



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:04 AM GMT

PDB ID : 1ZEF
Title : structure of alkaline phosphatase from human placenta in complex with its uncompetitive inhibitor L-Phe
Authors : Llinas, P.; Stura, E.A.; Menez, A.; Kiss, Z.; Stigbrand, T.; Millan, J.L.; Le Du, M.H.
Deposited on : 2005-04-18
Resolution : 1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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

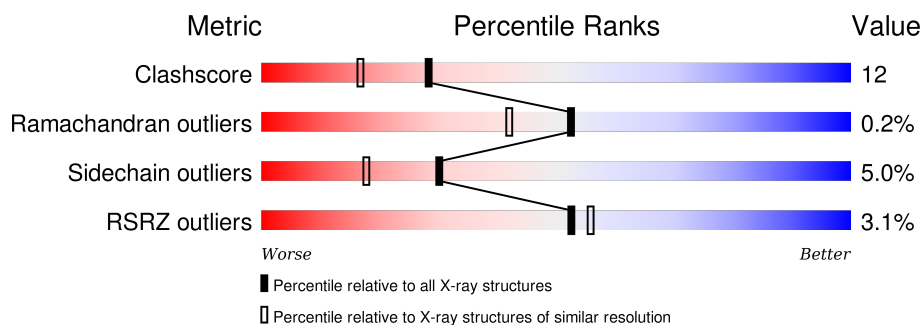
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	484	

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	NAG	A	801	-	-	-	X
3	PHE	A	802	-	-	X	X
3	PHE	A	804	-	-	X	X

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 4427 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.

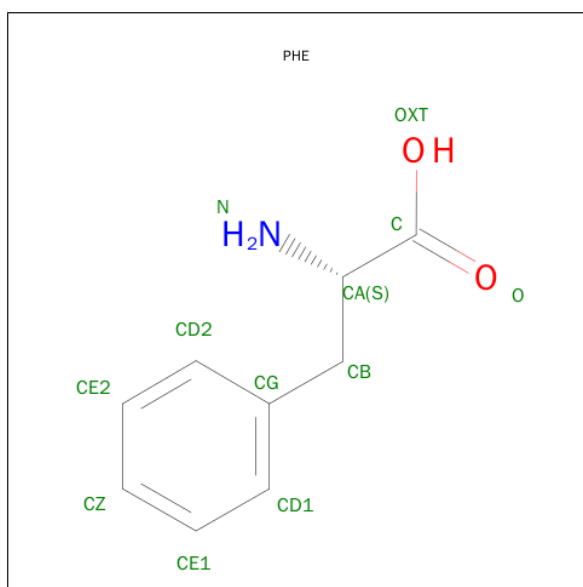
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	481	Total	C	N	O	P	S	0	0	0
			3669	2292	653	705	1	18			

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is PHENYLALANINE (three-letter code: PHE) (formula: $C_9H_{11}NO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			12	9	1	2		
3	A	1	Total	C	N	O	0	0
			12	9	1	2		

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Ca	0	0
			1	1		

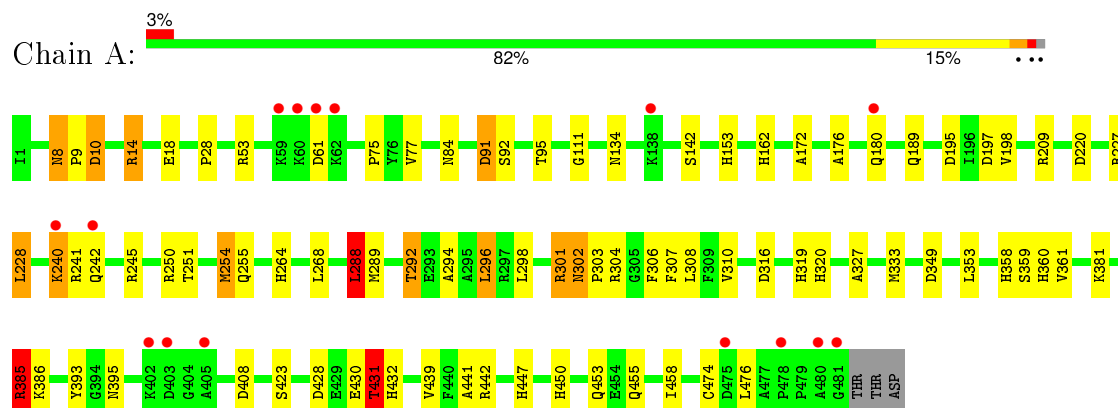
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	702	Total 702	O 702	0	0

3 Residue-property plots

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

- Molecule 1: Alkaline phosphatase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	87.79Å 114.94Å 106.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 1.90 24.95 – 1.89	Depositor EDS
% Data completeness (in resolution range)	100.0 (15.00-1.90) 98.6 (24.95-1.89)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.79 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.126 , 0.173 0.140 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	17.7	Xtriage
Anisotropy	0.286	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 57.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 43024 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	4427	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.49% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG, CA, NAG, SEP

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	0.78	0/3739	0.94	16/5072 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	301	ARG	NE-CZ-NH2	-8.75	115.93	120.30
1	A	301	ARG	NE-CZ-NH1	7.02	123.81	120.30
1	A	349	ASP	CB-CG-OD2	6.94	124.55	118.30
1	A	220	ASP	CB-CG-OD2	6.78	124.41	118.30
1	A	10	ASP	CB-CG-OD2	6.67	124.30	118.30
1	A	385	ARG	NE-CZ-NH2	6.49	123.55	120.30
1	A	428	ASP	CB-CG-OD2	6.21	123.89	118.30
1	A	385	ARG	CG-CD-NE	6.20	124.82	111.80
1	A	197	ASP	CB-CG-OD2	5.97	123.67	118.30
1	A	474	CYS	C-N-CA	-5.95	106.82	121.70
1	A	288	LEU	CB-CG-CD2	5.75	120.77	111.00
1	A	408	ASP	CB-CG-OD2	5.67	123.41	118.30
1	A	431	THR	N-CA-CB	-5.67	99.52	110.30
1	A	296	LEU	CB-CG-CD1	5.39	120.16	111.00
1	A	14	ARG	NE-CZ-NH2	5.23	122.92	120.30
1	A	53	ARG	NE-CZ-NH2	5.04	122.82	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	61	ASP	Peptide

5.2 Too-close contacts ⓘ

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	3669	0	3549	78	0
2	A	28	0	26	0	0
3	A	24	0	16	12	0
4	A	2	0	0	0	0
5	A	1	0	0	0	0
6	A	1	0	0	0	0
7	A	702	0	0	24	5
All	All	4427	0	3591	85	5

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 (85) 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:333:MET:HE2	7:A:1591:HOH:O	1.46	1.11
1:A:453:GLN:HG3	7:A:1054:HOH:O	1.51	1.09
1:A:92:SEP:P	3:A:802:PHE:N	2.35	0.99
3:A:804:PHE:HD1	3:A:804:PHE:O	1.51	0.94
3:A:804:PHE:O	3:A:804:PHE:CD1	2.20	0.94
1:A:301:ARG:NH2	7:A:1592:HOH:O	1.91	0.88
1:A:176:ALA:O	1:A:180:GLN:HG2	1.76	0.86
1:A:162:HIS:H	1:A:189:GLN:HE22	1.25	0.85
3:A:802:PHE:HE1	7:A:1595:HOH:O	1.64	0.79
1:A:333:MET:HB2	7:A:1591:HOH:O	1.84	0.77
1:A:431:THR:HG23	1:A:432:HIS:O	1.86	0.75
1:A:288:LEU:O	1:A:292:THR:HG23	1.90	0.71
1:A:360:HIS:HD2	1:A:430:GLU:OE1	1.75	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:450:HIS:HE1	7:A:985:HOH:O	1.76	0.68
1:A:333:MET:SD	7:A:1508:HOH:O	2.53	0.67
1:A:319:HIS:CE1	1:A:327:ALA:CB	2.79	0.65
1:A:264:HIS:CE1	7:A:1247:HOH:O	2.48	0.65
1:A:172:ALA:HA	1:A:228:LEU:HD22	1.79	0.64
1:A:153:HIS:HD2	7:A:957:HOH:O	1.83	0.60
3:A:804:PHE:C	3:A:804:PHE:CD1	2.75	0.60
1:A:28:PRO:CB	1:A:447:HIS:CE1	2.85	0.59
1:A:360:HIS:CD2	1:A:430:GLU:OE1	2.55	0.58
1:A:302:ASN:ND2	1:A:304:ARG:H	2.01	0.58
1:A:28:PRO:HB3	1:A:447:HIS:ND1	2.19	0.57
1:A:111:GLY:O	1:A:162:HIS:HD2	1.88	0.56
1:A:195:ASP:OD1	1:A:264:HIS:HE1	1.89	0.56
1:A:319:HIS:CE1	1:A:327:ALA:HB1	2.41	0.56
1:A:381:LYS:NZ	7:A:1265:HOH:O	2.38	0.55
1:A:209:ARG:HG2	7:A:1221:HOH:O	2.07	0.54
3:A:802:PHE:CD2	3:A:802:PHE:N	2.74	0.54
1:A:393:TYR:O	1:A:423:SER:HA	2.07	0.54
1:A:8:ASN:ND2	1:A:10:ASP:H	2.07	0.53
1:A:358:HIS:HD2	1:A:359:SER:O	1.91	0.53
1:A:385:ARG:HH21	1:A:385:ARG:HG2	1.73	0.53
1:A:8:ASN:HD22	1:A:9:PRO:N	2.07	0.52
1:A:302:ASN:C	1:A:302:ASN:HD22	2.12	0.52
1:A:28:PRO:HB3	1:A:447:HIS:CE1	2.44	0.52
1:A:385:ARG:NE	7:A:1469:HOH:O	2.43	0.52
1:A:320:HIS:CD2	3:A:802:PHE:HA	2.32	0.52
1:A:8:ASN:C	1:A:8:ASN:HD22	2.12	0.52
1:A:254:MET:HA	3:A:804:PHE:CZ	2.45	0.51
3:A:804:PHE:N	7:A:1575:HOH:O	2.43	0.51
1:A:302:ASN:HD22	1:A:303:PRO:N	2.08	0.51
3:A:802:PHE:N	3:A:802:PHE:HD2	2.08	0.50
1:A:162:HIS:HE1	7:A:1063:HOH:O	1.94	0.50
1:A:28:PRO:HB2	1:A:447:HIS:CE1	2.45	0.50
1:A:255:GLN:NE2	7:A:1172:HOH:O	2.44	0.49
1:A:84:ASN:HD21	1:A:91:ASP:H	1.59	0.49
1:A:439:VAL:HG21	1:A:458:ILE:HD11	1.95	0.49
1:A:353:LEU:HD12	1:A:458:ILE:HG23	1.94	0.49
1:A:92:SEP:O1P	3:A:802:PHE:N	2.40	0.47
1:A:251:THR:HG23	7:A:1053:HOH:O	2.15	0.47
1:A:28:PRO:CB	1:A:447:HIS:ND1	2.78	0.46
1:A:302:ASN:HD22	1:A:304:ARG:H	1.63	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:VAL:HA	1:A:439:VAL:O	2.16	0.45
1:A:18:GLU:OE2	7:A:1487:HOH:O	2.21	0.45
1:A:209:ARG:HA	1:A:227:ARG:HB2	1.99	0.45
1:A:162:HIS:H	1:A:189:GLN:NE2	2.04	0.45
1:A:14:ARG:HD2	7:A:1366:HOH:O	2.16	0.45
1:A:316:ASP:OD2	1:A:360:HIS:CE1	2.70	0.45
1:A:195:ASP:OD1	1:A:264:HIS:CE1	2.69	0.45
1:A:95:THR:HG22	1:A:455:GLN:HE22	1.83	0.44
1:A:316:ASP:OD2	1:A:360:HIS:HE1	2.01	0.44
1:A:319:HIS:ND1	1:A:327:ALA:CB	2.82	0.43
1:A:447:HIS:C	1:A:447:HIS:CD2	2.92	0.43
1:A:320:HIS:HE1	1:A:432:HIS:CD2	2.38	0.42
1:A:353:LEU:HD22	1:A:441:ALA:HB2	2.02	0.42
1:A:294:ALA:HB2	3:A:804:PHE:CZ	2.53	0.42
1:A:198:VAL:HG22	1:A:298:LEU:HD13	2.02	0.42
1:A:386:LYS:NZ	7:A:1299:HOH:O	2.40	0.42
1:A:75:PRO:HD2	1:A:442:ARG:HB3	2.02	0.41
1:A:308:LEU:HG	1:A:310:VAL:HG23	2.02	0.41
1:A:153:HIS:CD2	7:A:957:HOH:O	2.66	0.41
1:A:320:HIS:CE1	1:A:432:HIS:CD2	3.08	0.41
1:A:288:LEU:O	1:A:292:THR:CG2	2.65	0.41
1:A:142:SER:O	1:A:306:PHE:HA	2.21	0.41
1:A:333:MET:CE	7:A:1508:HOH:O	2.68	0.41
1:A:395:ASN:HD21	1:A:431:THR:CG2	2.33	0.41
1:A:251:THR:HB	7:A:1461:HOH:O	2.21	0.41
1:A:240:LYS:HD3	7:A:1153:HOH:O	2.21	0.41
1:A:250:ARG:O	1:A:254:MET:HG3	2.21	0.40
1:A:319:HIS:HD2	1:A:360:HIS:HB2	1.87	0.40
1:A:8:ASN:HD22	1:A:9:PRO:CD	2.34	0.40
1:A:289:MET:HE2	7:A:1508:HOH:O	2.22	0.40
1:A:307:PHE:C	1:A:307:PHE:CD1	2.95	0.40

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1068:HOH:O	7:A:1068:HOH:O[3_655]	1.34	0.86
7:A:1042:HOH:O	7:A:1570:HOH:O[3_655]	1.93	0.27
7:A:1062:HOH:O	7:A:1062:HOH:O[3_655]	1.94	0.26
7:A:1439:HOH:O	7:A:1548:HOH:O[3_655]	1.95	0.25
7:A:1089:HOH:O	7:A:1429:HOH:O[3_655]	2.17	0.03

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	478/484 (99%)	468 (98%)	9 (2%)	1 (0%)	52	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	361	VAL

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	377/386 (98%)	360 (96%)	17 (4%)	34	21

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ASN
1	A	91	ASP
1	A	134	ASN
1	A	228	LEU
1	A	240	LYS
1	A	241	ARG
1	A	242	GLN
1	A	245	ARG
1	A	254	MET
1	A	268	LEU

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Mol	Chain	Res	Type
1	A	288	LEU
1	A	292	THR
1	A	296	LEU
1	A	302	ASN
1	A	385	ARG
1	A	431	THR
1	A	476	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	ASN
1	A	84	ASN
1	A	127	ASN
1	A	134	ASN
1	A	153	HIS
1	A	162	HIS
1	A	189	GLN
1	A	193	ASN
1	A	235	GLN
1	A	255	GLN
1	A	264	HIS
1	A	302	ASN
1	A	358	HIS
1	A	360	HIS
1	A	445	GLN
1	A	450	HIS
1	A	455	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	SEP	A	92	1,4	8,9,10	1.69	1 (12%)	8,12,14	2.25	4 (50%)

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	SEP	A	92	1,4	-	0/6/8/10	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	92	SEP	P-OG	4.34	1.74	1.60

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	92	SEP	O3P-P-OG	-4.43	93.81	106.56
1	A	92	SEP	O-C-CA	-2.37	119.31	125.49
1	A	92	SEP	O3P-P-O2P	2.36	116.38	107.38
1	A	92	SEP	O3P-P-O1P	2.37	118.22	110.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	92	SEP	2	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 8 ligands modelled in this entry, 4 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$
2	NAG	A	801	1	14,14,15	0.69	0	15,19,21	1.05	1 (6%)
3	PHE	A	802	4	9,12,12	0.81	0	9,15,15	0.99	0
2	NAG	A	803	1	14,14,15	0.66	0	15,19,21	2.06	3 (20%)
3	PHE	A	804	-	9,12,12	1.27	2 (22%)	9,15,15	0.47	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
2	NAG	A	801	1	-	0/6/23/26	0/1/1/1
3	PHE	A	802	4	-	0/4/8/8	0/1/1/1
2	NAG	A	803	1	-	0/6/23/26	0/1/1/1
3	PHE	A	804	-	-	0/4/8/8	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	804	PHE	CE2-CD2	-2.50	1.33	1.38
3	A	804	PHE	CE1-CD1	-2.24	1.34	1.38

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	803	NAG	C6-C5-C4	-3.02	105.56	113.02
2	A	803	NAG	O6-C6-C5	-2.29	103.78	111.33
2	A	801	NAG	O7-C7-C8	-2.05	118.30	122.06
2	A	803	NAG	C1-O5-C5	5.96	119.82	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	802	PHE	6	0
3	A	804	PHE	6	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	480/484 (99%)	-0.22	15 (3%) 52 56	12, 18, 33, 49	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	61	ASP	6.3
1	A	481	GLY	5.4
1	A	242	GLN	4.2
1	A	60	LYS	3.8
1	A	403	ASP	3.8
1	A	475	ASP	3.5
1	A	478	PRO	3.0
1	A	480	ALA	2.6
1	A	405	ALA	2.5
1	A	138	LYS	2.4
1	A	240	LYS	2.4
1	A	62	LYS	2.4
1	A	59	LYS	2.3
1	A	402	LYS	2.2
1	A	180	GLN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	LLDF	B-factors(\AA^2)	Q<0.9
1	SEP	A	92	10/11	0.98	0.07	-	13,14,15,15	0

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	LLDF	B-factors(\AA^2)	Q<0.9
3	PHE	A	802	12/12	0.75	0.41	15.46	39,44,49,49	0
3	PHE	A	804	12/12	0.65	0.32	12.88	47,48,49,50	0
2	NAG	A	801	14/15	0.84	0.17	3.46	27,39,47,48	0
5	MG	A	903	1/1	0.99	0.07	-0.41	13,13,13,13	0
6	CA	A	904	1/1	1.00	0.04	-2.54	16,16,16,16	0
4	ZN	A	901	1/1	1.00	0.03	-3.12	14,14,14,14	0
4	ZN	A	902	1/1	1.00	0.02	-4.24	15,15,15,15	0
2	NAG	A	803	14/15	0.86	0.25	-	31,37,40,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.