Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 06:03 AM GMT

PDB ID	:	2VRQ
Title	:	STRUCTURE OF AN INACTIVE MUTANT OF ARABINOFURANOSIDASE FROM THERMOBACILLUS XYLANILYTICUS IN COMPLEX WITH A PENTASACCHARIDE
Authors	:	Paes, G.; Skov, L.K.; Odonohue, M.J.; Remond, C.; Kastrup, J.S.; Gajhede, M.; Mirza, O.
Deposited on	:	2008-04-09
Resolution	:	2.00 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

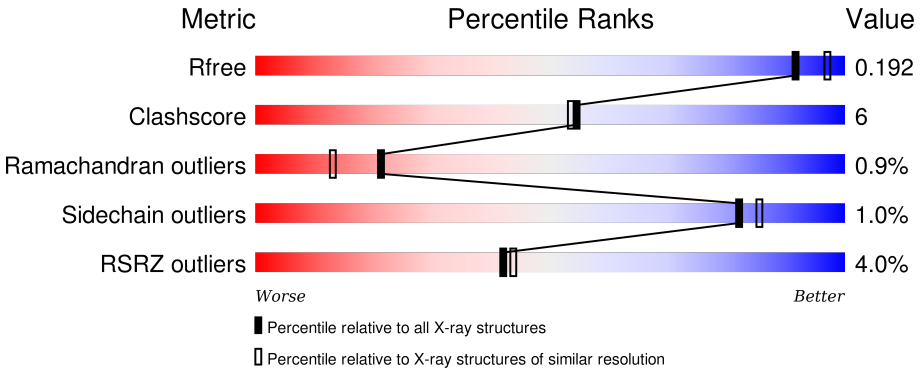
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.00 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))
R_{free}	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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. 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% 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	496	3% 87% 12%
1	B	496	4% 89% 10%
1	C	496	5% 85% 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	XYP	A	1499	-	-	-	X
2	XYP	B	1498	-	-	-	X
2	XYP	B	1500	-	-	-	X
3	PO4	B	1497	-	-	-	X
4	XYP	C	1498	-	-	-	X
4	XYP	C	1499	-	-	-	X
4	AHR	C	1500	-	-	-	X

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 13062 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 ALPHA-L-ARABINOFURANOSIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	493	Total	C	N	O	S	0	0	0
			3930	2487	694	726	23			
1	B	493	Total	C	N	O	S	0	0	0
			3930	2487	694	726	23			
1	C	493	Total	C	N	O	S	0	0	0
			3930	2487	694	726	23			

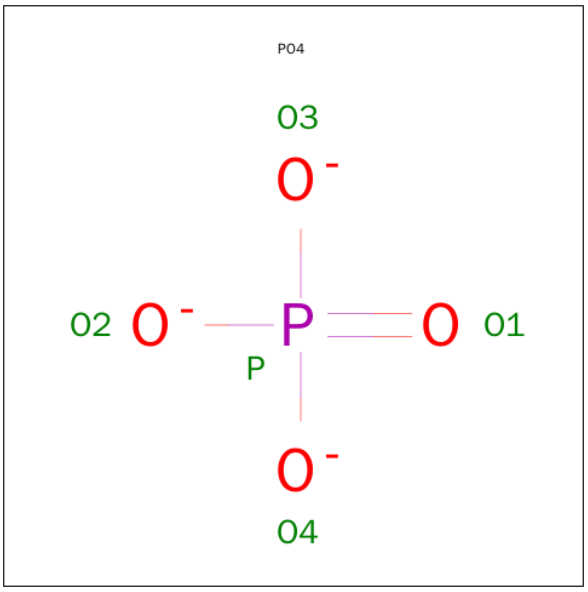
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	176	GLN	GLU	ENGINEERED MUTATION	UNP O69262
B	176	GLN	GLU	ENGINEERED MUTATION	UNP O69262
C	176	GLN	GLU	ENGINEERED MUTATION	UNP O69262

- Molecule 2 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	4	Total	C	O	0	0
			37	20	17		
2	B	4	Total	C	O	0	0
			37	20	17		

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total O P 5 4 1	0	0
3	C	1	Total O P 5 4 1	0	0

- Molecule 4 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	3	Total C O 28 15 13	0	0

- Molecule 5 is water.

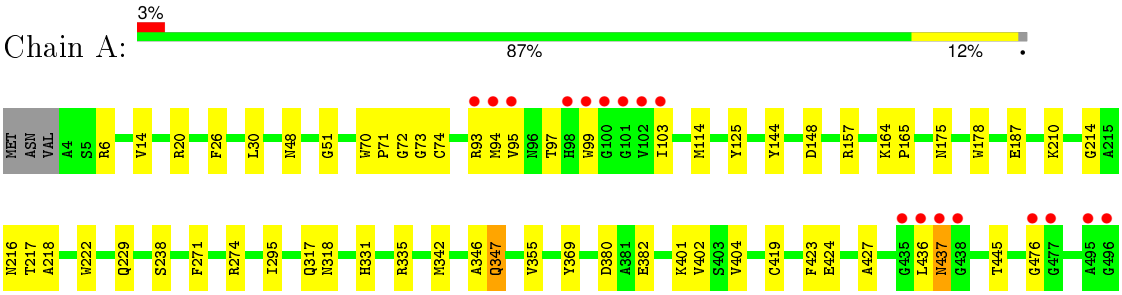
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	419	Total O 419 419	0	0
5	B	374	Total O 374 374	0	0
5	C	367	Total O 367 367	0	0

3 Residue-property plots (i)

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.

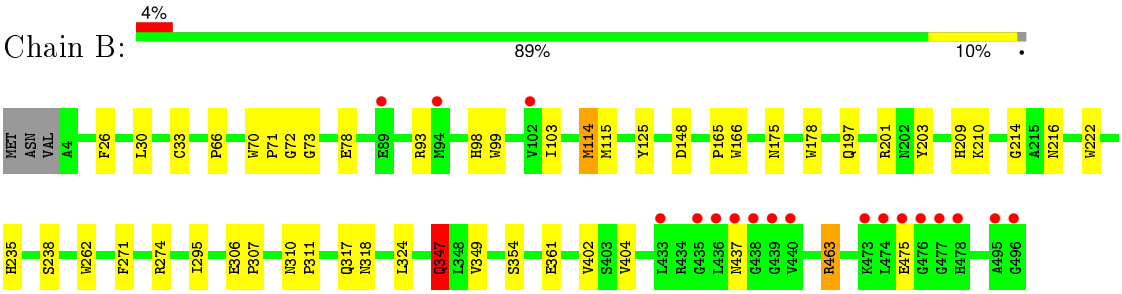
- Molecule 1: ALPHA-L-ARABINOFURANOSIDASE

Chain A:



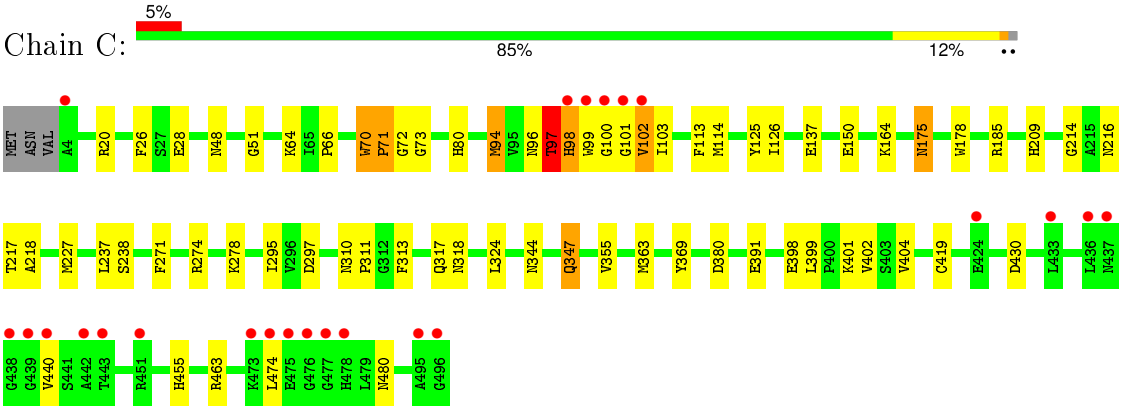
- Molecule 1: ALPHA-L-ARABINOFURANOSIDASE

Chain B:



- Molecule 1: ALPHA-L-ARABINOFURANOSIDASE

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α, β, γ	156.80Å 156.80Å 378.60Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	78.40 – 2.00 78.40 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (78.40-2.00) 100.0 (78.40-2.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.74 (at 2.00Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.182 , 0.201 0.177 , 0.192	Depositor DCC
R_{free} test set	1847 reflections (1.01%)	DCC
Wilson B-factor (Å^2)	20.4	Xtriage
Anisotropy	0.181	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 53.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.38$, $< L^2 > = 0.21$	Xtriage
Outliers	0 of 184421 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	13062	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.65% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: XYP, AHR, PO4

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	0.46	0/4038	0.59	0/5482
1	B	0.44	0/4038	0.57	1/5482 (0.0%)
1	C	0.43	0/4038	0.68	2/5482 (0.0%)
All	All	0.44	0/12114	0.61	3/16446 (0.0%)

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	2
1	B	0	1
All	All	0	3

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	70	TRP	C-N-CD	-21.17	74.03	120.60
1	C	70	TRP	C-N-CA	13.79	179.93	122.00
1	B	347	GLN	CB-CA-C	5.06	120.51	110.40

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	346	ALA	Peptide
1	A	72	GLY	Peptide

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Mol	Chain	Res	Type	Group
1	B	72	GLY	Peptide

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	3930	0	3778	51	0
1	B	3930	0	3778	37	0
1	C	3930	0	3778	67	0
2	A	37	0	31	4	0
2	B	37	0	31	1	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
4	C	28	0	24	1	0
5	A	419	0	0	4	0
5	B	374	0	0	4	0
5	C	367	0	0	7	0
All	All	13062	0	11420	150	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (150) 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:B:317:GLN:HE21	1:B:318:ASN:H	1.28	0.79
1:C:71:PRO:HD2	1:C:72:GLY:H	1.49	0.78
1:C:98:HIS:HB2	5:C:2104:HOH:O	1.82	0.77
1:A:317:GLN:HE21	1:A:318:ASN:H	1.29	0.76
1:C:26:PHE:O	1:C:347:GLN:HA	1.87	0.75
1:A:274:ARG:HH11	1:A:274:ARG:HG2	1.50	0.74
1:A:274:ARG:HG2	1:A:274:ARG:NH1	2.00	0.74
1:C:317:GLN:HE21	1:C:318:ASN:H	1.37	0.71
1:C:271:PHE:HE1	1:C:274:ARG:HD3	1.55	0.71
1:B:26:PHE:O	1:B:347:GLN:HA	1.91	0.71
1:B:73:GLY:HA2	1:B:175:ASN:CG	2.12	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:436:LEU:O	1:A:437:ASN:HB2	1.92	0.70
1:B:214:GLY:HA3	1:B:238:SER:O	1.92	0.70
1:A:73:GLY:HA2	1:A:175:ASN:CG	2.13	0.69
1:C:48:ASN:HD22	1:C:51:GLY:H	1.41	0.68
1:C:113:PHE:CD2	1:C:114:MET:HE2	2.27	0.68
2:B:1500:XYP:H5B2	5:B:2215:HOH:O	1.94	0.68
1:A:331:HIS:O	1:A:335:ARG:HG2	1.94	0.67
1:B:317:GLN:NE2	1:B:318:ASN:H	1.93	0.66
1:B:271:PHE:HE1	1:B:274:ARG:HD3	1.61	0.65
1:A:216:ASN:HD21	2:A:1499:XYP:H3B	1.62	0.64
1:A:26:PHE:O	1:A:347:GLN:HA	1.97	0.64
1:C:227:MET:CE	1:C:237:LEU:HD22	2.28	0.63
1:A:73:GLY:HA2	1:A:175:ASN:ND2	2.13	0.63
1:B:115:MET:HG2	5:B:2040:HOH:O	1.98	0.62
1:C:216:ASN:HD21	4:C:1499:XYP:H3B	1.64	0.62
1:C:113:PHE:HD2	1:C:114:MET:HE2	1.63	0.61
1:A:73:GLY:CA	1:A:175:ASN:ND2	2.64	0.61
1:C:113:PHE:HD2	1:C:114:MET:CE	2.14	0.60
1:A:214:GLY:HA3	1:A:238:SER:O	2.01	0.60
1:A:274:ARG:HH11	1:A:274:ARG:CG	2.13	0.60
1:C:271:PHE:CE1	1:C:274:ARG:HD3	2.36	0.60
1:B:209:HIS:CE1	1:B:235:HIS:CG	2.91	0.59
1:A:48:ASN:HD22	1:A:51:GLY:H	1.47	0.59
1:C:26:PHE:HE1	1:C:72:GLY:HA2	1.67	0.59
1:C:94:MET:HB2	5:C:2102:HOH:O	2.03	0.59
1:A:423:PHE:CE1	1:A:424:GLU:HG3	2.37	0.59
1:C:214:GLY:HA3	1:C:238:SER:O	2.03	0.59
1:C:297:ASP:HA	1:C:344:ASN:HD22	1.68	0.59
1:C:102:VAL:HG22	1:C:313:PHE:HZ	1.70	0.57
1:A:402:VAL:HG12	1:A:404:VAL:HG23	1.86	0.57
1:B:73:GLY:HA2	1:B:175:ASN:OD1	2.02	0.57
1:B:271:PHE:CE1	1:B:274:ARG:HD3	2.38	0.57
1:C:274:ARG:HE	1:C:278:LYS:HZ2	1.52	0.57
1:B:70:TRP:CD1	1:B:71:PRO:HA	2.40	0.57
1:B:30:LEU:HG	1:B:99:TRP:CG	2.40	0.56
1:B:463:ARG:HH11	1:B:463:ARG:HB2	1.71	0.56
1:C:102:VAL:HB	1:C:103:ILE:HD12	1.87	0.56
1:A:97:THR:HG21	1:B:201:ARG:CD	2.36	0.56
1:C:178:TRP:CZ2	1:C:216:ASN:HB2	2.41	0.55
1:B:78:GLU:OE2	1:B:98:HIS:ND1	2.40	0.55
1:C:102:VAL:HG23	1:C:103:ILE:H	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:LEU:HG	1:A:99:TRP:CG	2.42	0.54
1:C:113:PHE:CD2	1:C:114:MET:CE	2.90	0.54
1:A:317:GLN:NE2	1:A:318:ASN:H	2.01	0.54
1:A:93:ARG:HB3	1:A:103:ILE:CG2	2.38	0.53
1:C:96:ASN:O	1:C:98:HIS:N	2.41	0.53
1:A:48:ASN:ND2	1:A:51:GLY:H	2.05	0.53
1:C:274:ARG:NE	1:C:278:LYS:NZ	2.57	0.53
1:C:274:ARG:HE	1:C:278:LYS:NZ	2.06	0.52
1:C:274:ARG:NE	1:C:278:LYS:HZ2	2.08	0.52
1:C:440:VAL:HG23	1:C:474:LEU:HD21	1.93	0.51
1:A:20:ARG:HD3	1:A:380:ASP:OD2	2.11	0.51
1:B:361:GLU:HG2	5:B:2310:HOH:O	2.11	0.51
1:C:227:MET:HE2	1:C:237:LEU:HD22	1.92	0.51
1:C:402:VAL:HA	1:C:419:CYS:O	2.10	0.51
1:A:70:TRP:CD1	1:A:71:PRO:HA	2.45	0.51
1:B:402:VAL:HG12	1:B:404:VAL:HG23	1.93	0.51
1:B:238:SER:HA	1:B:295:ILE:O	2.12	0.50
1:C:96:ASN:OD1	1:C:99:TRP:HB2	2.12	0.50
1:C:178:TRP:CH2	1:C:216:ASN:HB2	2.47	0.49
1:A:144:TYR:O	1:A:157:ARG:HD3	2.12	0.49
1:C:164:LYS:HG2	5:C:2175:HOH:O	2.10	0.49
1:C:48:ASN:ND2	1:C:51:GLY:H	2.09	0.49
1:C:209:HIS:HD2	5:C:2232:HOH:O	1.94	0.49
1:C:430:ASP:HA	1:C:480:ASN:HD22	1.77	0.49
1:A:335:ARG:HG3	1:A:335:ARG:HH11	1.79	0.48
1:C:102:VAL:CG2	1:C:313:PHE:HZ	2.26	0.48
1:A:178:TRP:CZ2	1:A:216:ASN:HB2	2.49	0.48
1:C:217:THR:HG22	1:C:218:ALA:N	2.28	0.48
1:C:97:THR:HG23	1:C:99:TRP:CD1	2.48	0.47
1:A:73:GLY:C	1:A:175:ASN:ND2	2.68	0.47
1:A:164:LYS:HG2	5:A:2175:HOH:O	2.13	0.47
1:A:210:LYS:HE3	5:A:2204:HOH:O	2.14	0.47
1:A:401:LYS:HE3	1:A:427:ALA:HB2	1.96	0.47
1:C:71:PRO:CD	1:C:72:GLY:N	2.78	0.47
1:C:73:GLY:HA2	1:C:175:ASN:OD1	2.15	0.46
1:C:114:MET:HE3	1:C:126:ILE:HD11	1.97	0.46
1:C:238:SER:HA	1:C:295:ILE:O	2.15	0.46
1:C:317:GLN:NE2	1:C:318:ASN:H	2.07	0.46
1:A:355:VAL:O	1:A:369:TYR:HB2	2.15	0.45
1:A:436:LEU:O	1:A:437:ASN:CB	2.63	0.45
1:B:70:TRP:CG	1:B:71:PRO:HA	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:71:PRO:HD2	1:C:72:GLY:N	2.24	0.45
1:C:227:MET:HE3	1:C:237:LEU:HD22	1.96	0.45
1:A:187:GLU:HG3	5:A:2197:HOH:O	2.16	0.45
1:C:97:THR:O	1:C:99:TRP:N	2.49	0.45
1:A:97:THR:HG21	1:B:201:ARG:HD2	1.98	0.45
1:C:98:HIS:C	1:C:100:GLY:H	2.19	0.45
1:A:271:PHE:HE1	1:A:274:ARG:HD3	1.82	0.45
1:A:238:SER:HA	1:A:295:ILE:O	2.17	0.45
1:B:103:ILE:CD1	1:C:150:GLU:O	2.65	0.44
1:A:216:ASN:ND2	2:A:1499:XYP:H3B	2.30	0.44
1:C:355:VAL:O	1:C:369:TYR:HB2	2.17	0.44
1:C:80:HIS:HD2	1:C:137:GLU:OE2	2.01	0.44
1:A:229:GLN:OE1	1:C:185:ARG:HD3	2.18	0.43
1:C:398:GLU:HG3	1:C:399:LEU:HG	2.00	0.43
1:A:99:TRP:CH2	2:A:1497:XYP:H2B	2.53	0.43
1:B:197:GLN:HB2	1:B:210:LYS:HD3	2.01	0.43
1:B:317:GLN:NE2	5:B:2288:HOH:O	2.48	0.43
1:A:402:VAL:HA	1:A:419:CYS:O	2.19	0.43
1:B:103:ILE:HD11	5:C:2156:HOH:O	2.17	0.43
1:A:95:VAL:HG11	1:B:203:TYR:HE1	1.83	0.43
1:A:271:PHE:CZ	1:A:274:ARG:NH1	2.87	0.43
1:C:402:VAL:HG12	1:C:404:VAL:HG23	2.01	0.43
1:C:20:ARG:HD3	1:C:380:ASP:OD2	2.19	0.43
1:A:14:VAL:HG13	1:A:382:GLU:HB3	2.01	0.42
1:C:71:PRO:CD	1:C:72:GLY:H	2.18	0.42
1:A:217:THR:HG22	1:A:218:ALA:N	2.34	0.42
1:B:178:TRP:HB3	1:B:222:TRP:CZ3	2.55	0.42
1:B:262:TRP:CH2	1:B:324:LEU:HD12	2.55	0.42
1:B:178:TRP:CZ2	1:B:216:ASN:HB2	2.54	0.42
1:C:114:MET:CE	1:C:126:ILE:HD11	2.50	0.42
1:C:324:LEU:HD23	1:C:419:CYS:HB3	2.01	0.42
1:C:73:GLY:HA2	1:C:175:ASN:CG	2.40	0.42
1:A:148:ASP:HB3	1:A:165:PRO:HG3	2.02	0.42
1:C:391:GLU:HG3	1:C:401:LYS:CB	2.50	0.42
1:C:455:HIS:O	1:C:463:ARG:HD2	2.19	0.42
1:B:148:ASP:HB3	1:B:165:PRO:HG3	2.02	0.42
1:C:28:GLU:HG3	1:C:72:GLY:HA3	2.02	0.42
1:A:97:THR:HG21	1:B:201:ARG:HG3	2.00	0.42
1:C:70:TRP:CG	1:C:71:PRO:N	2.87	0.41
1:C:310:ASN:HA	1:C:311:PRO:HD2	1.87	0.41
1:A:178:TRP:HB3	1:A:222:TRP:CZ3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:LEU:HD12	1:A:99:TRP:CE2	2.55	0.41
1:B:347:GLN:O	1:B:354:SER:HA	2.21	0.41
1:B:310:ASN:HA	1:B:311:PRO:HD2	1.97	0.41
1:A:6:ARG:NH2	5:A:2003:HOH:O	2.53	0.41
1:B:306:GLU:HA	1:B:307:PRO:HD3	1.96	0.41
1:A:342:MET:HE2	1:A:342:MET:HB2	1.82	0.41
1:B:33:CYS:HA	1:B:349:VAL:O	2.21	0.41
1:C:102:VAL:HG22	1:C:313:PHE:CZ	2.54	0.41
1:A:74:CYS:SG	2:A:1500:AHR:H2'	2.61	0.41
1:A:271:PHE:CE1	1:A:274:ARG:NH1	2.89	0.40
1:B:93:ARG:HD2	1:B:103:ILE:HG21	2.04	0.40
1:C:80:HIS:HE1	5:C:2136:HOH:O	2.02	0.40
1:B:178:TRP:CH2	1:B:216:ASN:HB2	2.57	0.40
1:C:98:HIS:C	1:C:100:GLY:N	2.75	0.40
1:C:64:LYS:HD3	5:C:2063:HOH:O	2.21	0.40
1:B:114:MET:HG2	1:B:166:TRP:CD2	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	491/496 (99%)	468 (95%)	20 (4%)	3 (1%)	30 22
1	B	491/496 (99%)	469 (96%)	19 (4%)	3 (1%)	30 22
1	C	491/496 (99%)	466 (95%)	18 (4%)	7 (1%)	14 6
All	All	1473/1488 (99%)	1403 (95%)	57 (4%)	13 (1%)	21 13

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	437	ASN

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Mol	Chain	Res	Type
1	B	437	ASN
1	C	71	PRO
1	C	97	THR
1	C	98	HIS
1	A	347	GLN
1	A	476	GLY
1	C	102	VAL
1	C	347	GLN
1	B	347	GLN
1	B	66	PRO
1	C	66	PRO
1	C	101	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	416/419 (99%)	412 (99%)	4 (1%)	82	85
1	B	416/419 (99%)	412 (99%)	4 (1%)	82	85
1	C	416/419 (99%)	411 (99%)	5 (1%)	78	81
All	All	1248/1257 (99%)	1235 (99%)	13 (1%)	82	85

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	94	MET
1	A	114	MET
1	A	125	TYR
1	A	445	THR
1	B	114	MET
1	B	125	TYR
1	B	463	ARG
1	B	475	GLU
1	C	94	MET
1	C	97	THR

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Mol	Chain	Res	Type
1	C	125	TYR
1	C	175	ASN
1	C	363	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	ASN
1	A	176	GLN
1	A	183	ASN
1	A	317	GLN
1	A	437	ASN
1	A	480	ASN
1	B	183	ASN
1	B	317	GLN
1	B	437	ASN
1	C	21	ASN
1	C	48	ASN
1	C	80	HIS
1	C	176	GLN
1	C	183	ASN
1	C	209	HIS
1	C	317	GLN
1	C	344	ASN
1	C	437	ASN
1	C	480	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)

11 carbohydrates 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	XYP	A	1497	2	9,9,10	1.15	0	12,12,14	1.16	1 (8%)
2	XYP	A	1498	2	9,9,10	1.25	1 (11%)	12,12,14	2.55	6 (50%)
2	XYP	A	1499	2	10,10,10	0.98	0	12,14,14	0.75	0
2	AHR	A	1500	2	9,9,10	0.74	0	12,12,14	1.23	2 (16%)
2	XYP	B	1498	2	9,9,10	0.76	0	12,12,14	0.40	0
2	XYP	B	1499	2	9,9,10	1.29	1 (11%)	12,12,14	1.58	3 (25%)
2	XYP	B	1500	2	10,10,10	0.97	0	12,14,14	1.06	1 (8%)
2	AHR	B	1501	2	9,9,10	0.94	0	12,12,14	1.28	1 (8%)
4	XYP	C	1498	4	9,9,10	1.11	0	12,12,14	1.68	4 (33%)
4	XYP	C	1499	4	10,10,10	1.02	0	12,14,14	1.04	0
4	AHR	C	1500	4	9,9,10	0.66	0	12,12,14	1.68	2 (16%)

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	XYP	A	1497	2	-	0/0/14/17	0/1/1/1
2	XYP	A	1498	2	-	0/0/14/17	0/1/1/1
2	XYP	A	1499	2	-	0/0/17/17	0/1/1/1
2	AHR	A	1500	2	-	0/2/15/18	0/1/1/1
2	XYP	B	1498	2	-	0/0/14/17	0/1/1/1
2	XYP	B	1499	2	-	0/0/14/17	0/1/1/1
2	XYP	B	1500	2	-	0/0/17/17	0/1/1/1
2	AHR	B	1501	2	-	0/2/15/18	0/1/1/1
4	XYP	C	1498	4	-	0/0/14/17	0/1/1/1
4	XYP	C	1499	4	-	0/0/17/17	0/1/1/1
4	AHR	C	1500	4	-	0/2/15/18	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1499	XYP	C4B-C3B	2.16	1.55	1.52
2	A	1498	XYP	C4B-C3B	2.25	1.55	1.52

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1497	XYP	C4B-C3B-C2B	-2.95	108.32	111.24
2	B	1499	XYP	C4B-C3B-C2B	-2.75	108.52	111.24
2	A	1498	XYP	C4B-C3B-C2B	-2.65	108.62	111.24
4	C	1498	XYP	C4B-C3B-C2B	-2.36	108.91	111.24
2	A	1498	XYP	O3B-C3B-C4B	-2.09	106.23	110.00
4	C	1498	XYP	O4B-C4B-C3B	2.11	114.36	110.12
2	B	1499	XYP	O5B-C5B-C4B	2.25	114.52	110.31
2	A	1500	AHR	O2'-C2'-C3'	2.27	115.58	111.23
4	C	1498	XYP	O2B-C2B-C3B	2.51	115.16	110.12
2	A	1500	AHR	C1'-C2'-C3'	2.56	105.77	101.64
2	B	1501	AHR	C1'-C2'-C3'	2.69	105.97	101.64
2	B	1500	XYP	O5B-C5B-C4B	2.82	115.44	110.86
2	B	1499	XYP	C5B-C4B-C3B	2.85	112.92	109.54
2	A	1498	XYP	O5B-C5B-C4B	3.24	116.37	110.31
4	C	1500	AHR	C1'-C2'-C3'	3.26	106.89	101.64
2	A	1498	XYP	O2B-C2B-C3B	3.38	116.93	110.12
4	C	1498	XYP	C5B-C4B-C3B	3.41	113.57	109.54
2	A	1498	XYP	C5B-C4B-C3B	3.45	113.63	109.54
4	C	1500	AHR	O2'-C2'-C3'	4.02	118.94	111.23
2	A	1498	XYP	C1B-C2B-C3B	4.62	115.00	109.54

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1497	XYP	1	0
2	A	1499	XYP	2	0
2	A	1500	AHR	1	0
2	B	1500	XYP	1	0
4	C	1499	XYP	1	0

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	$\#\|Z\| > 2$
3	PO4	B	1497	-	4,4,4	0.22	0	6,6,6	0.27	0
3	PO4	C	1497	-	4,4,4	0.55	0	6,6,6	0.26	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
3	PO4	B	1497	-	-	0/0/0/0	0/0/0/0
3	PO4	C	1497	-	-	0/0/0/0	0/0/0/0

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, 95^{th} 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	493/496 (99%)	-0.19	17 (3%) 49 50	11, 19, 44, 67	0
1	B	493/496 (99%)	-0.07	18 (3%) 45 47	11, 22, 46, 76	0
1	C	493/496 (99%)	-0.02	24 (4%) 33 35	12, 22, 46, 78	0
All	All	1479/1488 (99%)	-0.09	59 (3%) 42 44	11, 21, 46, 78	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	496	GLY	8.4
1	C	100	GLY	7.9
1	B	496	GLY	7.0
1	C	99	TRP	6.9
1	C	98	HIS	6.4
1	B	436	LEU	5.8
1	C	101	GLY	5.7
1	A	496	GLY	5.7
1	C	437	ASN	5.4
1	C	495	ALA	5.0
1	A	437	ASN	4.7
1	C	440	VAL	4.6
1	A	495	ALA	4.4
1	C	474	LEU	4.4
1	B	437	ASN	4.1
1	B	439	GLY	4.1
1	A	94	MET	4.1
1	C	438	GLY	4.0
1	A	99	TRP	4.0
1	B	438	GLY	3.9
1	A	101	GLY	3.9
1	A	103	ILE	3.7
1	B	495	ALA	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	473	LYS	3.7
1	B	476	GLY	3.5
1	B	440	VAL	3.5
1	A	438	GLY	3.2
1	C	436	LEU	3.2
1	C	439	GLY	3.2
1	B	475	GLU	3.1
1	B	474	LEU	3.1
1	C	476	GLY	3.1
1	B	435	GLY	3.1
1	A	95	VAL	3.0
1	A	102	VAL	3.0
1	A	435	GLY	3.0
1	C	433	LEU	2.9
1	A	93	ARG	2.8
1	B	94	MET	2.7
1	C	102	VAL	2.7
1	C	451	ARG	2.6
1	C	475	GLU	2.6
1	A	476	GLY	2.4
1	C	478	HIS	2.4
1	B	433	LEU	2.3
1	B	477	GLY	2.3
1	C	477	GLY	2.3
1	B	102	VAL	2.3
1	C	473	LYS	2.3
1	A	100	GLY	2.2
1	A	477	GLY	2.2
1	A	98	HIS	2.2
1	C	442	ALA	2.2
1	B	478	HIS	2.2
1	C	4	ALA	2.1
1	A	436	LEU	2.1
1	C	443	THR	2.1
1	B	89	GLU	2.1
1	C	424	GLU	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)

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, 95^{th} 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	LLDF	B-factors(Å^2)	Q<0.9
4	XYP	C	1498	9/10	0.87	0.27	8.37	36,37,45,48	0
4	XYP	C	1499	10/10	0.80	0.28	8.35	48,53,63,70	0
2	XYP	A	1499	10/10	0.85	0.22	6.65	39,49,60,65	0
2	XYP	B	1500	10/10	0.77	0.17	5.12	35,47,51,59	0
2	XYP	B	1498	9/10	0.92	0.23	2.10	38,41,52,57	0
4	AHR	C	1500	9/10	0.89	0.15	2.03	19,26,32,35	0
2	XYP	A	1497	9/10	0.85	0.29	1.66	45,48,55,60	0
2	XYP	A	1498	9/10	0.91	0.16	0.64	26,32,41,42	0
2	AHR	A	1500	9/10	0.92	0.15	0.62	16,23,29,30	0
2	AHR	B	1501	9/10	0.93	0.12	0.16	19,22,27,30	0
2	XYP	B	1499	9/10	0.96	0.11	-0.18	22,28,33,37	0

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. 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, 95^{th} 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	LLDF	B-factors(Å^2)	Q<0.9
3	PO4	B	1497	5/5	0.97	0.18	3.59	26,27,46,52	0
3	PO4	C	1497	5/5	0.98	0.11	0.58	16,23,25,25	0

6.5 Other polymers (i)

There are no such residues in this entry.