



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 6, 2023 – 08:27 AM EDT

PDB ID : 1KH9
Title : E. COLI ALKALINE PHOSPHATASE MUTANT (D153GD330N) COMPLEX WITH PHOSPHATE
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Deposited on : 2001-11-29
Resolution : 2.50 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 : 2.35
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) : 2.35

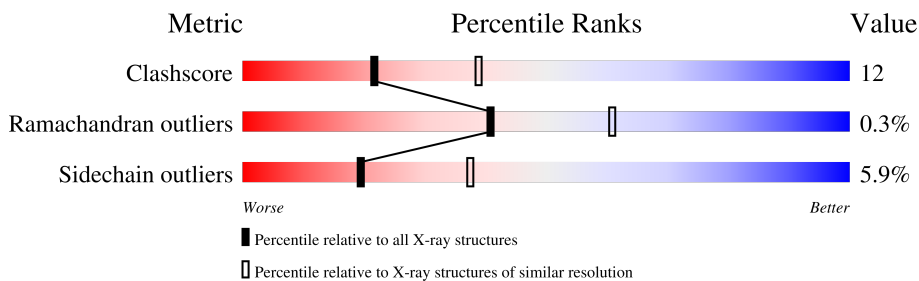
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)

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	449	
1	B	449	

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	PO4	B	453	-	X	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6665 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 Alkaline phosphatase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	444	3252	2009	577	655	11	0	0	0
1	B	444	3252	2009	577	655	11	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	15	ASN	ASP	conflict	UNP P00634
A	35	ASN	ASP	conflict	UNP P00634
A	176	GLN	GLU	conflict	UNP P00634
A	228	GLU	GLN	conflict	UNP P00634
A	230	GLU	GLN	conflict	UNP P00634
A	330	ASN	ASP	engineered mutation	UNP P00634
B	15	ASN	ASP	conflict	UNP P00634
B	35	ASN	ASP	conflict	UNP P00634
B	176	GLN	GLU	conflict	UNP P00634
B	228	GLU	GLN	conflict	UNP P00634
B	230	GLU	GLN	conflict	UNP P00634
B	330	ASN	ASP	engineered mutation	UNP P00634

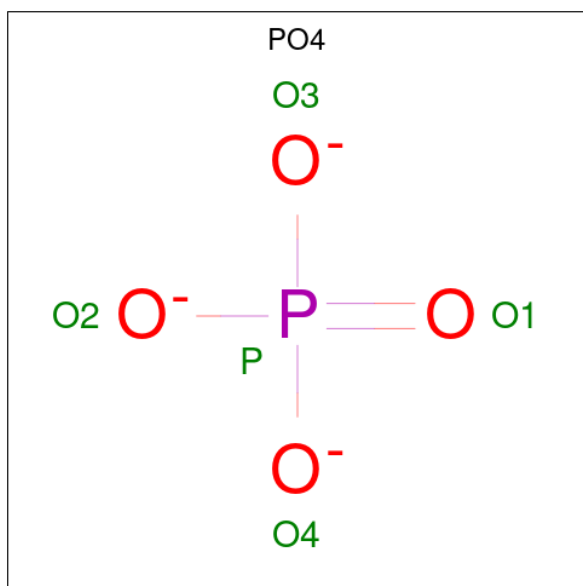
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

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

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

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



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

- Molecule 5 is water.

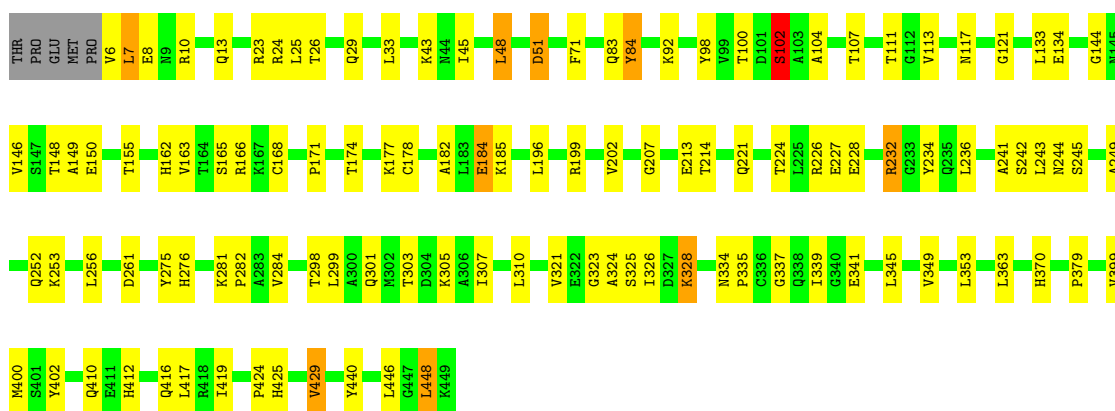
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	69	Total O 69 69	0	0
5	B	78	Total O 78 78	0	0

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. 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: Alkaline phosphatase

Chain A: 



- Molecule 1: Alkaline phosphatase

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, α , β , γ	164.01Å 164.01Å 138.88Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	10.00 – 2.50 19.86 – 2.50	Depositor EDS
% Data completeness (in resolution range)	83.4 (10.00-2.50) 83.4 (19.86-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.69 (at 2.50Å)	Xtrriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.196 , 0.250 0.287 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	43.5	Xtrriage
Anisotropy	0.559	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 65.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	6665	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.43% 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, ZN, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.53	1/3305 (0.0%)	0.78	2/4486 (0.0%)
1	B	0.51	0/3305	0.76	2/4486 (0.0%)
All	All	0.52	1/6610 (0.0%)	0.77	4/8972 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	102	SER	CA-C	7.05	1.71	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	48	LEU	CA-CB-CG	6.36	129.94	115.30
1	B	97	ASP	N-CA-C	-5.88	95.12	111.00
1	A	323	GLY	N-CA-C	-5.25	99.98	113.10
1	B	323	GLY	N-CA-C	-5.13	100.29	113.10

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	3252	0	3189	85	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3252	0	3190	76	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	1	0	0	0	0
4	A	4	0	0	1	0
4	B	5	0	0	2	0
5	A	69	0	0	4	0
5	B	78	0	0	3	0
All	All	6665	0	6379	154	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 12.

All (154) 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:102:SER:OG	4:B:453:PO4:P	2.03	1.17
1:B:102:SER:HG	4:B:453:PO4:P	1.93	0.92
1:B:178:CYS:HB3	1:B:181:ASN:HD22	1.36	0.89
1:A:7:LEU:H	1:A:7:LEU:HD13	1.44	0.82
1:A:334:ASN:HD22	1:A:337:GLY:H	1.30	0.77
1:A:325:SER:HA	1:A:328:LYS:HD2	1.69	0.75
1:B:208:ALA:HB2	1:B:258:LEU:HB3	1.69	0.74
1:A:335:PRO:HB3	1:A:400:MET:HE3	1.72	0.71
1:A:111:THR:CG2	1:A:113:VAL:HG12	2.21	0.71
1:A:168:CYS:SG	1:A:177:LYS:HB2	2.30	0.70
1:B:48:LEU:HD13	1:B:321:VAL:HB	1.73	0.69
1:A:23:ARG:HD2	1:B:440:TYR:CE2	2.27	0.69
1:B:220:TRP:CZ2	1:B:232:ARG:HD3	2.27	0.69
1:A:6:VAL:N	1:A:29:GLN:HG2	2.08	0.68
1:A:48:LEU:HD13	1:A:321:VAL:HB	1.75	0.68
1:B:224:THR:OG1	1:B:227:GLU:HG3	1.93	0.68
1:A:174:THR:HG23	1:A:178:CYS:HB2	1.78	0.66
1:A:111:THR:HG22	1:A:113:VAL:HG12	1.77	0.66
1:B:267:ARG:HH21	1:B:267:ARG:HG2	1.62	0.65
1:A:249:ALA:HA	1:A:253:LYS:O	1.97	0.65
1:B:182:ALA:HB3	1:B:185:LYS:HD3	1.79	0.65
1:A:13:GLN:HG2	1:A:23:ARG:O	1.97	0.64
1:B:298:THR:OG1	1:B:301:GLN:HG3	1.99	0.62
1:A:107:THR:O	1:A:111:THR:HB	2.00	0.62
1:B:120:LEU:O	1:B:162:HIS:HA	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:LEU:HD22	1:A:10:ARG:HE	1.66	0.60
1:B:213:GLU:O	1:B:225:LEU:HD22	2.01	0.60
1:A:48:LEU:HG	1:A:349:VAL:HG22	1.83	0.60
1:A:163:VAL:HG12	1:A:165:SER:H	1.68	0.59
1:A:148:THR:HG23	1:A:299:LEU:HD13	1.84	0.59
1:A:144:GLY:HA2	1:A:202:VAL:O	2.03	0.59
1:A:146:VAL:HG22	1:A:321:VAL:HG13	1.86	0.58
1:B:363:LEU:HD13	1:B:424:PRO:O	2.02	0.58
1:B:120:LEU:HD12	1:B:166:ARG:HA	1.87	0.57
1:A:419:ILE:CD1	1:A:429:VAL:HG22	2.34	0.57
1:A:182:ALA:HB1	1:A:184:GLU:OE1	2.03	0.57
1:B:218:GLY:O	1:B:221:GLN:HG2	2.03	0.57
1:A:33:LEU:HD12	1:B:427:ALA:HB1	1.86	0.56
1:A:339:ILE:HD11	1:A:400:MET:HE1	1.88	0.56
1:A:303:THR:O	1:A:307:ILE:HG13	2.06	0.56
1:A:412:HIS:HE1	4:A:453:PO4:O1	1.71	0.56
1:B:48:LEU:HB2	1:B:366:VAL:HG22	1.87	0.56
1:B:121:GLY:O	1:B:162:HIS:HD2	1.89	0.55
1:A:419:ILE:HD11	1:A:429:VAL:HG22	1.89	0.55
1:B:353:LEU:O	1:B:357:LYS:HG3	2.06	0.55
1:A:334:ASN:ND2	1:A:337:GLY:H	1.99	0.54
1:A:379:PRO:HA	1:A:399:VAL:HG21	1.89	0.54
1:A:182:ALA:HB3	1:A:185:LYS:HD3	1.90	0.54
1:A:134:GLU:OE2	1:A:162:HIS:HE1	1.91	0.54
1:A:7:LEU:H	1:A:7:LEU:CD1	2.19	0.53
1:B:228:GLU:HB2	5:B:1103:HOH:O	2.07	0.53
1:A:7:LEU:HD21	1:A:25:LEU:HA	1.91	0.53
1:A:10:ARG:O	1:A:24:ARG:HD3	2.09	0.53
1:A:111:THR:HG21	1:A:113:VAL:HG12	1.90	0.53
1:A:7:LEU:HG	1:A:26:THR:OG1	2.09	0.52
1:B:10:ARG:NH2	1:B:29:GLN:OE1	2.42	0.52
1:B:148:THR:HG23	1:B:299:LEU:HD13	1.91	0.51
1:B:163:VAL:HG23	1:B:194:GLN:NE2	2.25	0.51
1:B:310:LEU:HD23	1:B:317:PHE:CD1	2.46	0.51
1:A:298:THR:OG1	1:A:301:GLN:HG3	2.11	0.50
1:B:235:GLN:HE22	1:B:246:VAL:HG13	1.76	0.50
1:B:267:ARG:HG2	1:B:267:ARG:NH2	2.26	0.50
1:A:202:VAL:HB	1:A:310:LEU:HD11	1.94	0.50
1:B:89:LEU:O	1:B:116:TYR:HA	2.11	0.50
1:A:102:SER:CB	1:A:166:ARG:HH12	2.24	0.50
1:A:199:ARG:NH2	1:A:232:ARG:O	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:LEU:HD22	1:A:10:ARG:NE	2.28	0.49
1:B:253:LYS:N	1:B:254:PRO:HD3	2.28	0.49
1:A:104:ALA:HB2	1:A:117:ASN:HA	1.95	0.49
1:A:275:TYR:O	1:A:276:HIS:HB2	2.12	0.49
1:B:383:ALA:HB1	5:B:1092:HOH:O	2.12	0.48
1:A:51:ASP:O	1:A:326:ILE:HB	2.13	0.48
1:B:370:HIS:CE1	1:B:412:HIS:CD2	3.01	0.48
1:A:121:GLY:O	1:A:162:HIS:HD2	1.96	0.48
1:B:13:GLN:HG2	1:B:23:ARG:O	2.13	0.48
1:B:369:ASP:N	1:B:369:ASP:OD1	2.47	0.48
1:A:199:ARG:HA	1:A:234:TYR:OH	2.14	0.48
1:A:402:TYR:HB3	1:A:410:GLN:HG3	1.96	0.48
1:B:370:HIS:CE1	1:B:412:HIS:CG	3.01	0.48
1:A:281:LYS:CG	1:A:282:PRO:HD2	2.44	0.48
1:A:440:TYR:CD2	1:B:23:ARG:HD3	2.48	0.48
1:A:424:PRO:O	1:A:425:HIS:HB2	2.13	0.47
1:A:23:ARG:HD2	1:B:440:TYR:CD2	2.48	0.47
1:A:146:VAL:CG2	1:A:321:VAL:HG13	2.44	0.47
1:B:145:ASN:ND2	5:B:1033:HOH:O	2.47	0.47
1:A:149:ALA:HB2	1:A:324:ALA:CB	2.45	0.47
1:B:204:LEU:HD23	1:B:257:GLY:HA3	1.96	0.47
1:B:150:GLU:HG2	1:B:207:GLY:HA2	1.96	0.46
1:A:149:ALA:HB2	1:A:324:ALA:HB1	1.97	0.46
1:A:102:SER:HB2	1:A:166:ARG:HH12	1.79	0.46
1:A:100:THR:HG22	5:A:1080:HOH:O	2.14	0.46
1:B:46:ILE:HG22	1:B:48:LEU:HD22	1.98	0.46
1:B:299:LEU:HD11	1:B:321:VAL:HG13	1.97	0.45
1:A:276:HIS:HA	5:A:1121:HOH:O	2.16	0.45
1:A:325:SER:HA	1:A:328:LYS:HB2	1.98	0.45
1:A:334:ASN:ND2	5:A:1047:HOH:O	2.50	0.45
1:B:446:LEU:HB3	1:B:448:LEU:HD13	1.99	0.45
1:A:337:GLY:O	1:A:341:GLU:HG2	2.16	0.45
1:B:90:ASN:HB3	1:B:93:THR:OG1	2.16	0.45
1:A:84:TYR:O	1:A:84:TYR:HD1	1.99	0.45
1:A:224:THR:OG1	1:A:227:GLU:HG3	2.16	0.45
1:B:142:ALA:HB3	1:B:317:PHE:HB3	1.99	0.45
1:B:226:ARG:O	1:B:229:ALA:HB3	2.17	0.45
1:B:229:ALA:O	1:B:234:TYR:HD1	2.00	0.45
1:A:448:LEU:HD12	1:A:448:LEU:HA	1.57	0.44
1:B:134:GLU:OE2	1:B:162:HIS:HE1	2.00	0.44
1:B:358:LYS:HE3	1:B:358:LYS:HB2	1.74	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:363:LEU:HD13	1:A:424:PRO:O	2.18	0.44
1:A:370:HIS:CE1	1:A:412:HIS:CE1	3.06	0.44
1:B:40:LYS:O	1:B:424:PRO:HB3	2.18	0.44
1:B:284:VAL:HG12	1:B:285:THR:N	2.33	0.44
1:A:48:LEU:HD12	1:A:345:LEU:HD11	1.99	0.44
1:B:151:LEU:HD22	1:B:206:GLY:O	2.17	0.44
1:A:207:GLY:HA2	1:A:261:ASP:O	2.18	0.43
1:A:133:LEU:HD23	1:A:133:LEU:C	2.37	0.43
1:A:163:VAL:HG13	1:A:178:CYS:SG	2.59	0.43
1:B:52:GLY:HA2	1:B:370:HIS:O	2.19	0.43
1:B:111:THR:HG21	1:B:129:HIS:HB2	2.01	0.43
1:A:150:GLU:H	1:A:150:GLU:HG2	1.60	0.43
1:B:310:LEU:C	1:B:312:LYS:H	2.22	0.43
1:B:8:GLU:O	1:B:71:PHE:CZ	2.71	0.43
1:A:45:ILE:HD12	1:A:446:LEU:HG	2.00	0.42
1:B:275:TYR:O	1:B:276:HIS:HB2	2.18	0.42
1:B:144:GLY:O	1:B:319:LEU:HA	2.20	0.42
1:A:171:PRO:HG2	1:A:213:GLU:HB3	2.00	0.42
1:A:345:LEU:O	1:A:349:VAL:HG23	2.19	0.42
1:B:379:PRO:HA	1:B:399:VAL:HG21	2.01	0.42
1:B:277:GLY:O	1:B:281:LYS:HB2	2.19	0.42
1:A:236:LEU:HA	1:A:256:LEU:O	2.20	0.42
1:B:292:ARG:NH2	1:B:297:PRO:O	2.52	0.42
1:A:228:GLU:O	1:A:232:ARG:HG3	2.20	0.42
1:B:214:THR:HA	1:B:224:THR:HA	2.02	0.42
1:A:243:LEU:O	1:A:305:LYS:HE2	2.20	0.41
1:A:98:TYR:CE1	1:B:68:ALA:HB2	2.55	0.41
1:A:242:SER:O	1:A:245:SER:HB3	2.20	0.41
1:B:146:VAL:HG13	1:B:319:LEU:HD11	2.02	0.41
1:A:244:ASN:HA	1:A:305:LYS:HZ3	1.85	0.41
5:A:1007:HOH:O	1:B:123:ASP:HB2	2.20	0.41
1:B:424:PRO:O	1:B:425:HIS:HB2	2.21	0.41
1:B:178:CYS:HB3	1:B:181:ASN:ND2	2.19	0.41
1:B:337:GLY:O	1:B:341:GLU:HG2	2.20	0.41
1:A:98:TYR:HE1	1:B:68:ALA:HB2	1.86	0.41
1:B:149:ALA:HB2	1:B:324:ALA:CB	2.50	0.41
1:B:196:LEU:HD12	1:B:196:LEU:HA	1.89	0.41
1:B:15:ASN:O	1:B:21:GLY:HA3	2.20	0.41
1:B:10:ARG:HB2	1:B:71:PHE:CD1	2.56	0.40
1:B:48:LEU:O	1:B:366:VAL:HA	2.21	0.40
1:A:48:LEU:HD12	1:A:345:LEU:CD1	2.50	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:SER:HB2	1:A:166:ARG:NH1	2.36	0.40
1:A:199:ARG:O	1:A:199:ARG:HG2	2.21	0.40
1:B:165:SER:HB3	1:B:178:CYS:SG	2.62	0.40
1:B:7:LEU:HB2	1:B:10:ARG:HE	1.86	0.40
1:A:226:ARG:NH1	1:A:236:LEU:HD23	2.36	0.40
1:A:416:GLN:HG2	1:B:59:THR:OG1	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	442/449 (98%)	422 (96%)	18 (4%)	2 (0%)	29	48
1	B	442/449 (98%)	414 (94%)	27 (6%)	1 (0%)	47	68
All	All	884/898 (98%)	836 (95%)	45 (5%)	3 (0%)	41	61

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	241	ALA
1	A	8	GLU
1	B	311	SER

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	331/340 (97%)	310 (94%)	21 (6%)	18	34
1	B	331/340 (97%)	313 (95%)	18 (5%)	22	42
All	All	662/680 (97%)	623 (94%)	39 (6%)	19	37

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LEU
1	A	43	LYS
1	A	51	ASP
1	A	71	PHE
1	A	83	GLN
1	A	84	TYR
1	A	92	LYS
1	A	102	SER
1	A	155	THR
1	A	184	GLU
1	A	196	LEU
1	A	214	THR
1	A	221	GLN
1	A	232	ARG
1	A	252	GLN
1	A	284	VAL
1	A	328	LYS
1	A	353	LEU
1	A	417	LEU
1	A	429	VAL
1	A	448	LEU
1	B	51	ASP
1	B	71	PHE
1	B	84	TYR
1	B	147	SER
1	B	151	LEU
1	B	155	THR
1	B	163	VAL
1	B	196	LEU
1	B	209	LYS
1	B	221	GLN
1	B	232	ARG
1	B	252	GLN
1	B	269	LEU
1	B	287	THR

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Mol	Chain	Res	Type
1	B	291	GLN
1	B	314	GLU
1	B	315	LYS
1	B	417	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	GLN
1	A	15	ASN
1	A	83	GLN
1	A	162	HIS
1	A	235	GLN
1	A	244	ASN
1	A	263	ASN
1	A	334	ASN
1	A	388	GLN
1	B	9	ASN
1	B	83	GLN
1	B	145	ASN
1	B	162	HIS
1	B	181	ASN
1	B	235	GLN
1	B	263	ASN
1	B	334	ASN
1	B	375	GLN
1	B	410	GLN
1	B	435	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](#)

Of 7 ligands modelled in this entry, 5 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	PO4	A	453	2,1	0,3,4	-	-	0,3,6	-	-
4	PO4	B	453	2	4,4,4	1.82	1 (25%)	6,6,6	4.22	6 (100%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	453	PO4	P-O4	-3.49	1.44	1.54

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	453	PO4	O2-P-O1	-4.93	92.86	110.89
4	B	453	PO4	O4-P-O1	-4.79	93.36	110.89
4	B	453	PO4	O4-P-O2	4.79	123.34	107.97
4	B	453	PO4	O3-P-O1	-4.13	95.78	110.89
4	B	453	PO4	O3-P-O2	3.95	120.64	107.97
4	B	453	PO4	O4-P-O3	2.06	114.60	107.97

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	453	PO4	1	0
4	B	453	PO4	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](#)

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.