Full wwPDB X-ray Structure Validation Report (i)

Jun 18, 2024 – 01:49 AM EDT

PDB ID	:	3CZP
Title	:	Crystal structure of putative polyphosphate kinase 2 from Pseudomonas aeruginosa PA01
Authors	:	Nocek, B.; Evdokimova, E.; Osipiuk, J.; Savchenko, A.; Edwards, A.M.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on	:	2008-04-29
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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

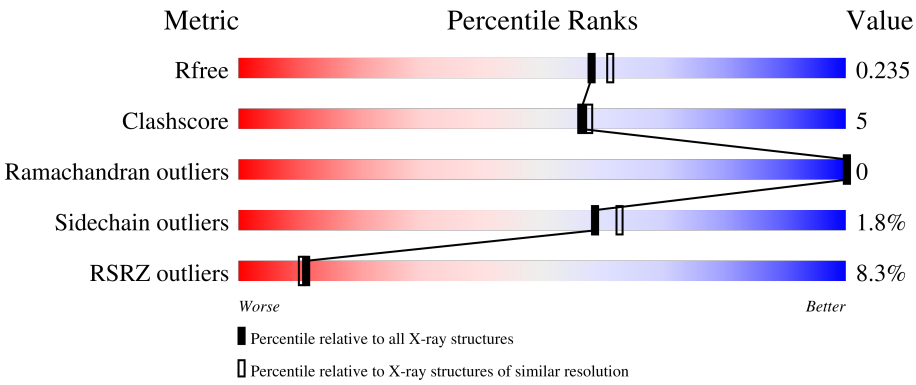
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 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}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (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 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 <=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	500	7% 82% 11% 7%
1	B	500	8% 80% 11% • 8%

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	ACT	B	602	-	-	X	-
4	GOL	A	609	-	-	X	-

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 8481 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.

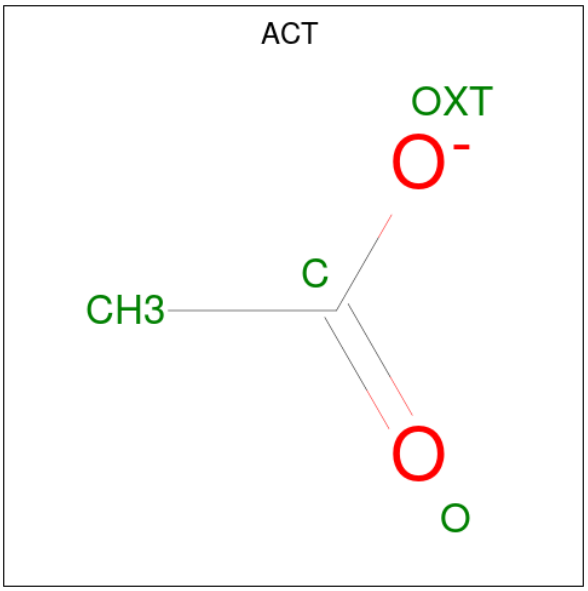
- Molecule 1 is a protein called Putative polyphosphate kinase 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	466	3925	2507	701	708	2	7	0	7	0
1	B	458	3825	2446	684	686	2	7	0	2	0

There are 8 discrepancies between the modelled and reference sequences:

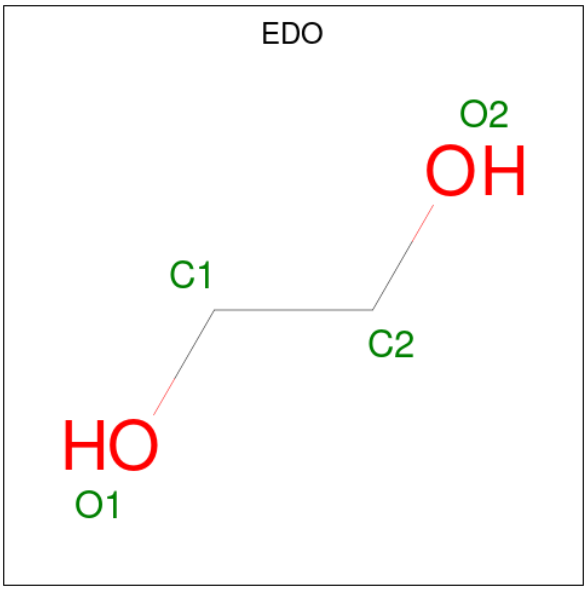
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP Q9HYF1
A	0	HIS	-	EXPRESSION TAG	UNP Q9HYF1
A	497	GLY	-	EXPRESSION TAG	UNP Q9HYF1
A	498	ALA	-	EXPRESSION TAG	UNP Q9HYF1
B	-1	GLY	-	EXPRESSION TAG	UNP Q9HYF1
B	0	HIS	-	EXPRESSION TAG	UNP Q9HYF1
B	497	GLY	-	EXPRESSION TAG	UNP Q9HYF1
B	498	ALA	-	EXPRESSION TAG	UNP Q9HYF1

- Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



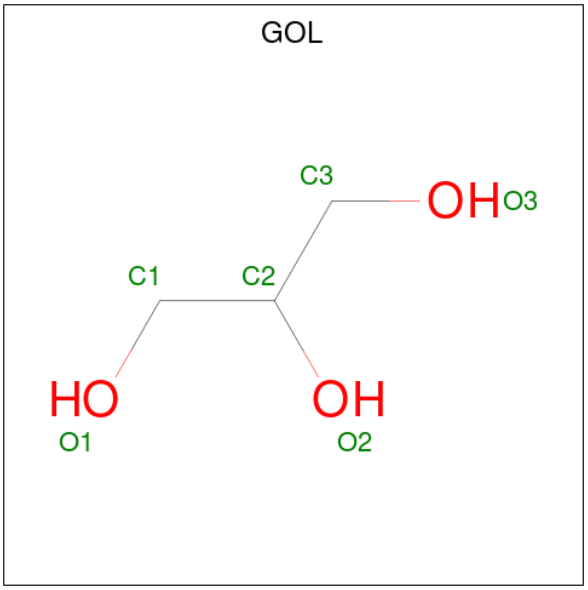
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	4	2	2	0	0
			Total	C	O		
2	A	1	4	2	2	0	0
			Total	C	O		
2	A	1	4	2	2	0	0
			Total	C	O		
2	A	1	4	2	2	0	0
			Total	C	O		
2	B	1	4	2	2	0	0

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



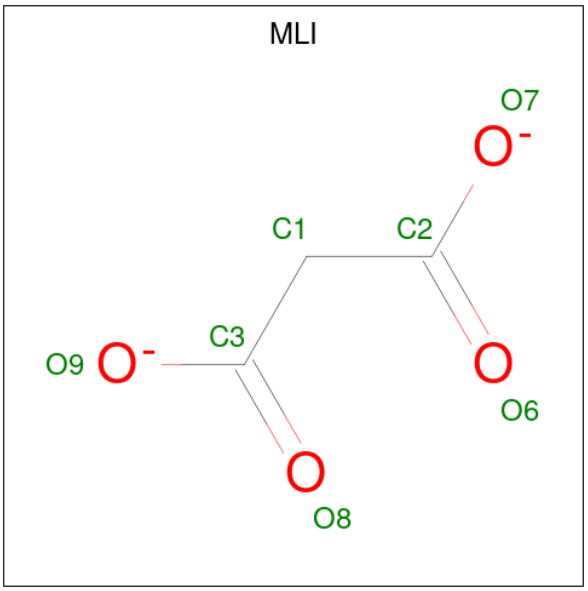
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	4	2	2	0	0
			Total	C	O		
3	B	1	4	2	2	0	0
			Total	C	O		
3	B	1	4	2	2	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	A	1	6	3	3	0	0
			Total	C	O		
4	A	1	6	3	3	0	0
			Total	C	O		
4	A	1	6	3	3	0	0
			Total	C	O		
4	A	1	6	3	3	0	0

- Molecule 5 is MALONATE ION (three-letter code: MLI) (formula: $C_3H_2O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	B	1	7	3	4	0	0

- Molecule 6 is water.

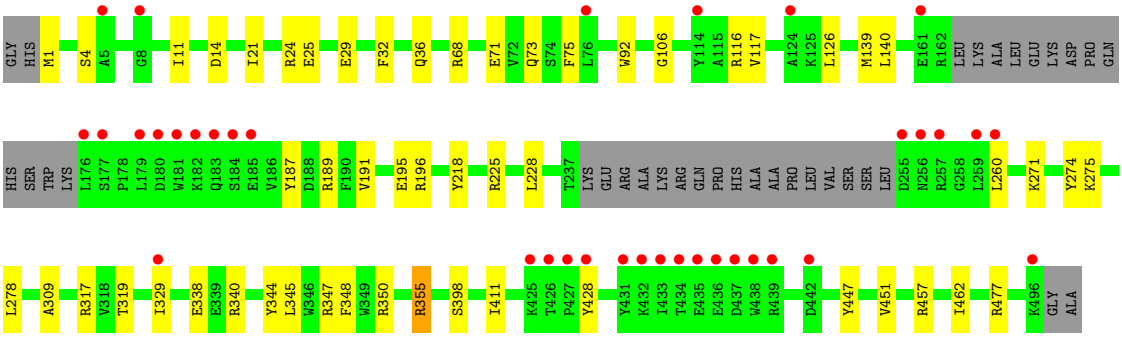
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	323	323	323	0	0
			Total	O		
6	B	345	345	345	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

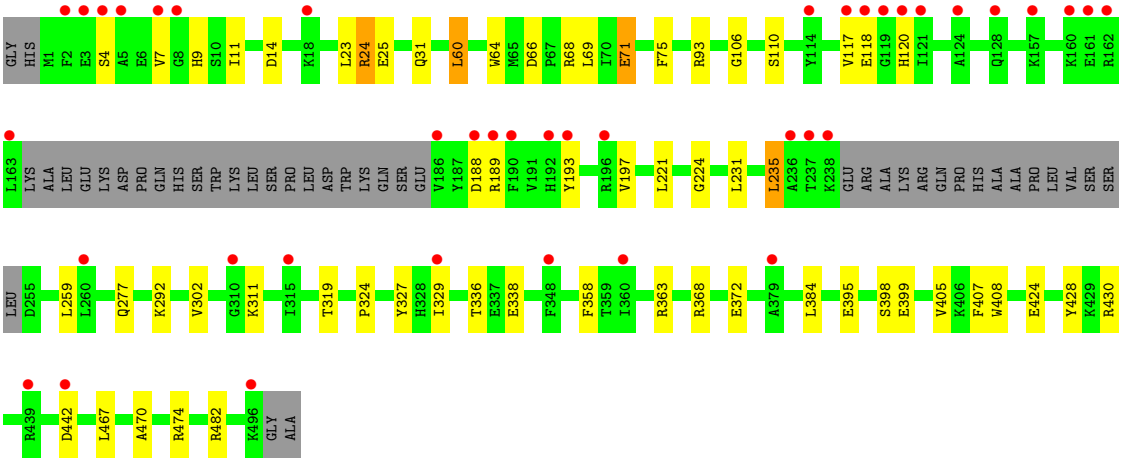
• Molecule 1: Putative polyphosphate kinase 2

Chain A:



• Molecule 1: Putative polyphosphate kinase 2

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	97.09Å 100.73Å 120.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.00 38.59 – 2.00	Depositor EDS
% Data completeness (in resolution range)	95.0 (40.00-2.00) 94.7 (38.59-2.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.68 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.173 , 0.231 0.180 , 0.235	Depositor DCC
R_{free} test set	3811 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	31.8	Xtriage
Anisotropy	0.695	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 43.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.017 for k,h,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	8481	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.83% 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, 0.333 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: ACT, EDO, GOL, MLI

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	0.91	0/4027	0.83	2/5423 (0.0%)
1	B	0.87	4/3915 (0.1%)	0.83	3/5273 (0.1%)
All	All	0.89	4/7942 (0.1%)	0.83	5/10696 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	71	GLU	CG-CD	5.30	1.59	1.51
1	B	235	LEU	CB-CG	5.28	1.67	1.52
1	B	302	VAL	CB-CG1	5.17	1.63	1.52
1	B	470	ALA	CA-CB	5.13	1.63	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	93	ARG	NE-CZ-NH1	5.85	123.22	120.30
1	A	340	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	B	14	ASP	CB-CG-OD1	5.13	122.92	118.30
1	A	355	ARG	NE-CZ-NH2	-5.04	117.78	120.30
1	B	474	ARG	NE-CZ-NH2	-5.02	117.79	120.30

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	3925	0	3874	47	0
1	B	3825	0	3784	38	0
2	A	16	0	12	1	0
2	B	4	0	3	2	0
3	A	4	0	6	0	0
3	B	8	0	12	2	0
4	A	24	0	32	12	0
5	B	7	0	2	0	0
6	A	323	0	0	3	0
6	B	345	0	0	4	0
All	All	8481	0	7725	78	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 5.

All (78) 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:31:GLN:HE22	1:B:66:ASP:H	1.11	0.95
1:B:259:LEU:HD21	1:B:467[A]:LEU:HD11	1.58	0.86
1:A:225:ARG:HG2	4:A:602:GOL:H31	1.63	0.81
1:A:24:ARG:HD3	4:A:609:GOL:H11	1.67	0.76
1:B:277:GLN:HE21	1:B:482:ARG:HH12	1.37	0.71
1:B:424:GLU:HG2	6:B:947:HOH:O	1.90	0.71
1:B:259:LEU:CD2	1:B:467[A]:LEU:HD11	2.24	0.67
1:B:69:LEU:HD21	3:B:603:EDO:H12	1.77	0.66
1:B:277:GLN:NE2	1:B:482:ARG:HH12	1.93	0.66
1:A:228:LEU:CD2	4:A:603:GOL:H12	2.27	0.64
1:A:68:ARG:HG2	1:B:329:ILE:HG21	1.79	0.64
1:A:319:THR:HG21	1:A:329:ILE:HD11	1.81	0.63
1:A:139[B]:MSE:SE	1:A:140:LEU:HD23	2.48	0.63
1:A:24:ARG:CG	4:A:609:GOL:H11	2.30	0.61
1:A:1:MSE:HB3	1:A:195:GLU:OE2	2.00	0.61
1:A:24:ARG:HD3	4:A:609:GOL:C1	2.30	0.61
1:B:259:LEU:HD21	1:B:467[B]:LEU:HD21	1.82	0.60
1:B:11:ILE:HD13	1:B:221:LEU:HD23	1.85	0.59
1:B:60:LEU:HD22	1:B:64:TRP:CE2	2.37	0.58
1:A:24:ARG:CD	4:A:609:GOL:H11	2.31	0.58
1:A:116:ARG:HG2	1:A:126:LEU:HD22	1.87	0.57
1:A:344:TYR:O	1:A:347[A]:ARG:HG2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:319:THR:HG21	1:B:329:ILE:HD11	1.86	0.56
1:A:309:ALA:HA	1:A:411:ILE:HD13	1.87	0.56
1:A:355:ARG:NE	6:A:841:HOH:O	2.40	0.54
1:A:25:GLU:OE1	1:B:430:ARG:NH2	2.38	0.53
1:A:329:ILE:HG21	1:B:68:ARG:HG2	1.91	0.53
1:A:260:LEU:HD11	1:A:451:VAL:HB	1.92	0.51
1:A:29:GLU:OE2	1:B:430:ARG:HG2	2.10	0.50
2:A:601:ACT:H3	6:B:764:HOH:O	2.10	0.50
1:A:24:ARG:HD3	4:A:609:GOL:H31	1.94	0.50
1:B:398:SER:O	2:B:602:ACT:CH3	2.60	0.50
1:A:344:TYR:O	1:A:347[B]:ARG:HG2	2.10	0.50
1:B:324:PRO:HA	1:B:327:TYR:CE2	2.47	0.49
1:B:24:ARG:HD3	6:B:711:HOH:O	2.12	0.49
1:A:196:ARG:NH1	6:A:895:HOH:O	2.41	0.49
1:B:368:ARG:HA	1:B:372:GLU:HB2	1.93	0.49
1:A:24:ARG:HD3	4:A:609:GOL:C3	2.43	0.49
1:A:338[B]:GLU:OE1	1:B:336:THR:OG1	2.22	0.49
1:B:259:LEU:CG	1:B:467[B]:LEU:HD21	2.43	0.49
1:A:187:TYR:O	1:A:191:VAL:HG22	2.12	0.49
1:B:259:LEU:CD2	1:B:467[B]:LEU:HD21	2.44	0.48
1:B:408:TRP:HB3	1:B:467[A]:LEU:HD23	1.95	0.48
1:A:25:GLU:HG2	1:B:428:TYR:CZ	2.49	0.48
1:B:398:SER:O	2:B:602:ACT:H3	2.14	0.47
1:A:21:ILE:HG12	4:A:609:GOL:H2	1.95	0.47
1:B:7:VAL:HG22	1:B:9:HIS:CE1	2.50	0.46
1:B:193:TYR:O	1:B:197:VAL:HG23	2.15	0.46
1:B:231:LEU:O	1:B:235:LEU:HG	2.15	0.46
1:A:139[A]:MSE:SE	1:A:345:LEU:HD12	2.65	0.46
1:A:71[B]:GLU:HG2	1:A:73:GLN:NE2	2.31	0.45
1:A:428:TYR:CZ	1:B:25:GLU:HB3	2.52	0.45
1:B:69:LEU:HD11	3:B:603:EDO:H11	1.97	0.45
1:A:117:VAL:O	1:A:189:ARG:NH2	2.49	0.45
1:A:338[B]:GLU:OE1	1:B:338:GLU:HB2	2.16	0.45
1:A:271:LYS:O	1:A:275:LYS:HG3	2.17	0.45
1:B:118:GLU:HB3	1:B:120:HIS:CE1	2.52	0.44
1:A:274:TYR:CZ	1:A:278:LEU:HD22	2.53	0.44
1:A:398[B]:SER:OG	1:A:462:ILE:HG23	2.17	0.44
1:A:14:ASP:OD2	6:A:764:HOH:O	2.21	0.44
1:B:395:GLU:O	1:B:399:GLU:HG3	2.18	0.43
1:B:11:ILE:HD11	6:B:957:HOH:O	2.18	0.43
1:B:75:PHE:HB2	1:B:106:GLY:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:317:ARG:HG3	1:A:477:ARG:HD3	2.00	0.43
1:B:117:VAL:HG13	1:B:189:ARG:HG3	2.00	0.43
1:A:92:TRP:CH2	1:A:139[B]:MSE:CE	3.02	0.43
1:A:228:LEU:HD21	4:A:603:GOL:H31	2.00	0.42
1:B:405:VAL:HG11	1:B:407:PHE:CZ	2.55	0.42
1:A:347[B]:ARG:HD3	1:A:348:PHE:CZ	2.55	0.42
1:A:75:PHE:HB2	1:A:106:GLY:O	2.20	0.42
1:A:11:ILE:HD12	1:A:218:TYR:HA	2.01	0.41
1:A:225:ARG:HG2	4:A:602:GOL:C3	2.43	0.41
1:B:23:LEU:HD21	1:B:224:GLY:HA3	2.02	0.41
1:A:24:ARG:HG2	4:A:609:GOL:H11	2.01	0.41
1:A:347[B]:ARG:HG3	1:A:348:PHE:CD2	2.56	0.41
1:A:447:TYR:O	1:A:451:VAL:HG23	2.21	0.40
1:A:32:PHE:O	1:A:36:GLN:HG2	2.21	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	467/500 (93%)	459 (98%)	8 (2%)	0	100	100
1	B	454/500 (91%)	440 (97%)	14 (3%)	0	100	100
All	All	921/1000 (92%)	899 (98%)	22 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	402/418 (96%)	399 (99%)	3 (1%)	84	88
1	B	390/418 (93%)	378 (97%)	12 (3%)	40	40
All	All	792/836 (95%)	777 (98%)	15 (2%)	59	61

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	SER
1	A	457[A]	ARG
1	A	457[B]	ARG
1	B	4	SER
1	B	24	ARG
1	B	60	LEU
1	B	71	GLU
1	B	110	SER
1	B	188	ASP
1	B	292	LYS
1	B	311	LYS
1	B	358	PHE
1	B	363	ARG
1	B	384	LEU
1	B	442	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	306	ASN
1	B	31	GLN
1	B	120	HIS
1	B	277	GLN

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)

13 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	GOL	A	610	-	5,5,5	0.33	0	5,5,5	0.91	0
2	ACT	A	607	-	3,3,3	0.87	0	3,3,3	1.09	0
2	ACT	B	602	-	3,3,3	1.04	0	3,3,3	1.66	1 (33%)
3	EDO	B	603	-	3,3,3	0.49	0	2,2,2	0.20	0
4	GOL	A	609	-	5,5,5	0.71	0	5,5,5	1.26	0
3	EDO	A	604	-	3,3,3	0.66	0	2,2,2	0.20	0
5	MLI	B	605	-	6,6,6	1.23	0	7,7,7	1.26	1 (14%)
4	GOL	A	603	-	5,5,5	0.49	0	5,5,5	0.76	0
2	ACT	A	608	-	3,3,3	0.92	0	3,3,3	1.67	1 (33%)
2	ACT	A	601	-	3,3,3	0.84	0	3,3,3	1.72	1 (33%)
4	GOL	A	602	-	5,5,5	0.92	0	5,5,5	1.57	1 (20%)
3	EDO	B	606	-	3,3,3	0.43	0	2,2,2	0.48	0
2	ACT	A	606	-	3,3,3	0.85	0	3,3,3	1.59	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
4	GOL	A	610	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	B	603	-	-	1/1/1/1	-
4	GOL	A	609	-	-	2/4/4/4	-
3	EDO	A	604	-	-	1/1/1/1	-
5	MLI	B	605	-	-	2/4/4/4	-
4	GOL	A	603	-	-	2/4/4/4	-
4	GOL	A	602	-	-	2/4/4/4	-
3	EDO	B	606	-	-	1/1/1/1	-

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	602	GOL	C3-C2-C1	2.60	121.35	111.80
5	B	605	MLI	C3-C1-C2	-2.41	104.43	112.95
2	B	602	ACT	OXT-C-O	-2.32	113.42	122.03
2	A	601	ACT	OXT-C-O	-2.23	113.75	122.03
2	A	608	ACT	OXT-C-O	-2.20	113.85	122.03

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	609	GOL	O2-C2-C3-O3
4	A	602	GOL	O1-C1-C2-C3
4	A	610	GOL	C1-C2-C3-O3
4	A	609	GOL	C1-C2-C3-O3
4	A	603	GOL	C1-C2-C3-O3
4	A	602	GOL	O1-C1-C2-O2
4	A	610	GOL	O2-C2-C3-O3
3	A	604	EDO	O1-C1-C2-O2
3	B	603	EDO	O1-C1-C2-O2
4	A	603	GOL	O2-C2-C3-O3
3	B	606	EDO	O1-C1-C2-O2
5	B	605	MLI	C2-C1-C3-O8
5	B	605	MLI	C2-C1-C3-O9

There are no ring outliers.

6 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	602	ACT	2	0
3	B	603	EDO	2	0
4	A	609	GOL	8	0
4	A	603	GOL	2	0
2	A	601	ACT	1	0
4	A	602	GOL	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)

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	460/500 (92%)	0.55	36 (7%)	13	12	16, 29, 50, 59	0
1	B	452/500 (90%)	0.67	40 (8%)	10	9	13, 29, 55, 86	1 (0%)
All	All	912/1000 (91%)	0.61	76 (8%)	11	10	13, 29, 53, 86	1 (0%)

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	427	PRO	9.7
1	A	176	LEU	8.9
1	B	2	PHE	7.5
1	A	255	ASP	7.1
1	B	7	VAL	6.8
1	B	238	LYS	6.2
1	A	428	TYR	6.1
1	A	431	TYR	5.4
1	B	5	ALA	5.4
1	A	182	LYS	5.3
1	B	157	LYS	5.2
1	B	124	ALA	5.0
1	A	177	SER	5.0
1	A	426	THR	4.9
1	B	4	SER	4.6
1	B	496	LYS	4.5
1	A	436	GLU	4.3
1	A	435	GLU	4.2
1	A	439	ARG	4.1
1	B	237	THR	3.9
1	A	432	LYS	3.9
1	B	236	ALA	3.8
1	B	379	ALA	3.8
1	B	121	ILE	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	434	THR	3.7
1	B	161	GLU	3.6
1	A	76	LEU	3.6
1	B	196	ARG	3.5
1	A	433	ILE	3.5
1	B	3	GLU	3.4
1	B	192	HIS	3.3
1	B	8	GLY	3.1
1	B	117	VAL	3.0
1	B	119	GLY	3.0
1	A	438	TRP	2.9
1	A	257	ARG	2.9
1	A	185	GLU	2.9
1	A	496	LYS	2.8
1	B	260	LEU	2.8
1	A	180	ASP	2.8
1	B	439	ARG	2.7
1	B	188	ASP	2.7
1	A	179	LEU	2.7
1	B	128	GLN	2.7
1	A	259	LEU	2.7
1	B	163	LEU	2.7
1	B	162	ARG	2.6
1	A	329	ILE	2.6
1	B	118	GLU	2.6
1	A	256	ASN	2.5
1	A	114	TYR	2.4
1	B	329	ILE	2.4
1	A	161	GLU	2.4
1	B	315	ILE	2.4
1	A	425	LYS	2.4
1	B	160	LYS	2.4
1	A	442	ASP	2.4
1	B	193	TYR	2.3
1	B	189	ARG	2.3
1	A	260	LEU	2.2
1	B	114	TYR	2.2
1	B	348	PHE	2.2
1	A	5	ALA	2.2
1	B	360	ILE	2.1
1	A	181	TRP	2.1
1	A	183	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	186	VAL	2.1
1	A	184	SER	2.1
1	A	437	ASP	2.1
1	B	442	ASP	2.1
1	B	120	HIS	2.1
1	A	8	GLY	2.1
1	A	124	ALA	2.0
1	B	18	LYS	2.0
1	B	190	PHE	2.0
1	B	310	GLY	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)

There are no monosaccharides in this entry.

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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	GOL	A	602	6/6	0.74	0.40	52,57,58,58	0
2	ACT	A	606	4/4	0.81	0.17	67,67,67,67	0
4	GOL	A	610	6/6	0.84	0.16	69,71,71,71	0
3	EDO	B	606	4/4	0.85	0.16	54,54,55,58	0
2	ACT	A	608	4/4	0.86	0.27	56,56,57,57	0
3	EDO	B	603	4/4	0.87	0.17	59,61,62,64	0
4	GOL	A	609	6/6	0.89	0.46	42,52,53,54	0
2	ACT	A	607	4/4	0.89	0.21	55,55,56,56	0
4	GOL	A	603	6/6	0.89	0.34	53,56,57,58	0
3	EDO	A	604	4/4	0.89	0.33	57,59,59,60	0
5	MLI	B	605	7/7	0.89	0.13	37,47,52,60	0
2	ACT	B	602	4/4	0.90	0.28	56,56,56,57	0
2	ACT	A	601	4/4	0.94	0.13	62,62,62,63	0

6.5 Other polymers (i)

There are no such residues in this entry.