



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 6, 2024 – 01:35 AM EST

PDB ID : 1YPP
Title : ACID ANHYDRIDE HYDROLASE
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Deposited on : 1996-05-29
Resolution : 2.40 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

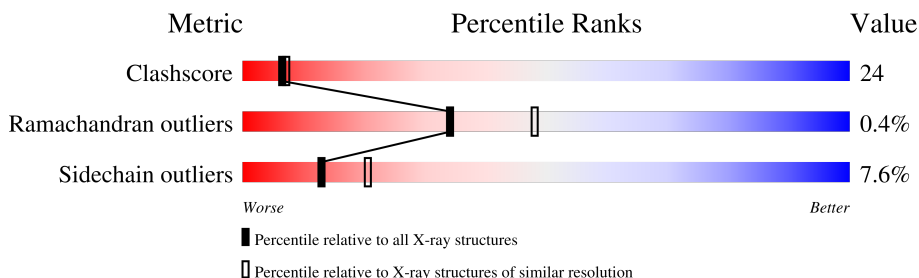
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	286	53% (green), 37% (yellow), 8% (orange), 2% (red), 0% (grey)
1	B	286	53% (green), 38% (yellow), 7% (orange), 2% (red), 0% (grey)

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4746 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 INORGANIC PYROPHOSPHATASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	282	2248	1444	369	432	3	0	0	0
1	B	282	2248	1444	369	432	3	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	73	ALA	LYS	conflict	UNP P00817
A	266	PRO	LEU	conflict	UNP P00817
B	73	ALA	LYS	conflict	UNP P00817
B	266	PRO	LEU	conflict	UNP P00817

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	Mn	0	0
			4	4		
2	B	4	Total	Mn	0	0
			4	4		

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



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

- Molecule 4 is water.

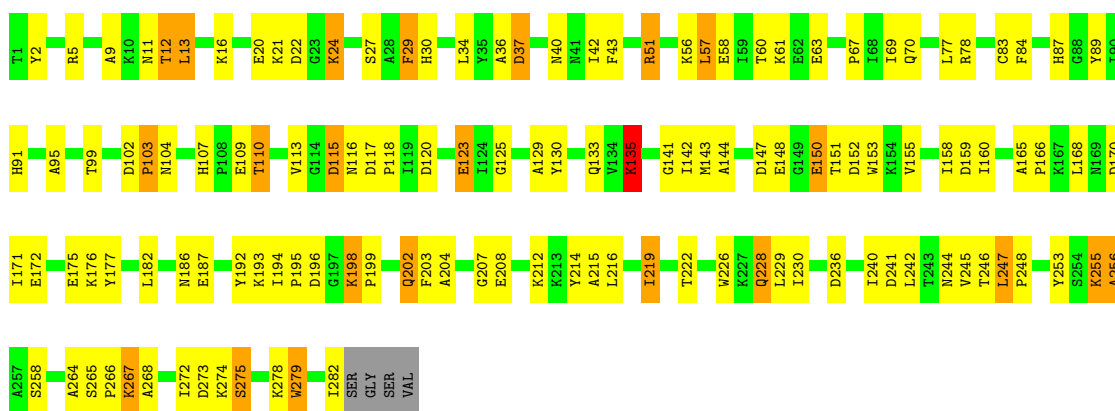
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	110	Total	O	0	0
			110	110		
4	B	112	Total	O	0	0
			112	112		

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. 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.

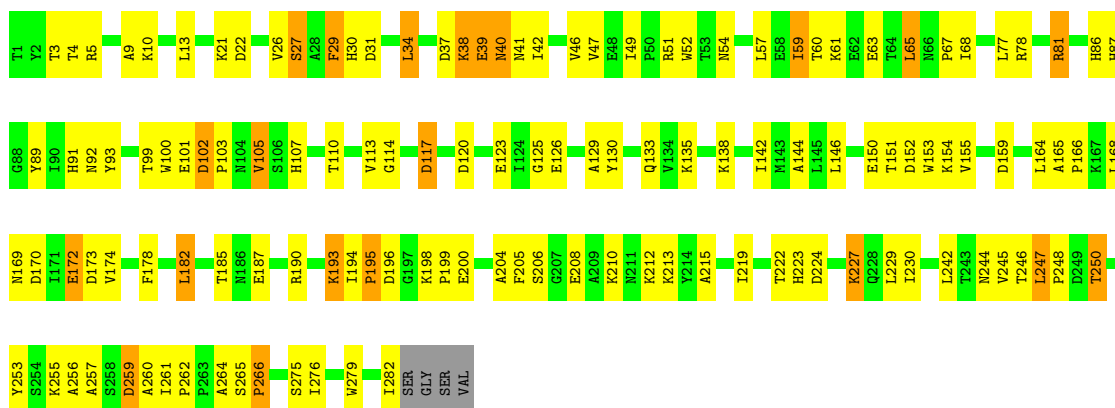
• Molecule 1: INORGANIC PYROPHOSPHATASE

Chain A:  53% 37% 8%



• Molecule 1: INORGANIC PYROPHOSPHATASE

Chain B:  53% 38% 7%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	116.00Å 106.20Å 56.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.40 9.98 – 2.40	Depositor EDS
% Data completeness (in resolution range)	79.0 (10.00-2.40) 79.2 (9.98-2.40)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.35 (at 2.41Å)	Xtriage
Refinement program	PROLSQ	Depositor
R, R_{free}	(Not available) , (Not available) 0.166 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	31.2	Xtriage
Anisotropy	0.926	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 81.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4746	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.22% 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: PO4, MN

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	1.08	1/2307 (0.0%)	1.59	31/3139 (1.0%)
1	B	1.05	0/2307	1.55	25/3139 (0.8%)
All	All	1.07	1/4614 (0.0%)	1.57	56/6278 (0.9%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	150	GLU	CD-OE2	-5.32	1.19	1.25

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	190	ARG	CD-NE-CZ	19.05	150.27	123.60
1	A	120	ASP	CB-CG-OD1	12.25	129.32	118.30
1	A	117	ASP	CB-CG-OD1	10.96	128.17	118.30
1	B	190	ARG	NE-CZ-NH2	10.05	125.32	120.30
1	A	152	ASP	CB-CG-OD1	9.62	126.95	118.30
1	A	78	ARG	NE-CZ-NH1	-8.99	115.80	120.30
1	B	57	LEU	CA-CB-CG	8.92	135.81	115.30
1	B	120	ASP	CB-CG-OD1	8.65	126.08	118.30
1	A	37	ASP	CB-CG-OD1	7.85	125.36	118.30
1	B	117	ASP	CB-CG-OD1	7.72	125.24	118.30
1	B	5	ARG	NE-CZ-NH1	7.45	124.02	120.30
1	A	177	TYR	CB-CG-CD1	-7.38	116.57	121.00
1	B	78	ARG	NE-CZ-NH2	7.04	123.82	120.30
1	B	159	ASP	CB-CG-OD2	6.99	124.59	118.30
1	A	110	THR	CA-C-N	6.93	132.44	117.20
1	A	236	ASP	CB-CG-OD1	6.80	124.42	118.30
1	A	159	ASP	CB-CG-OD2	6.77	124.39	118.30
1	A	172	GLU	OE1-CD-OE2	-6.57	115.42	123.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	29	PHE	CB-CG-CD1	6.47	125.33	120.80
1	A	135	LYS	CA-CB-CG	6.33	127.33	113.40
1	B	135	LYS	CA-CB-CG	6.22	127.09	113.40
1	A	117	ASP	CA-CB-CG	6.21	127.06	113.40
1	A	110	THR	CA-C-O	-6.20	107.08	120.10
1	B	117	ASP	CA-CB-CG	6.17	126.97	113.40
1	A	279	TRP	CA-CB-CG	6.04	125.17	113.70
1	B	5	ARG	CD-NE-CZ	6.01	132.01	123.60
1	B	152	ASP	CB-CG-OD2	-5.94	112.96	118.30
1	A	268	ALA	CB-CA-C	5.91	118.96	110.10
1	A	192	TYR	CB-CG-CD1	5.83	124.50	121.00
1	B	250	THR	N-CA-CB	5.72	121.17	110.30
1	A	51	ARG	NE-CZ-NH2	-5.70	117.45	120.30
1	B	39	GLU	C-N-CA	5.64	135.81	121.70
1	B	190	ARG	NH1-CZ-NH2	-5.61	113.23	119.40
1	A	177	TYR	CB-CG-CD2	5.57	124.34	121.00
1	A	143	MET	CA-CB-CG	5.54	122.71	113.30
1	B	81	ARG	CD-NE-CZ	5.52	131.33	123.60
1	A	12	THR	N-CA-CB	5.48	120.72	110.30
1	A	51	ARG	CB-CG-CD	5.46	125.79	111.60
1	B	78	ARG	NE-CZ-NH1	-5.42	117.59	120.30
1	A	192	TYR	CB-CG-CD2	-5.34	117.80	121.00
1	B	102	ASP	CB-CG-OD1	5.25	123.02	118.30
1	A	37	ASP	CA-CB-CG	5.24	124.92	113.40
1	B	190	ARG	CA-CB-CG	5.20	124.85	113.40
1	A	91	HIS	CB-CA-C	-5.20	100.00	110.40
1	A	16	LYS	CA-CB-CG	5.19	124.81	113.40
1	A	208	GLU	OE1-CD-OE2	-5.19	117.07	123.30
1	A	219	ILE	CA-CB-CG1	5.18	120.85	111.00
1	A	103	PRO	C-N-CA	5.18	134.64	121.70
1	A	198	LYS	CA-CB-CG	5.15	124.74	113.40
1	B	63	GLU	N-CA-CB	5.11	119.80	110.60
1	B	51	ARG	CB-CG-CD	5.09	124.83	111.60
1	B	40	ASN	CB-CA-C	-5.07	100.25	110.40
1	B	266	PRO	N-CA-CB	5.05	109.37	103.30
1	B	170	ASP	CB-CG-OD2	5.05	122.84	118.30
1	A	29	PHE	CB-CG-CD1	5.04	124.32	120.80
1	A	187	GLU	OE1-CD-OE2	5.01	129.31	123.30

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	2248	0	2218	107	0
1	B	2248	0	2218	107	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0
3	A	10	0	0	1	0
3	B	10	0	0	0	0
4	A	110	0	0	13	0
4	B	112	0	0	14	0
All	All	4746	0	4436	213	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 24.

All (213) 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:99:THR:HB	1:A:222:THR:CG2	1.88	1.02
1:A:99:THR:HB	1:A:222:THR:HG23	1.46	0.98
1:B:215:ALA:O	1:B:219:ILE:HD12	1.64	0.97
1:B:99:THR:HB	1:B:222:THR:CG2	1.96	0.94
1:B:224:ASP:HA	1:B:227:LYS:HD3	1.56	0.87
1:B:150:GLU:OE1	4:B:437:HOH:O	1.93	0.86
1:A:247:LEU:O	1:A:253:TYR:HB2	1.79	0.82
1:A:70:GLN:CB	4:A:440:HOH:O	2.29	0.80
1:A:42:ILE:HD13	1:A:160:ILE:HG21	1.65	0.79
1:A:129:ALA:HB1	1:A:133:GLN:NE2	1.97	0.78
1:A:165:ALA:HB3	1:A:166:PRO:HD3	1.65	0.78
1:A:175:GLU:OE1	4:A:436:HOH:O	2.02	0.77
1:A:30:HIS:HD2	1:A:226:TRP:HE1	1.34	0.75
1:B:99:THR:HB	1:B:222:THR:HG22	1.69	0.74
1:B:282:ILE:HG22	1:B:282:ILE:O	1.87	0.73
1:A:36:ALA:HB3	1:A:42:ILE:HG22	1.69	0.73
1:B:59:ILE:HG13	1:B:68:ILE:HG12	1.69	0.73
1:A:130:TYR:CE1	1:A:133:GLN:HG3	2.22	0.73
1:A:274:LYS:N	1:A:274:LYS:HD2	2.03	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:13:LEU:HD13	1:A:77:LEU:HD21	1.70	0.73
1:A:202:GLN:NE2	4:A:481:HOH:O	2.16	0.72
1:B:196:ASP:OD2	4:B:483:HOH:O	2.06	0.72
1:A:274:LYS:HD2	1:A:274:LYS:H	1.54	0.71
1:A:147:ASP:O	4:A:411:HOH:O	2.10	0.70
1:A:195:PRO:HG3	1:A:282:ILE:HD11	1.74	0.69
1:B:130:TYR:H	1:B:133:GLN:HE21	1.41	0.69
1:A:70:GLN:HB3	4:A:440:HOH:O	1.89	0.68
1:A:109:GLU:HG2	1:A:214:TYR:OH	1.94	0.67
1:B:105:VAL:O	1:B:113:VAL:HA	1.93	0.67
1:A:51:ARG:NH1	4:A:406:HOH:O	2.26	0.66
1:A:142:ILE:HG12	1:A:153:TRP:CE3	2.30	0.66
1:B:126:GLU:OE1	4:B:476:HOH:O	2.13	0.66
1:A:255:LYS:NZ	1:A:258:SER:HB2	2.10	0.66
1:B:102:ASP:HB3	1:B:105:VAL:HG23	1.77	0.66
1:A:141:GLY:HA3	1:A:171:ILE:HD13	1.77	0.66
1:A:202:GLN:N	1:A:202:GLN:HE21	1.93	0.65
1:B:142:ILE:HG22	1:B:210:LYS:HB2	1.77	0.65
1:B:54:ASN:OD1	4:B:433:HOH:O	2.14	0.65
1:A:133:GLN:NE2	1:A:135:LYS:HE3	2.12	0.65
1:A:215:ALA:O	1:A:219:ILE:HD12	1.97	0.64
1:A:255:LYS:O	1:A:256:ALA:HB3	1.97	0.64
1:A:129:ALA:HB1	1:A:133:GLN:HE22	1.62	0.64
1:B:31:ASP:OD2	1:B:245:VAL:HG22	1.96	0.64
1:B:255:LYS:O	1:B:256:ALA:HB3	1.98	0.64
1:B:276:ILE:O	4:B:408:HOH:O	2.15	0.64
1:B:40:ASN:O	1:B:41:ASN:HB2	1.98	0.63
1:B:257:ALA:O	1:B:260:ALA:HB3	1.98	0.63
1:B:230:ILE:HG13	1:B:250:THR:HG21	1.81	0.63
1:A:61:LYS:HD2	1:A:240:ILE:HG12	1.80	0.62
1:A:99:THR:HB	1:A:222:THR:HG22	1.80	0.62
1:B:253:TYR:OH	1:B:255:LYS:HG3	2.00	0.62
1:B:99:THR:CB	1:B:222:THR:HG22	2.29	0.61
1:A:13:LEU:HD13	1:A:77:LEU:CD2	2.30	0.61
1:B:144:ALA:HB2	1:B:153:TRP:CZ3	2.36	0.61
1:B:194:ILE:HD11	1:B:200:GLU:HB2	1.83	0.61
1:B:60:THR:HG22	1:B:67:PRO:O	2.01	0.61
1:B:99:THR:HB	1:B:222:THR:HG21	1.83	0.61
1:A:255:LYS:O	1:A:256:ALA:CB	2.49	0.60
1:B:174:VAL:HG11	1:B:182:LEU:HD13	1.82	0.60
1:B:130:TYR:H	1:B:133:GLN:NE2	1.99	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:130:TYR:CE1	1:B:133:GLN:HB2	2.37	0.60
1:A:123:GLU:OE2	1:A:125:GLY:N	2.33	0.59
1:A:21:LYS:HD2	4:A:459:HOH:O	2.03	0.58
1:A:60:THR:HG22	1:A:67:PRO:O	2.03	0.58
1:A:147:ASP:O	1:A:148:GLU:HB2	2.02	0.58
1:B:142:ILE:HD12	1:B:155:VAL:HG22	1.86	0.58
1:A:202:GLN:HE21	1:A:202:GLN:H	1.51	0.58
1:A:248:PRO:HA	1:A:253:TYR:CG	2.38	0.58
1:A:255:LYS:HZ1	1:A:258:SER:HB2	1.68	0.57
1:A:30:HIS:CD2	1:A:226:TRP:HE1	2.18	0.57
1:A:158:ILE:HD13	1:A:168:LEU:HD12	1.85	0.57
1:B:61:LYS:CE	4:B:450:HOH:O	2.49	0.56
1:B:110:THR:HB	1:B:146:LEU:HD21	1.88	0.56
1:A:57:LEU:O	4:A:413:HOH:O	2.18	0.56
1:A:193:LYS:NZ	3:A:301:PO4:O2	2.35	0.56
1:B:125:GLY:HA3	4:B:454:HOH:O	2.05	0.56
1:B:168:LEU:HD23	1:B:173:ASP:HB3	1.88	0.56
1:B:230:ILE:HD12	1:B:242:LEU:HB3	1.87	0.55
1:A:2:TYR:HA	1:A:20:GLU:O	2.06	0.55
1:A:99:THR:CB	1:A:222:THR:CG2	2.75	0.55
1:A:142:ILE:HG12	1:A:153:TRP:HE3	1.72	0.55
1:A:30:HIS:CE1	1:A:242:LEU:HA	2.42	0.54
1:A:198:LYS:HB3	1:A:199:PRO:CD	2.38	0.54
1:A:129:ALA:CB	1:A:133:GLN:HE22	2.21	0.53
1:A:150:GLU:OE1	4:A:434:HOH:O	2.18	0.53
1:B:101:GLU:OE2	4:B:448:HOH:O	2.18	0.53
1:B:265:SER:N	1:B:266:PRO:CD	2.71	0.53
1:B:230:ILE:HA	1:B:242:LEU:HD13	1.91	0.53
1:B:21:LYS:HB2	1:B:26:VAL:HG11	1.89	0.53
1:B:100:TRP:CZ3	1:B:229:LEU:HD13	2.44	0.53
1:B:49:ILE:HG21	1:B:89:TYR:CD2	2.44	0.53
1:B:102:ASP:OD1	1:B:103:PRO:HD2	2.10	0.52
1:B:130:TYR:CZ	1:B:133:GLN:HB2	2.44	0.52
1:A:99:THR:CG2	1:A:222:THR:HG22	2.39	0.52
1:A:170:ASP:OD1	1:A:212:LYS:HB3	2.10	0.52
1:A:5:ARG:HG3	1:A:264:ALA:HB2	1.91	0.52
1:B:93:TYR:OH	1:B:154:LYS:NZ	2.42	0.52
1:B:13:LEU:HD13	1:B:77:LEU:CD2	2.39	0.52
1:B:165:ALA:HB3	1:B:166:PRO:HD3	1.92	0.52
1:B:27:SER:OG	1:B:30:HIS:HB2	2.10	0.51
1:A:102:ASP:OD1	1:A:104:ASN:HB2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:61:LYS:NZ	4:B:450:HOH:O	2.10	0.51
1:B:34:LEU:HD12	1:B:223:HIS:CG	2.45	0.51
1:A:24:LYS:HE3	1:A:255:LYS:CE	2.41	0.51
1:B:255:LYS:O	1:B:256:ALA:CB	2.59	0.51
1:A:165:ALA:HB3	1:A:166:PRO:CD	2.40	0.51
1:B:46:VAL:HG11	1:B:59:ILE:HD11	1.93	0.50
1:A:195:PRO:HD3	1:A:282:ILE:HD13	1.93	0.50
1:A:273:ASP:OD2	1:A:275:SER:OG	2.19	0.50
1:A:70:GLN:HB2	4:A:440:HOH:O	2.05	0.50
1:A:116:ASN:OD1	1:A:240:ILE:HD11	2.11	0.50
1:B:282:ILE:O	1:B:282:ILE:CG2	2.59	0.50
1:A:24:LYS:HE3	1:A:255:LYS:HE3	1.93	0.50
1:B:21:LYS:HB2	1:B:26:VAL:CG1	2.42	0.50
1:B:245:VAL:O	1:B:245:VAL:HG23	2.12	0.49
1:A:37:ASP:CG	1:A:40:ASN:HD22	2.15	0.49
1:B:195:PRO:HD3	1:B:282:ILE:HD11	1.94	0.49
1:A:103:PRO:O	1:A:113:VAL:HB	2.12	0.49
1:A:142:ILE:HD12	1:A:155:VAL:HG22	1.94	0.49
1:B:165:ALA:N	1:B:166:PRO:HD2	2.28	0.49
1:B:21:LYS:O	1:B:22:ASP:C	2.51	0.49
1:B:230:ILE:HG12	1:B:247:LEU:HD23	1.95	0.49
1:A:95:ALA:HB1	1:A:118:PRO:HB2	1.94	0.49
1:A:115:ASP:HB3	1:A:151:THR:O	2.13	0.49
1:B:86:HIS:NE2	1:B:187:GLU:OE2	2.36	0.49
1:A:244:ASN:ND2	1:A:247:LEU:HD23	2.28	0.48
1:A:193:LYS:O	1:A:196:ASP:HB2	2.13	0.48
1:A:198:LYS:CB	1:A:199:PRO:CD	2.92	0.48
1:A:202:GLN:NE2	1:A:202:GLN:N	2.60	0.48
1:A:11:ASN:ND2	1:A:272:ILE:HD11	2.29	0.48
1:A:170:ASP:OD1	1:A:212:LYS:CB	2.63	0.47
1:A:202:GLN:NE2	1:A:202:GLN:H	2.13	0.47
1:B:265:SER:N	1:B:266:PRO:HD3	2.28	0.47
1:B:38:LYS:O	1:B:38:LYS:NZ	2.45	0.47
1:A:244:ASN:OD1	1:A:253:TYR:HA	2.14	0.47
1:B:123:GLU:OE2	1:B:125:GLY:N	2.43	0.46
1:A:43:PHE:HZ	1:A:216:LEU:CD2	2.28	0.46
1:B:38:LYS:HZ2	1:B:38:LYS:HG3	1.65	0.46
1:A:246:THR:O	1:A:248:PRO:HD3	2.15	0.46
1:B:52:TRP:N	1:B:89:TYR:O	2.36	0.46
1:B:194:ILE:N	1:B:195:PRO:CD	2.78	0.46
1:B:247:LEU:O	1:B:253:TYR:HB2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:29:PHE:HE1	1:A:99:THR:O	2.00	0.45
1:A:58:GLU:CD	4:A:419:HOH:O	2.54	0.45
1:A:241:ASP:OD1	1:A:241:ASP:C	2.54	0.45
1:A:83:CYS:O	1:A:84:PHE:C	2.55	0.45
1:A:133:GLN:HE22	1:A:135:LYS:HE3	1.79	0.45
1:A:107:HIS:CD2	1:A:107:HIS:N	2.84	0.45
1:B:107:HIS:HB3	4:B:430:HOH:O	2.16	0.45
1:B:193:LYS:O	1:B:196:ASP:HB2	2.17	0.45
1:A:165:ALA:CB	1:A:166:PRO:HD3	2.43	0.45
1:A:60:THR:HB	1:A:69:ILE:HG12	1.99	0.45
1:B:244:ASN:OD1	1:B:253:TYR:HA	2.17	0.45
1:B:3:THR:HB	1:B:4:THR:H	1.63	0.45
1:A:56:LYS:HE2	1:A:89:TYR:OH	2.18	0.44
1:B:246:THR:O	1:B:248:PRO:HD3	2.17	0.44
1:B:261:ILE:HA	1:B:262:PRO:HD3	1.89	0.44
1:B:9:ALA:O	1:B:10:LYS:C	2.55	0.44
1:B:27:SER:HB2	1:B:65:LEU:HD12	1.99	0.44
1:B:91:HIS:NE2	1:B:185:THR:OG1	2.47	0.44
1:B:138:LYS:HE3	4:B:481:HOH:O	2.17	0.44
1:A:265:SER:N	1:A:266:PRO:CD	2.81	0.44
1:A:195:PRO:CG	1:A:282:ILE:HD11	2.44	0.44
1:A:245:VAL:HB	1:A:255:LYS:CD	2.47	0.44
1:A:158:ILE:HD13	1:A:168:LEU:CD1	2.48	0.44
1:B:37:ASP:HB3	1:B:42:ILE:HB	2.00	0.44
1:B:103:PRO:O	1:B:113:VAL:HB	2.18	0.44
1:B:256:ALA:HA	1:B:259:ASP:OD1	2.18	0.44
1:B:264:ALA:HB1	1:B:266:PRO:HD3	2.00	0.44
1:A:255:LYS:HZ3	1:A:258:SER:HB2	1.82	0.44
1:A:195:PRO:HD3	1:A:282:ILE:CD1	2.48	0.44
1:A:229:LEU:HG	1:A:242:LEU:HD21	1.99	0.44
1:B:144:ALA:HB3	1:B:204:ALA:HB3	1.99	0.43
1:A:22:ASP:N	4:A:491:HOH:O	2.50	0.43
1:A:228:GLN:OE1	4:A:451:HOH:O	2.21	0.43
1:B:81:ARG:NH2	1:B:275:SER:O	2.49	0.43
1:B:198:LYS:HA	1:B:199:PRO:HD3	1.82	0.43
1:B:99:THR:CG2	1:B:222:THR:HG22	2.48	0.43
1:B:261:ILE:HG23	1:B:262:PRO:HD2	2.00	0.43
1:A:203:PHE:HB3	1:A:207:GLY:HA2	2.01	0.43
1:B:172:GLU:H	1:B:172:GLU:HG2	1.38	0.43
1:A:229:LEU:CG	1:A:242:LEU:HD21	2.48	0.43
1:B:169:ASN:N	1:B:173:ASP:OD2	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:174:VAL:O	1:B:178:PHE:HB2	2.18	0.43
1:B:205:PHE:O	1:B:208:GLU:HB2	2.18	0.42
1:A:60:THR:HG23	1:A:63:GLU:HB2	2.01	0.42
1:B:61:LYS:HE2	4:B:450:HOH:O	2.17	0.42
1:A:265:SER:N	1:A:266:PRO:HD3	2.34	0.42
1:B:130:TYR:CD1	1:B:133:GLN:HB2	2.55	0.42
1:A:9:ALA:HB2	1:A:267:LYS:HB2	2.02	0.42
1:A:107:HIS:O	1:A:110:THR:O	2.38	0.42
1:B:164:LEU:O	1:B:165:ALA:C	2.56	0.42
1:B:208:GLU:OE1	1:B:210:LYS:NZ	2.41	0.42
1:B:102:ASP:HA	1:B:103:PRO:HD2	1.80	0.41
1:A:87:HIS:ND1	1:B:87:HIS:ND1	2.52	0.41
1:A:230:ILE:HD11	1:A:244:ASN:HD22	1.84	0.41
1:B:174:VAL:HG11	1:B:182:LEU:CD1	2.48	0.41
1:B:47:VAL:HG11	1:B:129:ALA:CB	2.50	0.41
1:A:278:LYS:HE3	4:B:478:HOH:O	2.20	0.41
1:B:107:HIS:H	1:B:107:HIS:CD2	2.39	0.41
1:B:92:ASN:OD1	1:B:129:ALA:N	2.27	0.41
1:B:114:GLY:HA2	1:B:151:THR:HB	2.02	0.41
1:B:142:ILE:CD1	1:B:155:VAL:HG22	2.50	0.41
1:B:153:TRP:CZ3	1:B:205:PHE:HE2	2.39	0.41
1:B:219:ILE:HD12	1:B:219:ILE:H	1.86	0.41
1:B:282:ILE:N	4:B:477:HOH:O	2.54	0.41
1:A:34:LEU:HD12	1:A:34:LEU:O	2.21	0.41
1:A:144:ALA:CB	1:A:204:ALA:HB3	2.51	0.41
1:B:99:THR:HG22	1:B:222:THR:HG22	2.02	0.40
1:B:107:HIS:CD2	1:B:107:HIS:N	2.89	0.40
1:A:194:ILE:HB	1:A:195:PRO:HD3	2.03	0.40
1:B:77:LEU:HA	1:B:77:LEU:HD23	1.76	0.40
1:A:99:THR:CB	1:A:222:THR:HG22	2.46	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	280/286 (98%)	261 (93%)	18 (6%)	1 (0%)	34	48
1	B	280/286 (98%)	262 (94%)	17 (6%)	1 (0%)	34	48
All	All	560/572 (98%)	523 (93%)	35 (6%)	2 (0%)	34	48

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	256	ALA
1	B	195	PRO

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	244/247 (99%)	226 (93%)	18 (7%)	13	22
1	B	244/247 (99%)	225 (92%)	19 (8%)	12	19
All	All	488/494 (99%)	451 (92%)	37 (8%)	13	20

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	THR
1	A	13	LEU
1	A	24	LYS
1	A	27	SER
1	A	57	LEU
1	A	115	ASP
1	A	123	GLU
1	A	135	LYS
1	A	176	LYS
1	A	182	LEU
1	A	186	ASN

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Mol	Chain	Res	Type
1	A	202	GLN
1	A	228	GLN
1	A	247	LEU
1	A	255	LYS
1	A	267	LYS
1	A	275	SER
1	A	279	TRP
1	B	27	SER
1	B	29	PHE
1	B	34	LEU
1	B	38	LYS
1	B	39	GLU
1	B	59	ILE
1	B	65	LEU
1	B	105	VAL
1	B	117	ASP
1	B	172	GLU
1	B	182	LEU
1	B	193	LYS
1	B	206	SER
1	B	212	LYS
1	B	213	LYS
1	B	227	LYS
1	B	247	LEU
1	B	259	ASP
1	B	279	TRP

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

Mol	Chain	Res	Type
1	A	11	ASN
1	A	30	HIS
1	A	40	ASN
1	A	133	GLN
1	A	202	GLN
1	B	40	ASN
1	B	41	ASN
1	B	107	HIS
1	B	133	GLN
1	B	169	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](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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
3	PO4	B	301	2	4,4,4	1.19	0	6,6,6	0.72	0
3	PO4	A	301	2	4,4,4	1.36	1 (25%)	6,6,6	0.86	0
3	PO4	A	302	2	4,4,4	1.96	1 (25%)	6,6,6	1.30	0
3	PO4	B	302	2	4,4,4	1.82	1 (25%)	6,6,6	1.17	1 (16%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	302	PO4	P-O1	3.82	1.59	1.50
3	B	302	PO4	P-O1	3.56	1.59	1.50
3	A	301	PO4	P-O3	2.24	1.61	1.54

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	302	PO4	O2-P-O1	-2.04	103.44	110.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	301	PO4	1	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](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.