



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2021 – 01:54 PM EDT

PDB ID : 3E3H
Title : Crystal structure of the OP hydrolase mutant from *Brevundimonas diminuta*
Authors : Li, P.; Reeves, T.E.; Grimsley, J.K.; Wild, J.R.
Deposited on : 2008-08-07
Resolution : 2.15 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 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 : 2.23.2
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) : 2.23.2

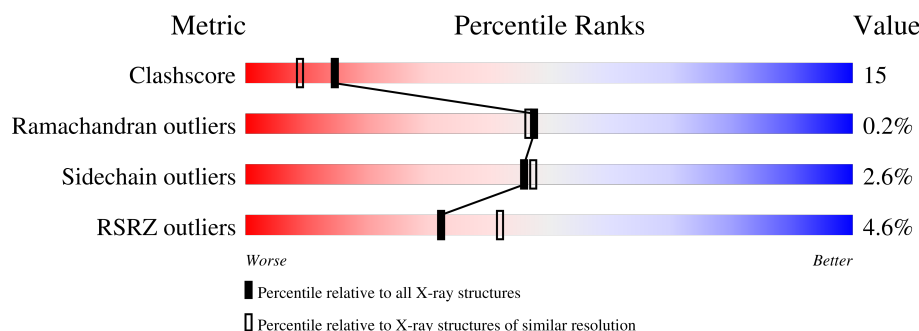
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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 $\leq 5\%$. 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	336	<div> <div>5%</div> <div> <div></div> <div>76%</div> <div>23%</div> <div>.</div> </div> </div>
1	B	336	<div> <div>4%</div> <div> <div></div> <div>75%</div> <div>23%</div> <div>.</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5625 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 Parathion hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	S	0	0	0
			2563	1620	455	481	7			
1	B	336	Total	C	N	O	S	0	0	0
			2563	1620	455	481	7			

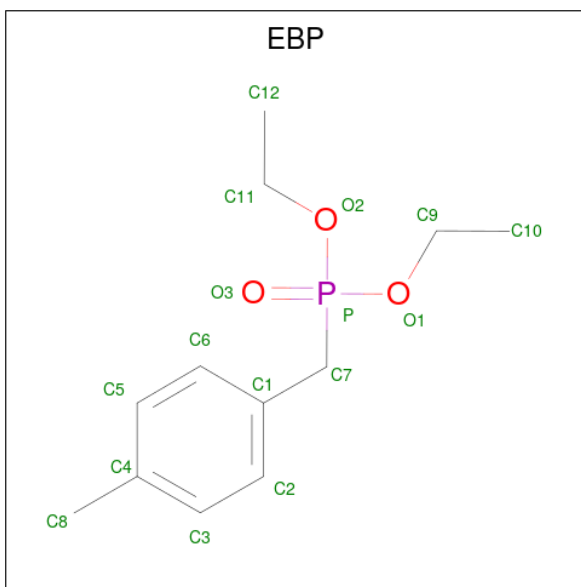
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	254	ARG	HIS	engineered mutation	UNP P0A434
A	257	PHE	HIS	engineered mutation	UNP P0A434
B	254	ARG	HIS	engineered mutation	UNP P0A434
B	257	PHE	HIS	engineered mutation	UNP P0A434

- Molecule 2 is COBALT (II) ION (three-letter code: CO) (formula: Co).

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

- Molecule 3 is DIETHYL 4-METHYLBENZYLPHOSPHONATE (three-letter code: EBP) (formula: C₁₂H₁₉O₃P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			16	12	3	1		
3	B	1	Total	C	O	P	0	0
			16	12	3	1		

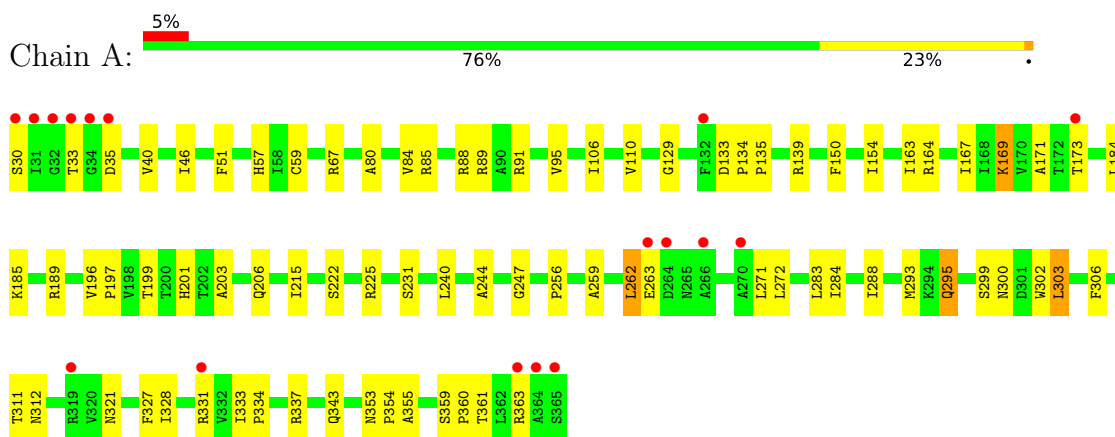
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	242	Total	O	0	0
			242	242		
4	B	221	Total	O	0	0
			221	221		

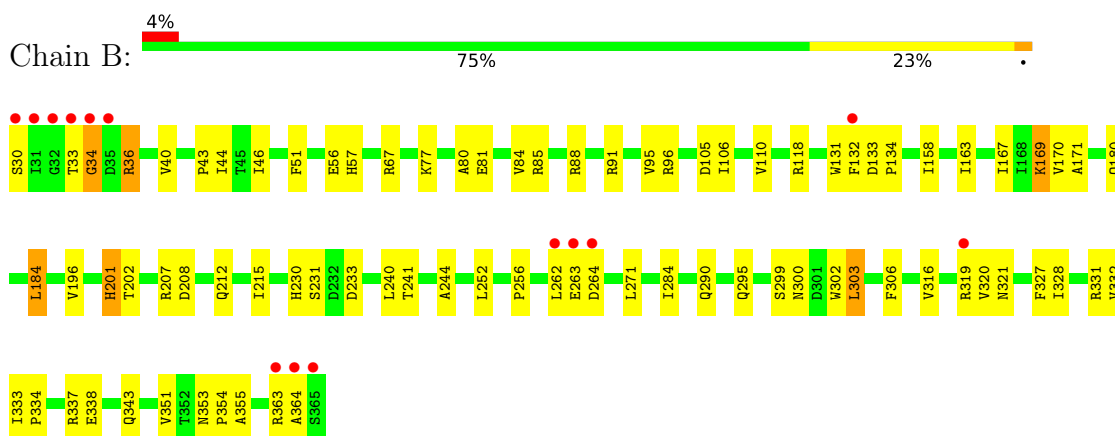
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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: Parathion hydrolase



• Molecule 1: Parathion hydrolase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	128.80Å 90.60Å 69.14Å 90.00° 91.74° 90.00°	Depositor
Resolution (Å)	50.00 – 2.15 27.47 – 2.15	Depositor EDS
% Data completeness (in resolution range)	93.2 (50.00-2.15) 93.1 (27.47-2.15)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	24.02 (at 2.16Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.189 , 0.218 0.181 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	23.8	Xtriage
Anisotropy	0.305	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 37.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.125 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5625	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.81% 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: CO, EBP, KCX

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	0.33	0/2597	0.62	1/3523 (0.0%)
1	B	0.32	0/2597	0.62	0/3523
All	All	0.32	0/5194	0.62	1/7046 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	203	ALA	N-CA-C	-5.58	95.92	111.00

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	2563	0	2587	77	0
1	B	2563	0	2587	79	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	16	0	19	1	0
3	B	16	0	19	2	0
4	A	242	0	0	36	0
4	B	221	0	0	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5625	0	5212	159	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 15.

All (159) 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:262:LEU:HD22	1:B:319:ARG:HH21	1.14	1.12
1:B:56:GLU:HA	4:B:918:HOH:O	1.52	1.08
1:A:173:THR:HB	4:A:895:HOH:O	1.71	0.90
1:A:163:ILE:HG21	4:A:912:HOH:O	1.74	0.86
1:B:262:LEU:CD2	1:B:319:ARG:HH21	1.88	0.86
1:B:163:ILE:HG21	4:B:908:HOH:O	1.77	0.84
1:B:262:LEU:HD22	1:B:319:ARG:NH2	1.95	0.82
1:B:363:ARG:HD3	4:B:845:HOH:O	1.79	0.82
1:B:338:GLU:HG3	4:B:891:HOH:O	1.78	0.81
1:A:283:LEU:HD23	4:A:939:HOH:O	1.85	0.76
1:B:36:ARG:HG2	1:B:43:PRO:HB2	1.66	0.76
1:A:173:THR:O	1:A:173:THR:HG23	1.87	0.75
1:A:311:THR:HA	4:A:911:HOH:O	1.87	0.74
1:A:196:VAL:HG21	4:A:942:HOH:O	1.88	0.74
1:A:327:PHE:CE1	1:A:331:ARG:HD2	2.22	0.74
1:B:180:GLN:O	1:B:184:LEU:HD23	1.88	0.73
1:A:271:LEU:HD23	4:A:925:HOH:O	1.88	0.73
1:A:263:GLU:HA	4:A:908:HOH:O	1.87	0.73
1:B:316:VAL:O	1:B:319:ARG:HG2	1.89	0.72
1:A:33:THR:HG23	4:A:929:HOH:O	1.89	0.71
1:B:337:ARG:HG3	4:B:916:HOH:O	1.90	0.71
1:A:312:ASN:HA	4:A:858:HOH:O	1.91	0.70
1:A:88:ARG:HB2	4:A:944:HOH:O	1.92	0.69
1:B:263:GLU:HA	4:B:854:HOH:O	1.93	0.68
1:B:302:TRP:N	4:B:918:HOH:O	2.27	0.68
1:B:30:SER:HB3	4:B:882:HOH:O	1.96	0.66
1:B:33:THR:HA	4:B:924:HOH:O	1.95	0.64
1:B:57:HIS:O	1:B:303:LEU:HA	1.98	0.63
1:B:215:ILE:HD12	4:B:844:HOH:O	1.98	0.63
1:A:333:ILE:HB	1:A:334:PRO:HD3	1.80	0.63
1:A:88:ARG:HD2	4:A:866:HOH:O	1.98	0.62
1:A:46:ILE:HD11	4:A:818:HOH:O	1.98	0.62
1:B:169:KCX:OQ1	1:B:201:HIS:HB2	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:110:VAL:HB	4:A:912:HOH:O	1.99	0.62
1:B:110:VAL:HB	4:B:908:HOH:O	2.00	0.62
1:B:36:ARG:HG3	1:B:44:ILE:O	2.00	0.62
1:B:88:ARG:HD2	4:B:812:HOH:O	1.99	0.61
1:A:283:LEU:HA	4:A:939:HOH:O	1.99	0.61
1:A:40:VAL:HG12	4:A:912:HOH:O	2.00	0.60
1:B:170:VAL:HG21	1:B:184:LEU:HD13	1.84	0.60
1:B:333:ILE:HB	1:B:334:PRO:HD3	1.81	0.60
1:A:353:ASN:HB2	1:A:354:PRO:HD3	1.84	0.59
1:B:252:LEU:HD12	1:B:284:ILE:HG12	1.84	0.59
1:B:96:ARG:HD3	4:B:832:HOH:O	2.03	0.58
1:B:85:ARG:HD2	4:B:902:HOH:O	2.04	0.58
1:B:106:ILE:HG22	1:B:106:ILE:O	2.04	0.58
1:B:244:ALA:O	1:B:295:GLN:NE2	2.36	0.58
1:B:171:ALA:HB2	1:B:201:HIS:HB3	1.84	0.58
1:A:106:ILE:HG22	1:A:106:ILE:O	2.04	0.57
1:B:202:THR:HB	1:B:208:ASP:HB2	1.86	0.57
1:A:89:ARG:HD3	4:A:843:HOH:O	2.03	0.57
1:B:319:ARG:HD2	4:B:887:HOH:O	2.05	0.57
1:B:30:SER:N	1:B:364:ALA:HB2	2.21	0.56
1:B:262:LEU:HD11	4:B:804:HOH:O	2.06	0.56
1:A:196:VAL:HG11	4:A:942:HOH:O	2.06	0.55
1:A:327:PHE:CD1	1:A:331:ARG:HD2	2.40	0.55
1:B:36:ARG:HD2	4:B:861:HOH:O	2.06	0.55
1:A:337:ARG:HG3	4:A:831:HOH:O	2.07	0.54
1:A:167:ILE:HD11	1:A:199:THR:HB	1.90	0.54
1:B:351:VAL:HG21	4:B:851:HOH:O	2.08	0.54
1:A:363:ARG:HA	4:A:878:HOH:O	2.06	0.54
1:A:33:THR:HA	4:A:868:HOH:O	2.08	0.54
1:A:171:ALA:CB	1:A:201:HIS:HB3	2.38	0.53
1:A:262:LEU:HD12	1:A:262:LEU:N	2.24	0.53
1:B:34:GLY:HA3	4:B:901:HOH:O	2.08	0.53
1:B:241:THR:HG21	1:B:290:GLN:HE21	1.73	0.53
1:A:244:ALA:O	4:A:718:HOH:O	2.18	0.53
1:B:331:ARG:HD3	4:B:773:HOH:O	2.08	0.53
1:A:46:ILE:CG2	1:A:355:ALA:HB1	2.39	0.52
1:B:212:GLN:HA	4:B:844:HOH:O	2.09	0.52
1:A:85:ARG:O	1:A:89:ARG:HG3	2.10	0.52
1:B:353:ASN:HB2	1:B:354:PRO:HD3	1.93	0.51
1:B:319:ARG:NE	4:B:804:HOH:O	2.42	0.51
1:A:171:ALA:HB2	1:A:201:HIS:HB3	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:171:ALA:CB	1:B:201:HIS:HB3	2.42	0.50
1:A:35:ASP:HA	4:A:765:HOH:O	2.11	0.50
1:A:80:ALA:O	1:A:84:VAL:HG23	2.11	0.50
1:A:337:ARG:HD3	1:A:343:GLN:HE22	1.76	0.50
1:A:169:KCX:OQ1	1:A:201:HIS:HB2	2.12	0.49
1:B:33:THR:HG22	4:B:924:HOH:O	2.11	0.49
1:B:46:ILE:HG13	4:B:903:HOH:O	2.12	0.49
1:B:46:ILE:CG2	1:B:355:ALA:HB1	2.42	0.49
1:B:363:ARG:HG2	1:B:364:ALA:N	2.28	0.48
1:A:57:HIS:O	1:A:303:LEU:HA	2.13	0.48
1:A:129:GLY:HA2	1:A:150:PHE:CE1	2.49	0.48
1:B:84:VAL:O	1:B:88:ARG:HG3	2.12	0.48
1:A:360:PRO:HD2	4:A:818:HOH:O	2.13	0.48
1:B:300:ASN:OD1	1:B:328:ILE:HG12	2.14	0.48
1:B:57:HIS:HB2	1:B:303:LEU:HB3	1.95	0.48
1:B:328:ILE:HD13	1:B:332:VAL:HG21	1.96	0.47
1:B:320:VAL:HG23	4:B:804:HOH:O	2.14	0.47
1:A:293:MET:CE	4:A:936:HOH:O	2.63	0.47
1:A:206:GLN:HG3	4:A:899:HOH:O	2.14	0.47
1:A:337:ARG:HD3	1:A:343:GLN:NE2	2.30	0.47
1:B:40:VAL:HG12	4:B:908:HOH:O	2.15	0.46
1:B:105:ASP:OD1	1:B:131:TRP:HB3	2.16	0.46
1:B:215:ILE:HB	4:B:844:HOH:O	2.15	0.46
1:A:30:SER:HB2	1:A:361:THR:CG2	2.46	0.46
1:A:359:SER:HA	4:A:818:HOH:O	2.16	0.45
1:A:133:ASP:N	1:A:134:PRO:CD	2.79	0.45
1:A:173:THR:HG22	4:A:802:HOH:O	2.15	0.45
3:A:702:EBP:H91	4:A:883:HOH:O	2.16	0.45
1:B:271:LEU:HD23	4:B:853:HOH:O	2.17	0.45
1:A:30:SER:HB2	1:A:361:THR:HG22	1.98	0.44
1:A:184:LEU:HD12	1:A:215:ILE:HD12	1.99	0.44
1:A:284:ILE:O	1:A:288:ILE:HG13	2.17	0.44
1:B:77:LYS:HE2	1:B:81:GLU:OE1	2.18	0.44
1:A:57:HIS:HB2	1:A:303:LEU:HB3	1.99	0.44
1:A:302:TRP:CH2	1:A:321:ASN:HB3	2.53	0.44
1:A:173:THR:O	1:A:173:THR:CG2	2.58	0.44
1:A:311:THR:O	1:A:312:ASN:HB2	2.18	0.43
1:B:302:TRP:CH2	1:B:321:ASN:HB3	2.54	0.43
1:B:252:LEU:CD1	1:B:284:ILE:HG12	2.47	0.43
1:A:256:PRO:HB3	1:A:327:PHE:CD2	2.54	0.43
1:A:35:ASP:HA	4:A:902:HOH:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:319:ARG:HG3	4:B:876:HOH:O	2.18	0.42
1:A:259:ALA:HB2	1:A:272:LEU:HB2	2.02	0.42
1:B:118:ARG:HG2	1:B:118:ARG:HH11	1.83	0.42
1:A:189:ARG:NH1	4:A:927:HOH:O	2.47	0.42
1:A:231:SER:HB3	1:A:240:LEU:CD2	2.49	0.42
1:B:230:HIS:O	1:B:233:ASP:HB2	2.20	0.42
1:A:40:VAL:HA	1:A:163:ILE:HG23	2.00	0.42
1:A:222:SER:HB2	1:A:363:ARG:HH21	1.84	0.42
1:B:91:ARG:HA	1:B:95:VAL:O	2.20	0.42
1:B:106:ILE:O	1:B:106:ILE:CG2	2.68	0.42
1:A:169:KCX:NZ	1:A:201:HIS:HB2	2.34	0.42
1:B:167:ILE:HA	1:B:196:VAL:CG1	2.49	0.42
1:B:132:PHE:HE2	1:B:201:HIS:CE1	2.37	0.42
1:B:231:SER:HB3	1:B:240:LEU:HD21	2.02	0.42
1:A:185:LYS:O	1:A:189:ARG:HG3	2.20	0.42
1:B:207:ARG:HD2	4:B:807:HOH:O	2.19	0.42
1:A:196:VAL:HG13	1:A:197:PRO:HD2	2.01	0.42
1:B:231:SER:HB3	1:B:240:LEU:CD2	2.49	0.41
1:A:150:PHE:O	1:A:154:ILE:HG13	2.19	0.41
1:B:201:HIS:C	1:B:201:HIS:CD2	2.92	0.41
1:B:80:ALA:O	1:B:84:VAL:HG23	2.20	0.41
1:B:88:ARG:NH1	4:B:915:HOH:O	2.53	0.41
1:B:337:ARG:NH2	4:B:872:HOH:O	2.53	0.41
1:A:184:LEU:HD12	1:A:215:ILE:CD1	2.49	0.41
1:A:91:ARG:HA	1:A:95:VAL:O	2.21	0.41
1:A:225:ARG:NE	4:A:873:HOH:O	2.53	0.41
1:B:256:PRO:HB3	1:B:327:PHE:CD2	2.55	0.41
1:A:247:GLY:CA	4:A:718:HOH:O	2.68	0.41
1:B:133:ASP:N	1:B:134:PRO:CD	2.84	0.41
1:B:110:VAL:HG11	1:B:158:ILE:HG21	2.02	0.41
3:B:701:EBP:H122	4:B:851:HOH:O	2.21	0.41
1:A:59:CYS:HB3	4:A:905:HOH:O	2.20	0.41
1:A:154:ILE:HG12	4:A:942:HOH:O	2.21	0.41
1:A:262:LEU:HD21	4:A:913:HOH:O	2.20	0.41
1:A:295:GLN:HG2	4:A:718:HOH:O	2.21	0.41
1:B:110:VAL:CG1	1:B:158:ILE:HG21	2.51	0.41
3:B:701:EBP:H71	3:B:701:EBP:H91	1.86	0.41
1:A:67:ARG:HG3	1:A:67:ARG:HH11	1.86	0.41
1:B:67:ARG:HG3	4:B:728:HOH:O	2.19	0.41
1:B:363:ARG:HA	4:B:882:HOH:O	2.21	0.40
1:B:337:ARG:HD3	1:B:343:GLN:HE22	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:300:ASN:OD1	1:A:328:ILE:HG12	2.22	0.40
1:A:135:PRO:O	1:A:139:ARG:HG3	2.21	0.40
1:A:154:ILE:O	1:A:164:ARG:HB3	2.22	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	333/336 (99%)	323 (97%)	10 (3%)	0	100	100
1	B	333/336 (99%)	319 (96%)	13 (4%)	1 (0%)	41	37
All	All	666/672 (99%)	642 (96%)	23 (4%)	1 (0%)	47	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	34	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	268/268 (100%)	262 (98%)	6 (2%)	52	55
1	B	268/268 (100%)	260 (97%)	8 (3%)	41	40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	536/536 (100%)	522 (97%)	14 (3%)	46	47

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	PHE
1	A	262	LEU
1	A	295	GLN
1	A	299	SER
1	A	303	LEU
1	A	306	PHE
1	B	36	ARG
1	B	51	PHE
1	B	184	LEU
1	B	201	HIS
1	B	264	ASP
1	B	299	SER
1	B	303	LEU
1	B	306	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	312	ASN
1	A	343	GLN
1	B	38	ASN
1	B	290	GLN
1	B	312	ASN
1	B	343	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	KCX	A	169	1,2	7,11,12	0.86	0	4,12,14	4.04	1 (25%)
1	KCX	B	169	1,2	7,11,12	0.52	0	4,12,14	3.85	1 (25%)

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
1	KCX	A	169	1,2	-	2/7/10/12	-
1	KCX	B	169	1,2	-	2/7/10/12	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	169	KCX	CE-NZ-CX	-7.96	109.47	122.95
1	B	169	KCX	CE-NZ-CX	-7.61	110.06	122.95

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	169	KCX	CG-CD-CE-NZ
1	A	169	KCX	CG-CD-CE-NZ
1	A	169	KCX	CE-CD-CG-CB
1	B	169	KCX	CE-CD-CG-CB

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	169	KCX	2	0
1	B	169	KCX	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 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	$\# Z > 2$
3	EBP	B	701	-	16,16,16	2.88	4 (25%)	21,21,21	1.21	3 (14%)
3	EBP	A	702	-	16,16,16	2.92	4 (25%)	21,21,21	1.23	3 (14%)

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	EBP	B	701	-	-	2/13/13/13	0/1/1/1
3	EBP	A	702	-	-	0/13/13/13	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	702	EBP	P-C7	-8.32	1.66	1.79
3	B	701	EBP	P-C7	-8.15	1.66	1.79
3	A	702	EBP	P-O3	5.90	1.64	1.48
3	B	701	EBP	P-O3	5.85	1.64	1.48
3	B	701	EBP	P-O1	-3.78	1.48	1.57
3	A	702	EBP	P-O1	-3.78	1.48	1.57
3	A	702	EBP	P-O2	-3.77	1.48	1.57
3	B	701	EBP	P-O2	-3.63	1.48	1.57

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	A	702	EBP	O3-P-C7	-3.54	106.00	114.19
3	B	701	EBP	O3-P-C7	-3.47	106.18	114.19
3	A	702	EBP	O1-P-C7	2.70	111.50	104.15
3	B	701	EBP	O1-P-C7	2.63	111.29	104.15
3	A	702	EBP	O2-P-C7	2.48	110.89	104.15
3	B	701	EBP	O2-P-C7	2.41	110.71	104.15

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	701	EBP	C9-O1-P-C7
3	B	701	EBP	C9-O1-P-O3

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	701	EBP	2	0
3	A	702	EBP	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 ⓘ

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, 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	335/336 (99%)	0.07	17 (5%) 28 36	15, 23, 43, 75	2 (0%)
1	B	335/336 (99%)	0.14	14 (4%) 36 45	14, 24, 43, 73	2 (0%)
All	All	670/672 (99%)	0.10	31 (4%) 32 42	14, 24, 43, 75	4 (0%)

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	34	GLY	13.1
1	A	34	GLY	12.2
1	B	33	THR	11.0
1	A	365	SER	10.1
1	A	30	SER	9.6
1	A	31	ILE	9.1
1	A	32	GLY	8.8
1	A	33	THR	8.7
1	B	30	SER	8.6
1	B	31	ILE	8.4
1	B	365	SER	8.4
1	B	32	GLY	7.8
1	B	364	ALA	5.0
1	B	35	ASP	4.2
1	A	364	ALA	4.2
1	A	264	ASP	3.9
1	A	132	PHE	3.9
1	B	132	PHE	3.8
1	B	363	ARG	3.8
1	A	35	ASP	3.7
1	A	363	ARG	3.6
1	B	262	LEU	3.6
1	B	264	ASP	3.5
1	B	319	ARG	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	173	THR	2.6
1	A	319	ARG	2.6
1	A	331	ARG	2.2
1	B	263	GLU	2.1
1	A	266	ALA	2.1
1	A	270	ALA	2.1
1	A	263	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	KCX	A	169	12/13	0.91	0.19	16,20,37,37	0
1	KCX	B	169	12/13	0.93	0.17	17,21,32,33	0

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
3	EBP	A	702	16/16	0.90	0.18	33,41,47,48	0
3	EBP	B	701	16/16	0.94	0.14	26,33,37,37	0
2	CO	B	603	1/1	0.99	0.13	22,22,22,22	0
2	CO	B	604	1/1	0.99	0.07	29,29,29,29	0
2	CO	A	601	1/1	0.99	0.06	26,26,26,26	0
2	CO	A	602	1/1	0.99	0.14	23,23,23,23	0

6.5 Other polymers [i](#)

There are no such residues in this entry.