



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:55 PM GMT

PDB ID : 4QCL
Title : Crystal structure of the catalytic core of human DNA polymerase alpha in ternary complex with an RNA-primed DNA template and dCTP
Authors : Baranovskiy, A.G.; Suwa, Y.; Babayeva, N.D.; Gu, J.; Tahirov, T.H.
Deposited on : 2014-05-12
Resolution : 2.20 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

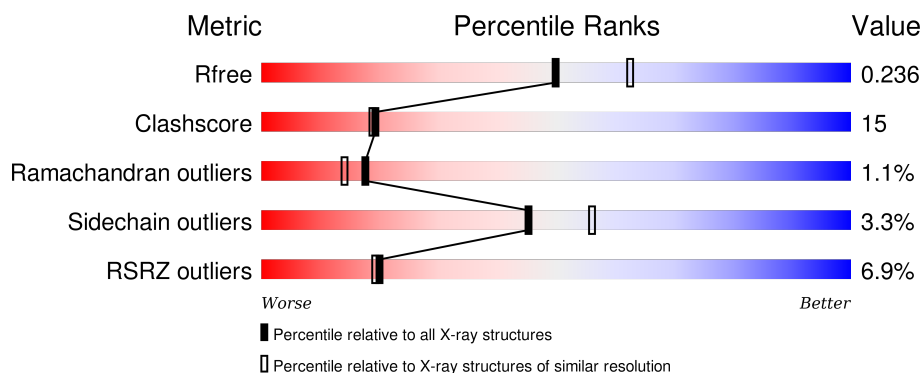
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	91344	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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	922	<div> <div>6%</div> <div>69% 22% 6%</div> </div>
2	B	11	<div> <div>9%</div> <div>64% 27% 9%</div> </div>
3	C	21	<div> <div>5%</div> <div>29% 33% 38%</div> </div>

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
9	EDO	A	1307	-	-	-	X

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 7910 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 DNA polymerase alpha catalytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	865	Total	C	N	O	S	0	0	0
			6947	4470	1162	1274	41			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	516	ALA	VAL	ENGINEERED MUTATION	UNP P09884

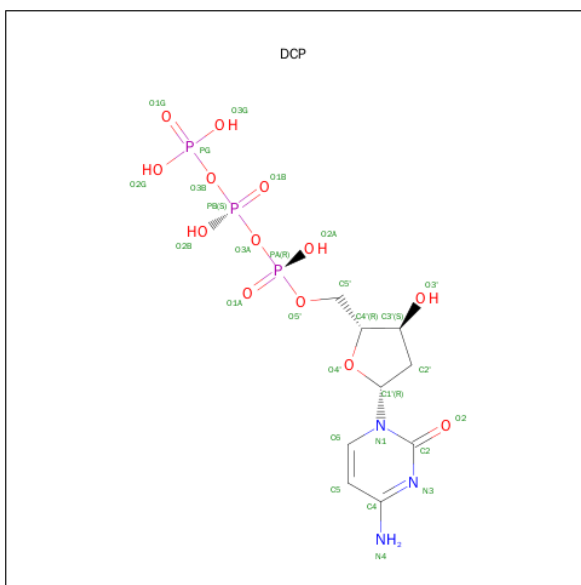
- Molecule 2 is DNA/RNA hybrid called RNA PRIMER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	11	Total	C	N	O	P	0	0	0
			232	105	44	73	10			

- Molecule 3 is a DNA chain called DNA TEMPLATE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	13	Total	C	N	O	P	0	0	0
			264	125	52	75	12			

- Molecule 4 is 2'-DEOXYCYTIDINE-5'-TRIPHOSPHATE (three-letter code: DCP) (formula: C₉H₁₆N₃O₁₃P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			28	9	3	13	3		

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

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

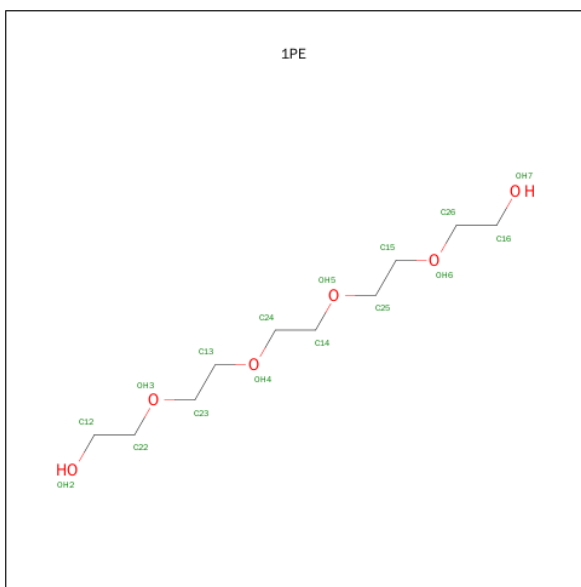
- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total Zn 1 1	0	0
6	A	2	Total Zn 2 2	0	0

- Molecule 7 is POTASSIUM ION (three-letter code: K) (formula: K).

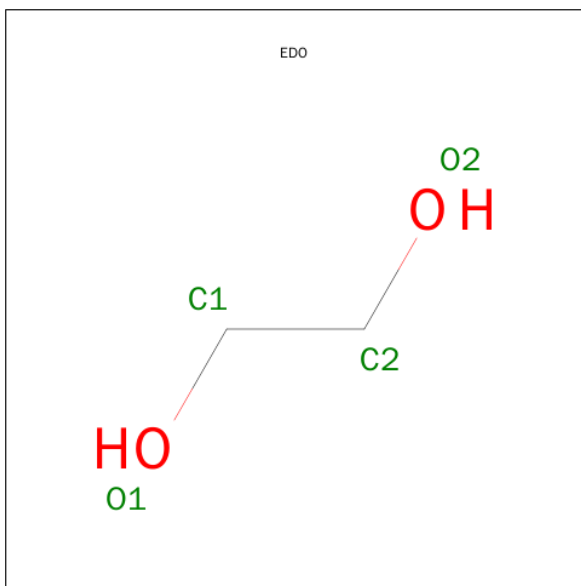
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total K 1 1	0	0

- Molecule 8 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			16	10	6		

- Molecule 9 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

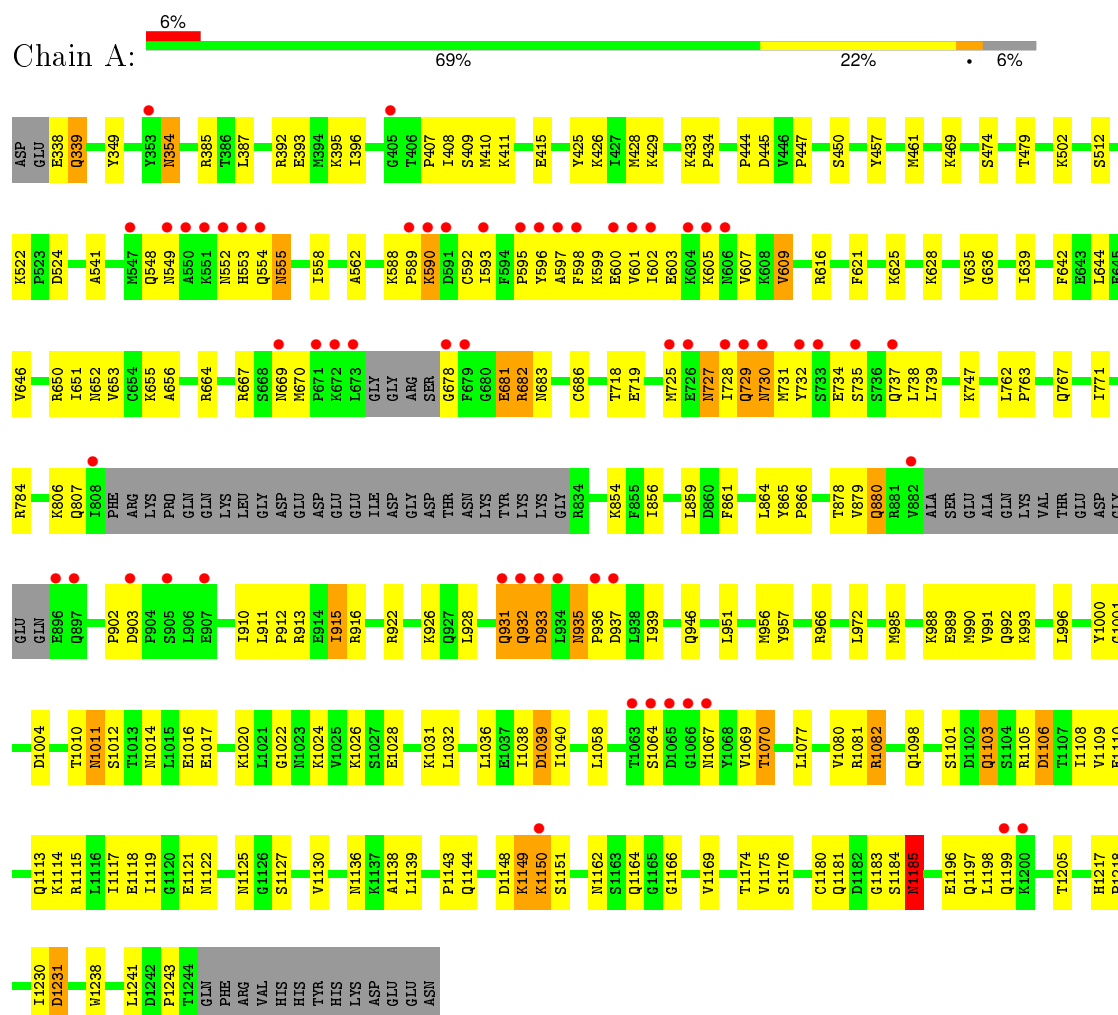
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	351	Total 351	O 351	0	0
10	B	23	Total 23	O 23	0	0
10	C	40	Total 40	O 40	0	0

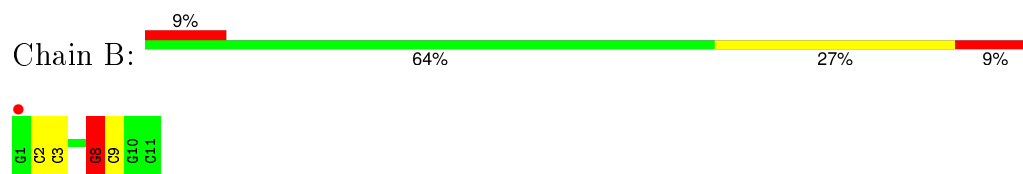
3 Residue-property plots

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.

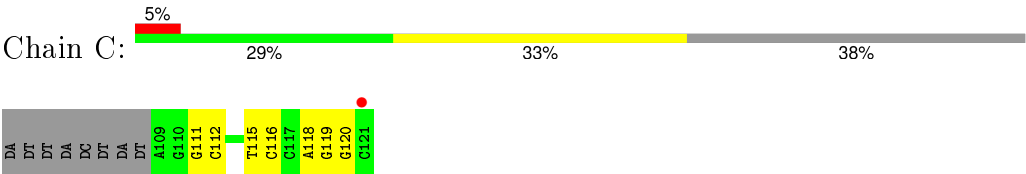
- Molecule 1: DNA polymerase alpha catalytic subunit



- Molecule 2: RNA PRIMER



- Molecule 3: DNA TEMPLATE



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	140.76Å 140.76Å 181.31Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.51 – 2.20 39.65 – 2.20	Depositor EDS
% Data completeness (in resolution range)	88.6 (29.51-2.20) 88.7 (39.65-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	36.68 (at 2.20Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.210 , 0.239 0.207 , 0.236	Depositor DCC
R_{free} test set	4801 reflections (5.41%)	DCC
Wilson B-factor (Å ²)	37.8	Xtriage
Anisotropy	0.076	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 63.0	EDS
Estimated twinning fraction	0.029 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	1 of 95866 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7910	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.17% 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, K, MG, EDO, 1PE, DCP

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	0.37	0/7089	0.61	1/9582 (0.0%)
2	B	0.44	0/259	0.89	2/402 (0.5%)
3	C	0.48	0/296	0.81	0/455
All	All	0.37	0/7644	0.64	3/10439 (0.0%)

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
2	B	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	8	G	O4'-C1'-N9	6.66	113.53	108.20
2	B	8	G	N9-C1'-C2'	5.83	121.58	114.00
1	A	1183	GLY	N-CA-C	-5.41	99.58	113.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	8	G	Sidechain

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	6947	0	7092	214	0
2	B	232	0	120	2	0
3	C	264	0	146	8	0
4	A	28	0	12	2	0
5	A	1	0	0	0	0
6	A	2	0	0	0	0
6	B	1	0	0	0	0
7	A	1	0	0	0	0
8	A	16	0	22	1	0
9	A	4	0	6	0	0
10	A	351	0	0	16	0
10	B	23	0	0	0	0
10	C	40	0	0	1	0
All	All	7910	0	7398	225	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 (225) 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:729:GLN:HE21	1:A:729:GLN:H	1.04	1.02
1:A:935:ASN:N	1:A:935:ASN:HD22	1.53	1.01
1:A:729:GLN:NE2	1:A:729:GLN:H	1.62	0.98
1:A:1113:GLN:HE21	1:A:1238:TRP:HE1	1.14	0.94
1:A:935:ASN:H	1:A:935:ASN:ND2	1.62	0.93
1:A:935:ASN:H	1:A:935:ASN:HD22	1.06	0.91
3:C:118:DA:H2''	3:C:119:DG:H5'	1.54	0.88
1:A:354:ASN:HD22	1:A:354:ASN:N	1.75	0.84
1:A:935:ASN:N	1:A:935:ASN:ND2	2.24	0.83
1:A:1026:LYS:HE2	1:A:1039:ASP:HA	1.61	0.82
3:C:115:DT:H2''	3:C:116:DC:C5'	2.09	0.82
1:A:457:TYR:HB2	1:A:461:MET:HE1	1.62	0.79
1:A:1113:GLN:NE2	1:A:1238:TRP:HE1	1.79	0.78
1:A:1139:LEU:HD11	1:A:1175:VAL:HG23	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:115:DT:H2"	3:C:116:DC:H5"	1.66	0.77
1:A:597:ALA:O	1:A:601:VAL:HG23	1.86	0.76
1:A:589:PRO:O	1:A:590:LYS:HG3	1.85	0.75
1:A:1149:LYS:HG2	1:A:1150:LYS:N	2.01	0.74
1:A:854:LYS:HG3	1:A:1011:ASN:HD22	1.54	0.73
1:A:1181:GLN:HB2	1:A:1205:THR:HG23	1.72	0.72
1:A:727:ASN:N	1:A:727:ASN:HD22	1.89	0.71
1:A:1069:VAL:HG12	1:A:1070:THR:H	1.55	0.71
1:A:644:LEU:HD23	1:A:681:GLU:HB3	1.74	0.69
1:A:616:ARG:HD2	10:A:1708:HOH:O	1.91	0.69
1:A:1143:PRO:HG2	1:A:1144:GLN:NE2	2.06	0.69
1:A:1130:VAL:HG12	10:A:1619:HOH:O	1.92	0.68
1:A:605:LYS:HE2	1:A:739:LEU:HD21	1.75	0.68
1:A:729:GLN:N	1:A:729:GLN:HE21	1.85	0.67
3:C:115:DT:H2"	3:C:116:DC:H5'	1.76	0.67
1:A:411:LYS:HE2	1:A:415:GLU:OE2	1.94	0.67
1:A:1185:ASN:HD22	1:A:1185:ASN:C	1.97	0.67
1:A:878:THR:O	1:A:902:PRO:HB3	1.95	0.66
1:A:1139:LEU:HD11	1:A:1175:VAL:CG2	2.26	0.66
1:A:1143:PRO:HG2	1:A:1144:GLN:HE22	1.61	0.66
1:A:990:MET:HE1	1:A:1032:LEU:HD11	1.78	0.66
1:A:1138:ALA:HA	1:A:1174:THR:HA	1.77	0.65
1:A:936:PRO:O	1:A:939:ILE:HG22	1.97	0.65
1:A:652:ASN:HD22	1:A:670:MET:HE3	1.61	0.64
1:A:392:ARG:HD3	1:A:396:ILE:HD13	1.80	0.64
1:A:1184:SER:O	1:A:1185:ASN:ND2	2.32	0.63
1:A:854:LYS:HG3	1:A:1011:ASN:HA	1.79	0.63
1:A:730:ASN:HD22	1:A:730:ASN:N	1.96	0.63
1:A:1149:LYS:CG	1:A:1150:LYS:N	2.61	0.62
1:A:1149:LYS:HD3	1:A:1150:LYS:HD2	1.80	0.62
1:A:469:LYS:HG2	1:A:474:SER:O	1.99	0.62
1:A:859:LEU:HD23	1:A:1040:ILE:HD13	1.80	0.62
1:A:727:ASN:ND2	1:A:727:ASN:N	2.45	0.61
1:A:428:MET:C	1:A:429:LYS:HD2	2.21	0.61
1:A:1230:ILE:HD12	1:A:1238:TRP:HH2	1.66	0.60
1:A:729:GLN:N	1:A:729:GLN:NE2	2.42	0.60
1:A:595:PRO:HG3	1:A:732:TYR:O	2.02	0.60
1:A:1181:GLN:HB2	1:A:1205:THR:CG2	2.31	0.60
1:A:1114:LYS:HE3	1:A:1118:GLU:OE2	2.02	0.59
1:A:990:MET:CE	1:A:1032:LEU:HD11	2.33	0.59
1:A:727:ASN:ND2	1:A:727:ASN:H	1.99	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1098:GLN:O	1:A:1101:SER:HB3	2.03	0.59
1:A:461:MET:HE2	10:A:1511:HOH:O	2.02	0.59
1:A:1180:CYS:SG	1:A:1198:LEU:HD13	2.43	0.59
1:A:859:LEU:CD2	1:A:1040:ILE:HD13	2.33	0.59
1:A:911:LEU:HB3	1:A:912:PRO:HD3	1.85	0.58
1:A:553:HIS:CG	1:A:553:HIS:O	2.56	0.58
1:A:1149:LYS:O	1:A:1151:SER:N	2.36	0.58
1:A:806:LYS:HG2	1:A:966:ARG:NH1	2.19	0.57
1:A:667:ARG:NH1	1:A:683:ASN:O	2.37	0.57
1:A:549:ASN:ND2	1:A:552:ASN:OD1	2.37	0.57
1:A:1113:GLN:HG3	1:A:1238:TRP:NE1	2.19	0.57
1:A:926:LYS:HG2	1:A:946:GLN:HG3	1.86	0.57
1:A:605:LYS:HE2	1:A:739:LEU:CD2	2.35	0.57
1:A:1185:ASN:ND2	1:A:1185:ASN:C	2.59	0.57
1:A:727:ASN:O	1:A:731:MET:HG3	2.05	0.56
1:A:1016:GLU:O	1:A:1020:LYS:HG3	2.04	0.56
1:A:502:LYS:HE3	10:A:1725:HOH:O	2.05	0.56
1:A:1069:VAL:HG12	1:A:1070:THR:N	2.20	0.56
1:A:864:LEU:HD22	1:A:1004:ASP:HB3	1.86	0.55
1:A:429:LYS:N	1:A:429:LYS:HD2	2.21	0.55
1:A:1115:ARG:O	1:A:1119:ILE:HG12	2.06	0.55
1:A:678:GLY:HA2	1:A:681:GLU:OE1	2.07	0.55
1:A:595:PRO:O	1:A:598:PHE:HB2	2.06	0.54
1:A:354:ASN:N	1:A:354:ASN:ND2	2.48	0.54
1:A:718:THR:HG22	1:A:719:GLU:N	2.23	0.54
1:A:387:LEU:HD22	1:A:479:THR:HA	1.89	0.53
1:A:596:TYR:O	1:A:597:ALA:HB3	2.08	0.53
1:A:725:MET:HA	1:A:728:ILE:CD1	2.38	0.53
1:A:916:ARG:HD3	10:A:1687:HOH:O	2.08	0.53
1:A:864:LEU:HD22	1:A:1004:ASP:CB	2.38	0.53
1:A:730:ASN:ND2	1:A:730:ASN:N	2.57	0.52
3:C:111:DG:H2'	3:C:112:DC:C6	2.44	0.52
1:A:1218:PRO:HG3	10:A:1664:HOH:O	2.08	0.52
1:A:682:ARG:NH1	10:A:1730:HOH:O	2.41	0.52
1:A:916:ARG:HH11	1:A:916:ARG:HG2	1.73	0.52
1:A:725:MET:HA	1:A:728:ILE:HD12	1.91	0.51
1:A:628:LYS:HD3	10:A:1715:HOH:O	2.10	0.51
3:C:118:DA:C2'	3:C:119:DG:H5'	2.35	0.51
1:A:457:TYR:HB2	1:A:461:MET:CE	2.37	0.51
1:A:922:ARG:O	1:A:926:LYS:HG3	2.10	0.51
1:A:1122:ASN:HA	1:A:1125:ASN:ND2	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:395:LYS:C	1:A:396:ILE:HD12	2.31	0.51
1:A:1138:ALA:HB2	1:A:1174:THR:HG22	1.93	0.51
1:A:652:ASN:HB2	1:A:670:MET:HE1	1.93	0.51
1:A:683:ASN:O	1:A:686:CYS:HB2	2.11	0.51
1:A:854:LYS:O	1:A:856:ILE:HD12	2.11	0.50
1:A:652:ASN:ND2	1:A:670:MET:HE3	2.25	0.50
1:A:1122:ASN:HA	1:A:1125:ASN:HD21	1.77	0.50
1:A:1139:LEU:CD1	1:A:1175:VAL:HG23	2.39	0.50
1:A:650:ARG:HH12	1:A:653:VAL:HG11	1.75	0.50
1:A:607:VAL:HB	1:A:609:VAL:HG12	1.94	0.50
1:A:928:LEU:O	1:A:931:GLN:HB2	2.12	0.49
1:A:1148:ASP:O	1:A:1148:ASP:OD1	2.31	0.49
1:A:854:LYS:HB2	10:A:1731:HOH:O	2.12	0.49
1:A:646:VAL:O	1:A:650:ARG:HG2	2.11	0.49
1:A:985:MET:O	1:A:989:GLU:HG3	2.13	0.49
1:A:913:ARG:HG3	10:A:1611:HOH:O	2.13	0.49
1:A:512:SER:HB2	1:A:664:ARG:O	2.13	0.49
1:A:593:ILE:O	1:A:593:ILE:HG13	2.13	0.49
1:A:1113:GLN:NE2	1:A:1238:TRP:NE1	2.52	0.49
1:A:597:ALA:C	1:A:601:VAL:HG23	2.32	0.49
1:A:428:MET:HB2	1:A:429:LYS:HD2	1.95	0.49
1:A:1117:ILE:O	1:A:1121:GLU:HG3	2.12	0.49
1:A:1077:LEU:O	1:A:1080:VAL:HG22	2.13	0.48
1:A:1014:ASN:OD1	1:A:1017:GLU:HB2	2.13	0.48
1:A:596:TYR:O	1:A:597:ALA:CB	2.61	0.48
1:A:444:PRO:O	1:A:445:ASP:HB2	2.12	0.48
1:A:1058:LEU:HD22	1:A:1070:THR:HG23	1.95	0.48
1:A:558:ILE:HB	1:A:732:TYR:OH	2.14	0.48
1:A:395:LYS:HG2	1:A:396:ILE:N	2.28	0.48
1:A:1106:ASP:O	1:A:1110:GLU:HG2	2.14	0.47
1:A:642:PHE:CZ	1:A:646:VAL:HG21	2.49	0.47
1:A:985:MET:HG2	10:A:1604:HOH:O	2.13	0.47
1:A:636:GLY:HA3	1:A:639:ILE:HD11	1.96	0.47
1:A:597:ALA:HA	1:A:600:GLU:OE1	2.15	0.47
1:A:588:LYS:HA	1:A:732:TYR:HE2	1.79	0.47
1:A:393:GLU:OE1	1:A:393:GLU:N	2.37	0.47
1:A:541:ALA:O	1:A:562:ALA:HA	2.14	0.47
1:A:1125:ASN:OD1	1:A:1127:SER:HB2	2.14	0.47
1:A:922:ARG:NE	1:A:946:GLN:OE1	2.46	0.47
1:A:879:VAL:HB	1:A:972:LEU:HD21	1.97	0.47
1:A:1149:LYS:CG	1:A:1150:LYS:H	2.28	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:916:ARG:HG2	1:A:916:ARG:NH1	2.31	0.46
1:A:865:TYR:HB2	1:A:866:PRO:HD3	1.96	0.46
3:C:120:DG:H2'	10:C:238:HOH:O	2.16	0.46
1:A:1149:LYS:HD3	1:A:1150:LYS:H	1.81	0.46
1:A:1139:LEU:N	1:A:1139:LEU:HD12	2.31	0.46
1:A:1000:TYR:CG	1:A:1001:GLY:N	2.84	0.46
1:A:991:VAL:O	1:A:996:LEU:HB2	2.15	0.45
1:A:408:ILE:HG22	1:A:409:SER:N	2.31	0.45
1:A:1010:THR:C	1:A:1012:SER:H	2.19	0.45
3:C:118:DA:H2''	3:C:119:DG:C5'	2.37	0.45
1:A:910:ILE:HD12	1:A:910:ILE:N	2.31	0.45
1:A:425:TYR:O	1:A:426:LYS:HB2	2.17	0.45
1:A:1113:GLN:HG3	1:A:1238:TRP:CD1	2.52	0.45
1:A:864:LEU:HD12	1:A:1036:LEU:HD11	1.99	0.45
1:A:338:GLU:O	1:A:339:GLN:HB2	2.17	0.45
1:A:595:PRO:HB2	1:A:735:SER:OG	2.17	0.45
1:A:553:HIS:HA	10:A:1626:HOH:O	2.18	0.44
1:A:1217:HIS:HB3	1:A:1218:PRO:HD3	2.00	0.44
1:A:650:ARG:NH1	1:A:653:VAL:HG11	2.33	0.44
1:A:861:PHE:HA	1:A:1038:ILE:HA	1.99	0.44
1:A:1081:ARG:HD2	10:A:1453:HOH:O	2.17	0.44
2:B:2:C:H2'	2:B:3:C:C6	2.53	0.44
1:A:599:LYS:O	1:A:603:GLU:HG2	2.18	0.43
8:A:1306:1PE:H221	10:A:1627:HOH:O	2.18	0.43
1:A:1031:LYS:HE3	1:A:1031:LYS:HB2	1.76	0.43
1:A:1022:GLY:HA3	1:A:1040:ILE:HD11	2.00	0.43
1:A:865:TYR:CD2	4:A:1301:DCP:H2'2	2.53	0.43
1:A:991:VAL:HG12	1:A:996:LEU:HB2	1.99	0.43
1:A:1241:LEU:O	1:A:1243:PRO:HD3	2.19	0.43
1:A:1098:GLN:NE2	1:A:1103:GLN:OE1	2.50	0.43
1:A:1230:ILE:HG22	1:A:1231:ASP:N	2.33	0.43
1:A:589:PRO:O	1:A:590:LYS:CG	2.63	0.43
1:A:932:GLN:HG2	1:A:932:GLN:H	1.61	0.43
1:A:880:GLN:HE21	1:A:880:GLN:HB3	1.54	0.43
1:A:1082:ARG:HG2	1:A:1136:ASN:O	2.19	0.43
1:A:1150:LYS:H	1:A:1150:LYS:HD2	1.84	0.43
1:A:784:ARG:NH2	1:A:951:LEU:HD13	2.34	0.43
1:A:349:TYR:CG	1:A:686:CYS:SG	3.12	0.43
1:A:447:PRO:HG2	1:A:450:SER:HB2	2.00	0.43
1:A:669:ASN:HD22	1:A:669:ASN:N	2.16	0.42
2:B:8:G:H1'	2:B:9:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:988:LYS:O	1:A:992:GLN:HG3	2.19	0.42
1:A:1196:GLU:HG3	1:A:1197:GLN:N	2.34	0.42
1:A:806:LYS:HE3	10:A:1651:HOH:O	2.18	0.42
1:A:865:TYR:CG	4:A:1301:DCP:H2'2	2.54	0.42
1:A:522:LYS:HE3	1:A:524:ASP:OD1	2.20	0.42
1:A:1024:LYS:O	1:A:1028:GLU:HG2	2.19	0.42
1:A:767:GLN:O	1:A:771:ILE:HG13	2.19	0.42
1:A:725:MET:O	1:A:728:ILE:HB	2.19	0.42
1:A:1136:ASN:OD1	1:A:1176:SER:HB2	2.18	0.42
1:A:1105:ARG:NH2	1:A:1108:ILE:CD1	2.83	0.42
1:A:1109:VAL:HG13	1:A:1230:ILE:CD1	2.50	0.42
1:A:806:LYS:HB3	1:A:806:LYS:HE2	1.88	0.42
1:A:541:ALA:HA	1:A:635:VAL:HG13	2.02	0.42
1:A:988:LYS:HB3	1:A:988:LYS:HE2	1.94	0.42
1:A:395:LYS:O	1:A:396:ILE:HD12	2.20	0.42
1:A:747:LYS:HD2	1:A:747:LYS:HA	1.85	0.42
1:A:1010:THR:C	1:A:1012:SER:N	2.73	0.41
1:A:410:MET:HG3	1:A:434:PRO:HB3	2.02	0.41
1:A:732:TYR:HA	1:A:738:LEU:HG	2.02	0.41
1:A:651:ILE:HG23	1:A:656:ALA:HB3	2.01	0.41
1:A:555:ASN:HA	1:A:555:ASN:HD22	1.53	0.41
1:A:1064:SER:O	1:A:1067:ASN:HB2	2.20	0.41
1:A:552:ASN:HD21	1:A:554:GLN:NE2	2.18	0.41
1:A:1115:ARG:HD2	1:A:1115:ARG:HA	1.89	0.41
1:A:669:ASN:ND2	1:A:669:ASN:N	2.68	0.41
1:A:728:ILE:O	1:A:731:MET:HB2	2.21	0.41
1:A:762:LEU:HB2	1:A:763:PRO:HD3	2.03	0.41
1:A:730:ASN:H	1:A:730:ASN:ND2	2.18	0.41
1:A:588:LYS:HD2	1:A:592:CYS:O	2.21	0.41
1:A:922:ARG:NH2	1:A:946:GLN:OE1	2.51	0.41
1:A:915:ILE:HG12	1:A:956:MET:SD	2.61	0.41
1:A:1144:GLN:H	1:A:1144:GLN:CD	2.24	0.41
1:A:989:GLU:O	1:A:993:LYS:HG3	2.21	0.41
1:A:621:PHE:O	1:A:625:LYS:HG2	2.21	0.41
1:A:1162:ASN:OD1	1:A:1169:VAL:N	2.50	0.41
1:A:807:GLN:HG2	10:A:1544:HOH:O	2.20	0.41
1:A:731:MET:HA	1:A:737:GLN:HB3	2.03	0.40
1:A:428:MET:CB	1:A:429:LYS:HD2	2.51	0.40
1:A:718:THR:CG2	1:A:719:GLU:N	2.85	0.40
1:A:433:LYS:HB3	1:A:433:LYS:HE2	1.86	0.40
1:A:385:ARG:HD2	1:A:457:TYR:CZ	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:548:GLN:H	1:A:725:MET:HE2	1.86	0.40
1:A:602:ILE:HG23	1:A:609:VAL:HG13	2.03	0.40
1:A:932:GLN:HB3	1:A:932:GLN:HE21	1.64	0.40
1:A:616:ARG:HH21	1:A:655:LYS:HB2	1.86	0.40
1:A:595:PRO:HG2	1:A:734:GLU:C	2.42	0.40
1:A:738:LEU:HA	1:A:738:LEU:HD23	1.89	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	857/922 (93%)	798 (93%)	50 (6%)	9 (1%)	17 14

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	933	ASP
1	A	1149	LYS
1	A	1150	LYS
1	A	590	LYS
1	A	1185	ASN
1	A	339	GLN
1	A	1103	GLN
1	A	407	PRO
1	A	1166	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	778/827 (94%)	752 (97%)	26 (3%)	45 56

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	354	ASN
1	A	555	ASN
1	A	609	VAL
1	A	681	GLU
1	A	682	ARG
1	A	727	ASN
1	A	729	GLN
1	A	730	ASN
1	A	880	GLN
1	A	903	ASP
1	A	915	ILE
1	A	931	GLN
1	A	932	GLN
1	A	933	ASP
1	A	935	ASN
1	A	937	ASP
1	A	957	TYR
1	A	1011	ASN
1	A	1039	ASP
1	A	1070	THR
1	A	1082	ARG
1	A	1106	ASP
1	A	1164	GLN
1	A	1185	ASN
1	A	1199	GLN
1	A	1231	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	354	ASN
1	A	548	GLN
1	A	554	GLN

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Mol	Chain	Res	Type
1	A	555	ASN
1	A	606	ASN
1	A	638	ASN
1	A	652	ASN
1	A	669	ASN
1	A	683	ASN
1	A	727	ASN
1	A	729	GLN
1	A	730	ASN
1	A	760	ASN
1	A	880	GLN
1	A	897	GLN
1	A	931	GLN
1	A	932	GLN
1	A	935	ASN
1	A	954	ASN
1	A	1011	ASN
1	A	1067	ASN
1	A	1098	GLN
1	A	1103	GLN
1	A	1111	ASN
1	A	1113	GLN
1	A	1132	GLN
1	A	1144	GLN
1	A	1181	GLN
1	A	1185	ASN
1	A	1199	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 8 ligands modelled in this entry, 5 are monoatomic - leaving 3 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	DCP	A	1301	5,6	21,29,29	1.22	2 (9%)	33,45,45	1.76	6 (18%)
8	1PE	A	1306	-	15,15,15	1.16	1 (6%)	14,14,14	0.36	0
9	EDO	A	1307	-	3,3,3	0.55	0	2,2,2	0.37	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	DCP	A	1301	5,6	-	0/18/34/34	0/2/2/2
8	1PE	A	1306	-	-	0/13/13/13	0/0/0/0
9	EDO	A	1307	-	-	0/1/1/1	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1301	DCP	PG-O3G	2.06	1.62	1.54
8	A	1306	1PE	OH7-C16	2.41	1.55	1.42
4	A	1301	DCP	C6-N1	2.96	1.40	1.35

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1301	DCP	PB-O3A-PA	-5.05	118.54	132.73
4	A	1301	DCP	PB-O3B-PG	-4.50	117.59	132.67
4	A	1301	DCP	C2'-C1'-N1	-2.97	106.94	114.16
4	A	1301	DCP	N4-C4-N3	2.07	120.27	116.50
4	A	1301	DCP	O4'-C1'-N1	3.02	112.94	107.72
4	A	1301	DCP	C2-N3-C4	3.92	121.15	115.61

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	1301	DCP	2	0
8	A	1306	1PE	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	865/922 (93%)	-0.02	59 (6%) 20 20	20, 47, 94, 114	0
2	B	11/11 (100%)	0.03	1 (9%) 11 11	25, 32, 82, 86	0
3	C	13/21 (61%)	-0.29	1 (7%) 16 16	26, 32, 75, 92	0
All	All	889/954 (93%)	-0.02	61 (6%) 20 19	20, 47, 94, 114	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	597	ALA	6.2
1	A	596	TYR	6.1
1	A	553	HIS	5.6
1	A	932	GLN	5.1
1	A	550	ALA	5.1
1	A	933	ASP	4.8
1	A	1065	ASP	4.7
1	A	591	ASP	4.6
1	A	604	LYS	4.5
1	A	595	PRO	4.4
1	A	552	ASN	4.2
1	A	598	PHE	4.2
1	A	732	TYR	4.0
1	A	931	GLN	3.9
1	A	896	GLU	3.8
1	A	602	ILE	3.6
1	A	897	GLN	3.6
1	A	551	LYS	3.5
1	A	1066	GLY	3.5
1	A	672	LYS	3.5
1	A	600	GLU	3.5
1	A	733	SER	3.5
1	A	730	ASN	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	678	GLY	3.3
1	A	590	LYS	3.3
1	A	671	PRO	3.2
1	A	673	LEU	3.1
1	A	735	SER	3.1
1	A	549	ASN	3.1
1	A	808	ILE	3.1
1	A	882	VAL	3.1
1	A	589	PRO	3.1
1	A	725	MET	3.0
1	A	1067	ASN	2.9
1	A	936	PRO	2.9
1	A	1063	THR	2.9
1	A	606	ASN	2.9
1	A	905	SER	2.8
1	A	605	LYS	2.7
1	A	728	ILE	2.7
1	A	1150	LYS	2.7
1	A	1064	SER	2.6
1	A	679	PHE	2.6
1	A	353	TYR	2.6
1	A	937	ASP	2.6
1	A	601	VAL	2.6
1	A	934	LEU	2.6
2	B	1	G	2.5
1	A	593	ILE	2.5
1	A	547	MET	2.5
1	A	405	GLY	2.4
1	A	907	GLU	2.4
1	A	1199	GLN	2.4
3	C	121	DC	2.2
1	A	726	GLU	2.2
1	A	737	GLN	2.1
1	A	903	ASP	2.1
1	A	554	GLN	2.1
1	A	669	ASN	2.1
1	A	729	GLN	2.1
1	A	1200	LYS	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

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
9	EDO	A	1307	4/4	0.91	0.13	3.19	45,59,59,62	0
4	DCP	A	1301	28/28	0.99	0.16	1.00	18,26,35,40	0
8	1PE	A	1306	16/16	0.95	0.10	-0.44	34,45,55,60	0
5	MG	A	1302	1/1	0.99	0.14	-0.62	21,21,21,21	0
7	K	A	1305	1/1	0.98	0.07	-1.54	54,54,54,54	0
6	ZN	B	501	1/1	0.98	0.13	-	72,72,72,72	0
6	ZN	A	1304	1/1	1.00	0.13	-	30,30,30,30	1
6	ZN	A	1303	1/1	1.00	0.14	-	34,34,34,34	0

6.5 Other polymers [i](#)

There are no such residues in this entry.