (i)

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	311/311 (100%)	254 (82%)	57 (18%)	1 9

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	9	VAL
1	A	11	ARG
1	A	18	ILE
1	A	22	PRO
1	A	26	ILE
1	A	38	LEU
1	A	39	THR
1	A	40	LYS
1	A	49	LEU
1	A	54	ARG
1	A	55	ARG
1	A	56	ARG
1	A	59	ARG
1	A	63	ASN

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Mol	Chain	Res	Type
1	A	72	ILE
1	A	73	ARG
1	A	77	VAL
1	A	81	LEU
1	A	87	ASN
1	A	91	LEU
1	A	98	SER
1	A	115	SER
1	A	118	GLU
1	A	119	ASP
1	A	120	ARG
1	A	133	GLN
1	A	136	LYS
1	A	140	LEU
1	A	141	LYS
1	A	143	GLU
1	A	146	LEU
1	A	148	ARG
1	A	153	LYS
1	A	158	THR
1	A	169	ASP
1	A	175	SER
1	A	176	ARG
1	A	177	LEU
1	A	200	MET
1	A	211	LEU
1	A	222	GLU
1	A	223	LYS
1	A	231	LEU
1	A	241	LEU
1	A	244	GLN
1	A	246	GLN
1	A	249	ARG
1	A	250	LYS
1	A	275	LEU
1	A	303	THR
1	A	305	ASN
1	A	316	THR
1	A	326	GLU
1	A	334	GLN
1	A	335	ASP
1	A	339	GLU

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

Mol	Chain	Res	Type
1	A	87	ASN
1	A	107	GLN
1	A	265	GLN
1	A	304	GLN
1	A	305	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)

3 monosaccharides 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	NAG	B	1	1,2	14,14,15	1.56	2 (14%)	17,19,21	1.18	3 (17%)
2	NAG	B	2	2	14,14,15	1.20	1 (7%)	17,19,21	2.46	5 (29%)
2	BMA	B	3	2	11,11,12	1.98	2 (18%)	15,15,17	3.08	9 (60%)

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	NAG	B	1	1,2	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	2	2	-	2/6/23/26	0/1/1/1
2	BMA	B	3	2	-	2/2/19/22	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	3	BMA	C4-C5	4.84	1.63	1.53
2	B	1	NAG	C4-C5	-4.09	1.44	1.53
2	B	3	BMA	C2-C3	-3.32	1.47	1.52
2	B	2	NAG	O5-C1	2.91	1.48	1.43
2	B	1	NAG	O3-C3	-2.36	1.37	1.43

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	3	BMA	C1-C2-C3	-8.16	99.63	109.67
2	B	2	NAG	C2-N2-C7	-5.89	114.51	122.90
2	B	2	NAG	C1-O5-C5	4.74	118.62	112.19
2	B	2	NAG	C3-C4-C5	4.05	117.47	110.24
2	B	3	BMA	O5-C5-C6	-3.79	101.26	107.20
2	B	3	BMA	C2-C3-C4	-3.68	104.53	110.89
2	B	3	BMA	O2-C2-C1	3.40	116.10	109.15
2	B	3	BMA	C3-C4-C5	2.78	115.20	110.24
2	B	3	BMA	O2-C2-C3	2.61	115.36	110.14
2	B	2	NAG	O5-C5-C6	2.58	111.24	107.20
2	B	2	NAG	C1-C2-N2	-2.56	106.12	110.49
2	B	1	NAG	O5-C5-C6	2.43	111.01	107.20
2	B	3	BMA	O5-C5-C4	2.33	116.49	110.83
2	B	1	NAG	O5-C5-C4	-2.29	105.25	110.83
2	B	1	NAG	C1-O5-C5	2.23	115.22	112.19
2	B	3	BMA	O4-C4-C3	-2.21	105.25	110.35
2	B	3	BMA	O3-C3-C2	2.13	114.07	109.99

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	3	BMA	O5-C5-C6-O6
2	B	3	BMA	C4-C5-C6-O6
2	B	2	NAG	O5-C5-C6-O6
2	B	2	NAG	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1	NAG	1	0
2	B	2	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.
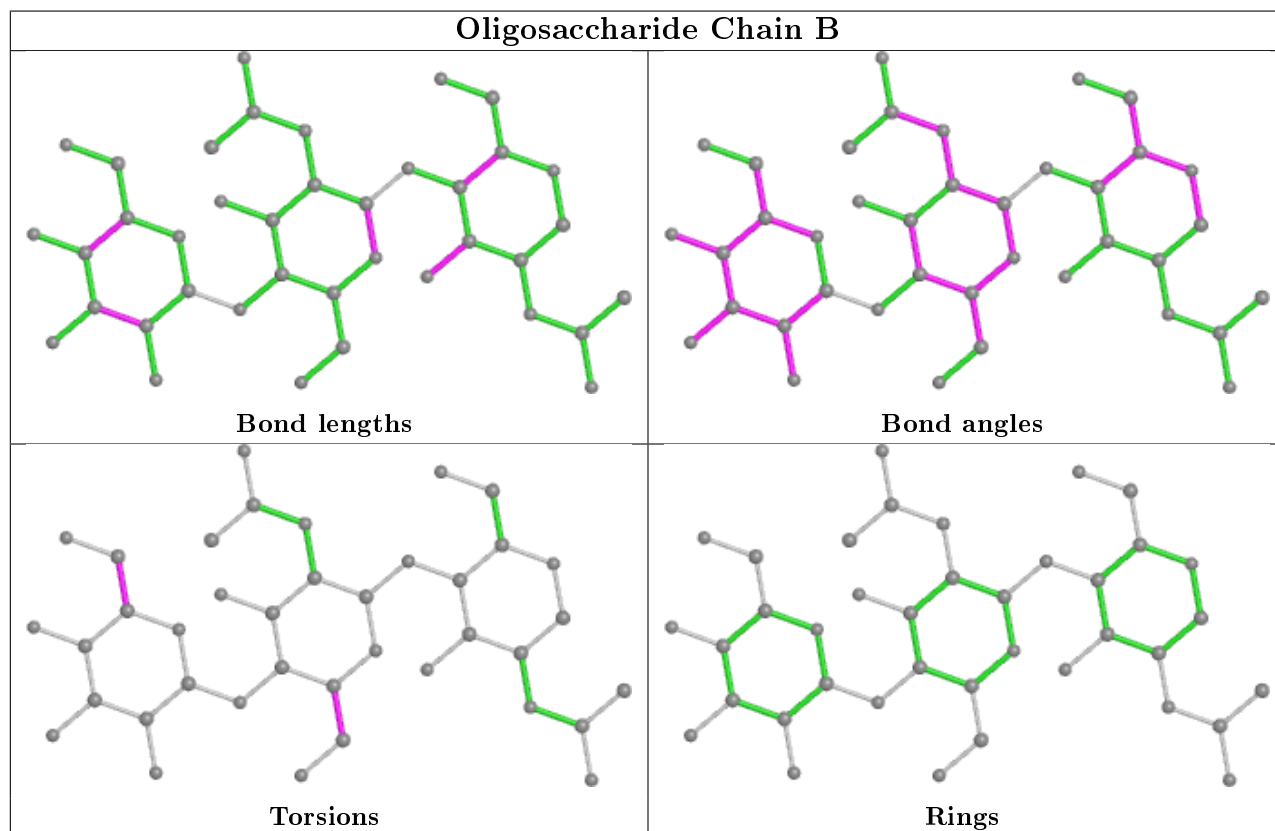
5.6 Ligand geometry ⓘ

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
4	VO4	A	343	1	1,4,4	0.49	0	-		
3	NAG	A	347	1	14,14,15	2.00	5 (35%)	17,19,21	1.88	3 (17%)

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
3	NAG	A	347	1	-	0/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	347	NAG	C4-C3	4.26	1.63	1.52
3	A	347	NAG	C4-C5	3.61	1.60	1.53
3	A	347	NAG	O5-C5	2.37	1.48	1.43
3	A	347	NAG	C6-C5	2.37	1.59	1.51
3	A	347	NAG	C3-C2	2.07	1.56	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	347	NAG	C6-C5-C4	5.00	124.71	113.00
3	A	347	NAG	C1-O5-C5	-4.11	106.63	112.19
3	A	347	NAG	C8-C7-N2	-2.50	111.87	116.10

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	343	VO4	4	0
3	A	347	NAG	2	0

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 (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.