Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 02:33 AM GMT

PDB ID	:	2HNY
Title	:	Crystal Structure of E138K Mutant HIV-1 Reverse Transcriptase in Complex with Nevirapine
Authors	:	Ren, J.; Nichols, C.E.; Stamp, A.; Chamberlain, P.P.; Stammers, D.K.
Deposited on	:	2006-07-13
Resolution	:	2.50 Å(reported)

The following versions of software and data (see references (i)) 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
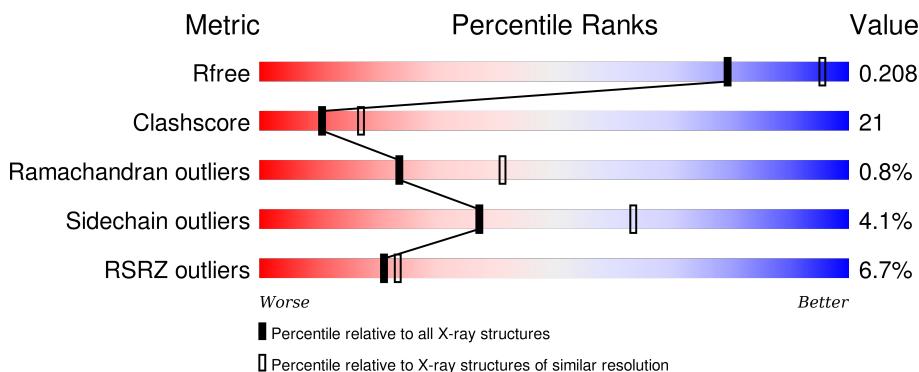
1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION
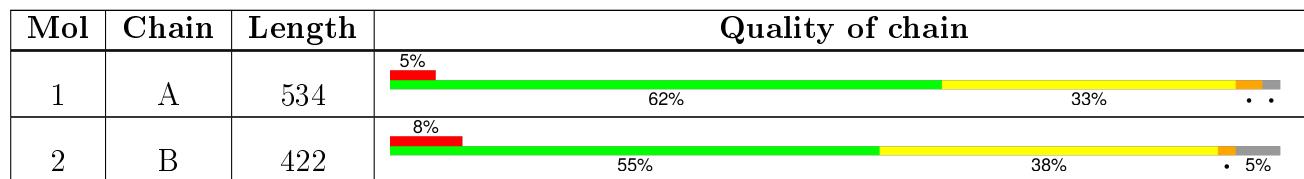
The reported resolution of this entry is 2.50 Å.

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))
R_{free}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (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 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 <=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	534	5% / 62% / 33% / · ·
2	B	422	8% / 55% / 38% / · 5%

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
3	PO4	A	1302	-	-	-	X

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 7744 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 Reverse transcriptase/ribonuclease H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	523	4295	2784	711	792	8	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	138	LYS	GLU	ENGINEERED	UNP P04585
A	280	CSD	CYS	MODIFIED RESIDUE	UNP P04585
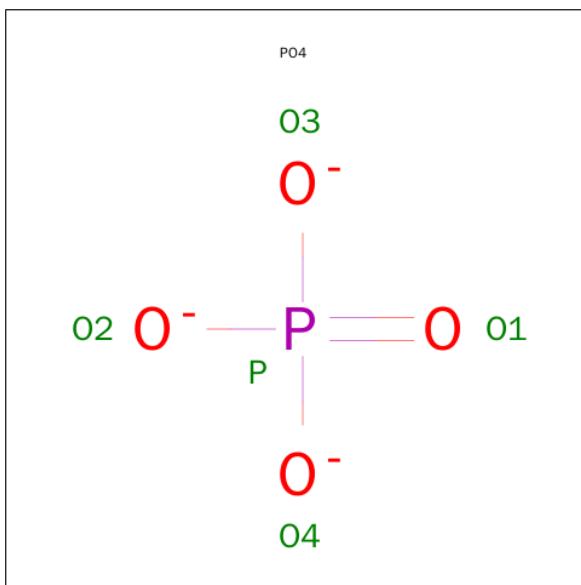
- Molecule 2 is a protein called Reverse transcriptase/ribonuclease H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	401	3334	2177	551	599	7	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	138	LYS	GLU	ENGINEERED	UNP P04585

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).
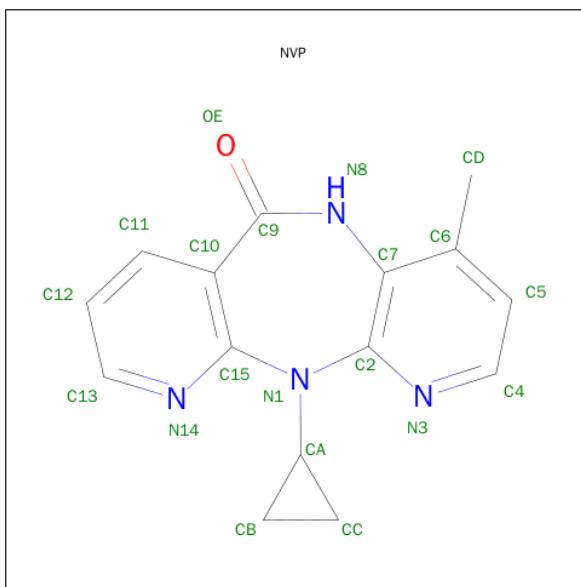
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 5	O 4	P 1	0	0
3	A	1	Total 5	O 4	P 1	0	0
3	A	1	Total 5	O 4	P 1	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 5 is 11-CYCLOPROPYL-5,11-DIHYDRO-4-METHYL-6H-DIPYRIDO[3,2-B:2',3'-E][1,4]DIAZEPIN-6-ONE (three-letter code: NVP) (formula: $C_{15}H_{14}N_4O$).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	A	1	20	15	4	1	0	0
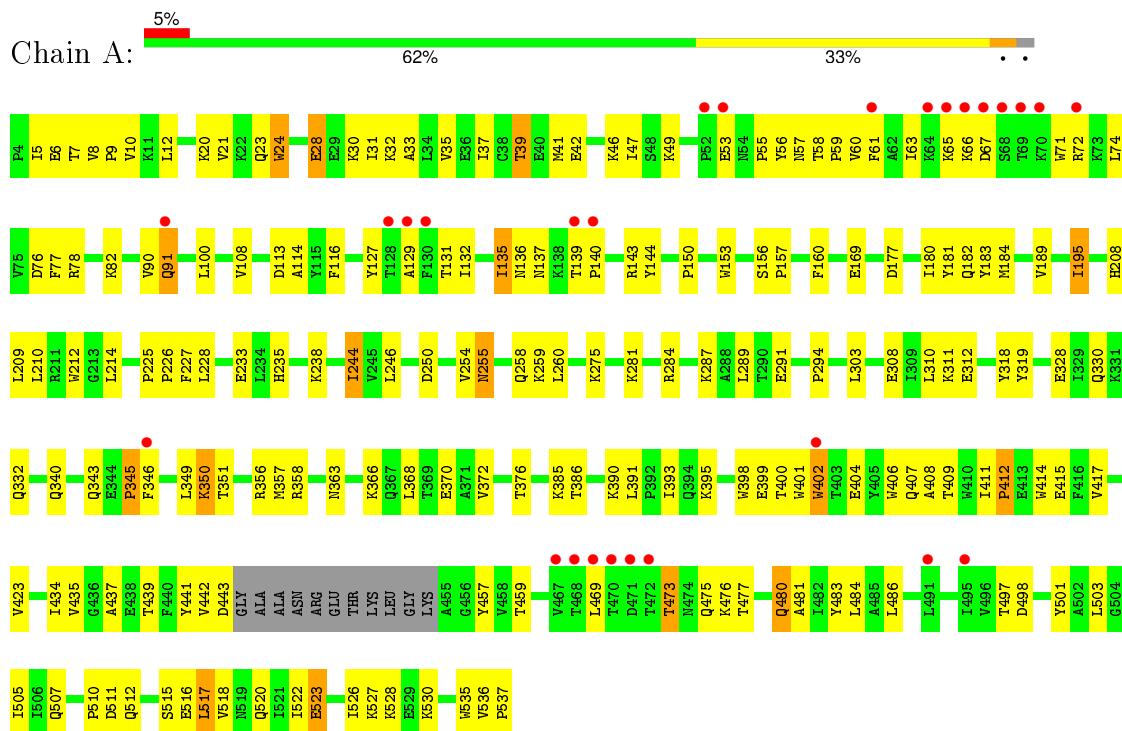
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	51	Total 51	O 51	0	0
6	B	28	Total 28	O 28	0	0
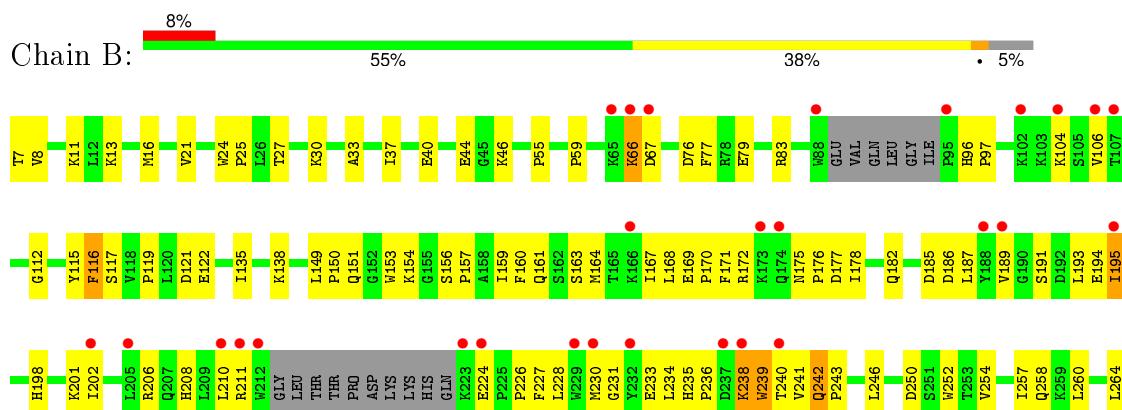
3 Residue-property plots ⓘ
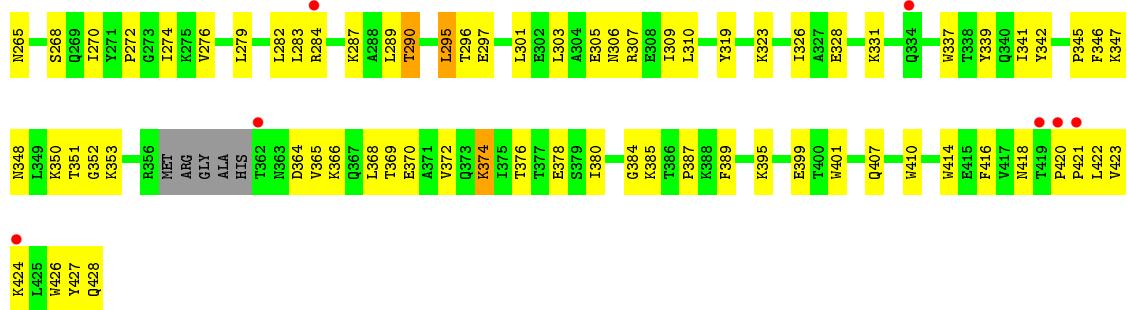
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: Reverse transcriptase/ribonuclease H

- Molecule 2: Reverse transcriptase/ribonuclease H

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	139.60Å　　115.00Å　　65.60Å 90.00°　　　90.00°　　　90.00°	Depositor
Resolution (Å)	19.94　–　2.50 19.94　–　2.50	Depositor EDS
% Data completeness (in resolution range)	99.5 (19.94-2.50) 99.5 (19.94-2.50)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	1.26 (at 2.50Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.214　,　0.284 0.204　,　0.208	Depositor DCC
R_{free} test set	1856 reflections (5.27%)	DCC
Wilson B-factor (Å^2)	56.8	Xtriage
Anisotropy	0.135	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 56.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$<|L|> = 0.50, <L^2> = 0.33$	Xtriage
Outliers	0 of 37062 reflections	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	7744	wwPDB-VP
Average B, all atoms (Å^2)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.24% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $<|L|>$, $<L^2>$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: CSD, PO4, MG, NVP

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	0.43	0/4401	0.63	0/5982
2	B	0.41	0/3431	0.64	0/4659
All	All	0.42	0/7832	0.63	0/10641

There are no bond length outliers.

There are no bond angle outliers.

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	4295	0	4338	167	0
2	B	3334	0	3366	169	0
3	A	15	0	0	0	0
4	A	1	0	0	0	0
5	A	20	0	14	0	0
6	A	51	0	0	7	0
6	B	28	0	0	1	0
All	All	7744	0	7718	327	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 21.

All (327) 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)
2:B:227:PHE:HB3	2:B:231:GLY:HA2	1.36	1.08
2:B:66:LYS:HD2	2:B:230:MET:HA	1.43	0.98
1:A:135:ILE:H	1:A:135:ILE:HD13	1.29	0.96
2:B:227:PHE:CB	2:B:231:GLY:HA2	1.99	0.91
1:A:33:ALA:O	1:A:37:ILE:HG12	1.71	0.90
1:A:6:GLU:HG2	6:A:1001:HOH:O	1.73	0.88
1:A:473:THR:HG23	1:A:476:LYS:HB2	1.56	0.88
1:A:113:ASP:HA	1:A:116:PHE:HD2	1.39	0.86
1:A:517:LEU:HA	1:A:520:GLN:HE21	1.41	0.84
2:B:331:LYS:O	2:B:424:LYS:HE2	1.76	0.84
2:B:270:ILE:O	2:B:272:PRO:HD3	1.80	0.81
1:A:23:GLN:HE22	1:A:60:VAL:H	1.29	0.80
1:A:469:LEU:HD11	1:A:480:GLN:HG3	1.63	0.79
2:B:135:ILE:O	2:B:138:LYS:HG3	1.82	0.79
2:B:295:LEU:HD12	2:B:295:LEU:N	1.97	0.78
1:A:136:ASN:HB2	1:A:139:THR:HB	1.65	0.78
1:A:63:ILE:HD11	1:A:74:LEU:HD22	1.66	0.77
1:A:24:TRP:HZ2	1:A:61:PHE:HD2	1.31	0.76
2:B:66:LYS:CD	2:B:230:MET:HA	2.14	0.76
2:B:274:ILE:HD11	2:B:310:LEU:HD21	1.66	0.76
2:B:66:LYS:HB2	2:B:407:GLN:HE22	1.51	0.75
2:B:7:THR:HG22	2:B:119:PRO:HB2	1.69	0.74
2:B:40:GLU:HG3	2:B:44:GLU:OE2	1.90	0.71
2:B:194:GLU:OE2	2:B:195:ILE:HG12	1.91	0.71
2:B:206:ARG:HD2	2:B:227:PHE:CE1	2.27	0.70
2:B:305:GLU:O	2:B:309:ILE:HG13	1.92	0.70
1:A:442:VAL:HB	1:A:481:ALA:HB1	1.74	0.70
1:A:308:GLU:OE1	1:A:311:LYS:HD2	1.92	0.69
2:B:164:MET:SD	2:B:167:ILE:HD11	2.33	0.69
1:A:31:ILE:HG21	1:A:135:ILE:HG23	1.74	0.69
1:A:131:THR:OG1	1:A:143:ARG:HG2	1.93	0.69
1:A:399:GLU:HG3	1:A:402:TRP:CE3	2.27	0.69
1:A:244:ILE:HD13	1:A:310:LEU:HD13	1.75	0.68
2:B:342:TYR:HB3	2:B:348:ASN:HD22	1.59	0.68
2:B:427:TYR:O	2:B:428:GLN:HB3	1.91	0.68
2:B:254:VAL:O	2:B:258:GLN:HG3	1.93	0.68
1:A:515:SER:HB2	6:A:1038:HOH:O	1.93	0.68
2:B:66:LYS:HB2	2:B:407:GLN:NE2	2.08	0.67
2:B:238:LYS:O	2:B:240:THR:HG23	1.93	0.67
1:A:46:LYS:HE3	1:A:116:PHE:HD1	1.60	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:LYS:HE3	1:A:71:TRP:CZ3	2.29	0.67
1:A:246:LEU:HD22	1:A:260:LEU:HD11	1.78	0.66
1:A:30:LYS:HE3	1:A:71:TRP:HZ3	1.60	0.66
1:A:24:TRP:HE1	1:A:61:PHE:HB3	1.61	0.66
2:B:168:LEU:O	2:B:172:ARG:HB2	1.95	0.66
2:B:295:LEU:HD12	2:B:295:LEU:H	1.59	0.65
2:B:238:LYS:HD2	2:B:238:LYS:N	2.11	0.65
2:B:282:LEU:HD21	2:B:296:THR:HG23	1.77	0.65
2:B:319:TYR:OH	2:B:385:LYS:HD3	1.95	0.65
1:A:65:LYS:HD2	1:A:72:ARG:HD2	1.78	0.65
2:B:66:LYS:HB3	2:B:66:LYS:NZ	2.10	0.65
1:A:507:GLN:HE22	2:B:421:PRO:HB3	1.61	0.65
2:B:175:ASN:HD21	2:B:201:LYS:CE	2.10	0.65
1:A:61:PHE:CZ	1:A:74:LEU:HD23	2.32	0.64
1:A:498:ASP:HA	1:A:536:VAL:O	1.97	0.64
1:A:281:LYS:HE3	1:A:284:ARG:CZ	2.28	0.64
1:A:42:GLU:OE2	1:A:49:LYS:HG3	1.97	0.63
1:A:480:GLN:C	1:A:480:GLN:HE21	2.02	0.63
1:A:294:PRO:HA	6:A:1027:HOH:O	1.98	0.63
2:B:246:LEU:HD12	2:B:307:ARG:HG2	1.81	0.63
1:A:28:GLU:HG3	1:A:135:ILE:CG2	2.29	0.62
2:B:284:ARG:O	2:B:287:LYS:NZ	2.29	0.62
1:A:46:LYS:HE3	1:A:116:PHE:CD1	2.34	0.62
1:A:399:GLU:HG3	1:A:402:TRP:CZ3	2.35	0.62
1:A:135:ILE:H	1:A:135:ILE:CD1	2.06	0.62
1:A:24:TRP:CZ2	1:A:61:PHE:HD2	2.16	0.62
2:B:420:PRO:HG2	2:B:423:VAL:HG12	1.80	0.62
2:B:171:PHE:CE2	2:B:178:ILE:HD11	2.35	0.62
1:A:235:HIS:HB2	1:A:238:LYS:O	2.00	0.61
1:A:357:MET:HE1	1:A:512:GLN:HE21	1.65	0.61
1:A:501:TYR:CZ	1:A:505:ILE:HD11	2.36	0.61
2:B:104:LYS:O	2:B:235:HIS:HA	2.01	0.61
1:A:393:ILE:HB	1:A:423:VAL:CG2	2.31	0.61
1:A:530:LYS:HA	6:A:1075:HOH:O	1.99	0.61
2:B:423:VAL:HG13	2:B:424:LYS:N	2.17	0.60
2:B:172:ARG:O	2:B:176:PRO:HG3	2.02	0.60
1:A:136:ASN:HB2	1:A:139:THR:CB	2.32	0.60
2:B:116:PHE:CE1	2:B:151:GLN:HG3	2.36	0.60
2:B:182:GLN:HB2	2:B:187:LEU:CD1	2.31	0.60
1:A:28:GLU:O	1:A:32:LYS:HD3	2.02	0.60
1:A:473:THR:HG23	1:A:476:LYS:CB	2.28	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:175:ASN:HD21	2:B:201:LYS:NZ	1.99	0.60
2:B:135:ILE:HB	2:B:138:LYS:HE2	1.82	0.60
1:A:72:ARG:HH21	1:A:74:LEU:HD13	1.67	0.59
2:B:59:PRO:HG2	2:B:76:ASP:HB3	1.84	0.59
1:A:181:TYR:CE1	1:A:183:TYR:HB2	2.36	0.59
1:A:28:GLU:OE1	1:A:31:ILE:HD12	2.02	0.59
1:A:63:ILE:CD1	1:A:74:LEU:HD22	2.32	0.59
2:B:116:PHE:HE1	2:B:151:GLN:HG3	1.68	0.59
2:B:368:LEU:O	2:B:372:VAL:HG23	2.03	0.59
1:A:255:ASN:ND2	1:A:289:LEU:HB3	2.17	0.59
1:A:28:GLU:HG3	1:A:135:ILE:HG22	1.85	0.58
2:B:171:PHE:HE2	2:B:178:ILE:HD11	1.68	0.58
1:A:523:GLU:O	1:A:527:LYS:HG2	2.02	0.58
1:A:516:GLU:O	1:A:520:GLN:HG3	2.02	0.58
2:B:8:VAL:O	2:B:121:ASP:HB2	2.04	0.58
2:B:254:VAL:HG13	2:B:283:LEU:HD22	1.84	0.58
1:A:376:THR:HG23	1:A:386:THR:HG22	1.85	0.57
1:A:156:SER:HB2	1:A:157:PRO:HD3	1.87	0.57
2:B:295:LEU:CD1	2:B:295:LEU:N	2.68	0.57
2:B:46:LYS:HZ3	2:B:116:PHE:HD2	1.51	0.57
2:B:164:MET:O	2:B:167:ILE:HG12	2.04	0.57
1:A:357:MET:CE	1:A:512:GLN:HE21	2.16	0.57
1:A:497:THR:O	1:A:535:TRP:HA	2.05	0.57
1:A:150:PRO:HG2	1:A:153:TRP:HB2	1.87	0.57
1:A:113:ASP:HA	1:A:116:PHE:CD2	2.30	0.56
2:B:163:SER:O	2:B:167:ILE:HG23	2.05	0.56
2:B:189:VAL:HG11	2:B:202:ILE:HD13	1.86	0.56
2:B:21:VAL:HB	2:B:59:PRO:HD3	1.86	0.56
1:A:406:TRP:CH2	2:B:418:ASN:HA	2.40	0.56
1:A:408:ALA:HB2	2:B:337:TRP:HH2	1.71	0.56
1:A:401:TRP:HA	1:A:404:GLU:HG2	1.88	0.56
2:B:151:GLN:HB3	2:B:185:ASP:OD1	2.06	0.55
2:B:233:GLU:N	2:B:233:GLU:OE2	2.40	0.55
1:A:356:ARG:HH21	1:A:358:ARG:HD2	1.71	0.55
1:A:356:ARG:NH2	6:A:1029:HOH:O	2.39	0.55
1:A:255:ASN:O	1:A:259:LYS:HG3	2.06	0.55
2:B:175:ASN:HD21	2:B:201:LYS:HE3	1.70	0.54
1:A:35:VAL:HG22	1:A:132:ILE:HG21	1.88	0.54
1:A:91:GLN:HE22	1:A:184:MET:H	1.55	0.54
1:A:340:GLN:HG3	1:A:351:THR:HG22	1.88	0.54
1:A:195:ILE:HG13	6:A:1022:HOH:O	2.05	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:VAL:HG12	1:A:91:GLN:HG2	1.89	0.54
1:A:53:GLU:O	1:A:55:PRO:HD3	2.08	0.53
1:A:363:ASN:HA	1:A:511:ASP:OD1	2.08	0.53
2:B:106:VAL:HG13	2:B:234:LEU:HB2	1.90	0.53
1:A:76:ASP:OD2	1:A:78:ARG:HG3	2.08	0.53
2:B:164:MET:HA	2:B:167:ILE:HG12	1.91	0.53
1:A:319:TYR:OH	1:A:385:LYS:HE2	2.09	0.53
1:A:254:VAL:O	1:A:258:GLN:HG3	2.09	0.53
2:B:227:PHE:CB	2:B:231:GLY:CA	2.82	0.52
2:B:242:GLN:HG3	2:B:352:GLY:HA2	1.90	0.52
2:B:66:LYS:HD2	2:B:230:MET:CA	2.29	0.52
1:A:65:LYS:O	1:A:67:ASP:N	2.42	0.52
2:B:195:ILE:N	2:B:195:ILE:HD13	2.24	0.52
2:B:169:GLU:N	2:B:170:PRO:HD2	2.24	0.52
2:B:191:SER:OG	2:B:198:HIS:ND1	2.39	0.52
1:A:503:LEU:O	1:A:507:GLN:HG3	2.10	0.52
1:A:23:GLN:HE22	1:A:60:VAL:HG12	1.74	0.52
1:A:72:ARG:HH21	1:A:74:LEU:CD1	2.22	0.52
1:A:131:THR:HG23	1:A:143:ARG:HG3	1.92	0.51
2:B:115:TYR:HB3	2:B:149:LEU:HB2	1.92	0.51
2:B:395:LYS:HG3	2:B:416:PHE:CE1	2.46	0.51
2:B:159:ILE:HG22	2:B:159:ILE:O	2.09	0.51
1:A:434:ILE:HB	1:A:437:ALA:HB3	1.91	0.51
2:B:257:ILE:HG22	2:B:283:LEU:HD11	1.93	0.51
1:A:209:LEU:O	1:A:214:LEU:HB2	2.10	0.51
1:A:366:LYS:HB3	1:A:366:LYS:NZ	2.24	0.51
1:A:20:LYS:HE2	1:A:55:PRO:HB2	1.93	0.51
1:A:246:LEU:HD13	1:A:303:LEU:CD1	2.41	0.50
2:B:224:GLU:O	2:B:226:PRO:HD3	2.12	0.50
1:A:395:LYS:HD3	1:A:414:TRP:CZ2	2.45	0.50
1:A:363:ASN:HA	1:A:511:ASP:CG	2.31	0.50
2:B:178:ILE:HG22	2:B:191:SER:HB3	1.93	0.50
2:B:66:LYS:CE	2:B:230:MET:H	2.24	0.50
2:B:164:MET:HA	2:B:167:ILE:CD1	2.41	0.50
1:A:345:PRO:O	1:A:346:PHE:HB2	2.11	0.50
2:B:66:LYS:HE3	2:B:230:MET:N	2.27	0.50
1:A:37:ILE:O	1:A:41:MET:HG3	2.12	0.49
1:A:23:GLN:NE2	1:A:60:VAL:HG12	2.26	0.49
1:A:47:ILE:HD12	1:A:144:TYR:CD2	2.47	0.49
1:A:246:LEU:HD22	1:A:260:LEU:CD1	2.40	0.49
2:B:175:ASN:ND2	2:B:201:LYS:CE	2.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10:VAL:HG11	1:A:153:TRP:CZ2	2.48	0.49
2:B:46:LYS:HD3	2:B:116:PHE:CD2	2.46	0.49
2:B:66:LYS:HE3	2:B:230:MET:CA	2.42	0.49
1:A:406:TRP:CZ3	1:A:407:GLN:HB2	2.47	0.49
1:A:72:ARG:NH2	1:A:74:LEU:HD13	2.28	0.49
1:A:480:GLN:O	1:A:483:TYR:HB3	2.13	0.48
1:A:368:LEU:O	1:A:372:VAL:HG23	2.13	0.48
1:A:90:VAL:HG12	1:A:91:GLN:N	2.27	0.48
2:B:150:PRO:HG2	2:B:153:TRP:HB2	1.96	0.48
1:A:417:VAL:O	1:A:417:VAL:HG13	2.12	0.48
2:B:372:VAL:HA	2:B:389:PHE:CE2	2.48	0.48
2:B:365:VAL:HG11	2:B:401:TRP:HB2	1.96	0.48
1:A:408:ALA:HA	2:B:364:ASP:OD1	2.14	0.48
1:A:399:GLU:HG3	1:A:402:TRP:HE3	1.76	0.48
2:B:387:PRO:HG2	2:B:389:PHE:CE1	2.48	0.48
2:B:297:GLU:O	2:B:301:LEU:HG	2.12	0.48
1:A:228:LEU:HD23	1:A:233:GLU:HA	1.96	0.48
2:B:66:LYS:CE	2:B:230:MET:HA	2.44	0.48
1:A:469:LEU:CD1	1:A:480:GLN:HG3	2.38	0.48
2:B:395:LYS:O	2:B:399:GLU:HG2	2.14	0.48
2:B:265:ASN:O	2:B:268:SER:HB3	2.13	0.48
2:B:161:GLN:O	2:B:164:MET:HB3	2.13	0.48
1:A:225:PRO:HA	1:A:226:PRO:C	2.34	0.48
1:A:535:TRP:CZ3	1:A:537:PRO:HD3	2.49	0.47
2:B:33:ALA:O	2:B:37:ILE:HG13	2.15	0.47
1:A:287:LYS:HG2	1:A:291:GLU:OE2	2.15	0.47
1:A:475:GLN:HB2	1:A:501:TYR:CD2	2.49	0.47
1:A:486:LEU:O	1:A:528:LYS:NZ	2.46	0.47
1:A:393:ILE:HB	1:A:423:VAL:HG22	1.95	0.47
1:A:518:VAL:O	1:A:522:ILE:HG13	2.14	0.47
1:A:398:TRP:CE2	1:A:411:ILE:HD12	2.49	0.47
2:B:66:LYS:CD	2:B:230:MET:CA	2.92	0.47
1:A:281:LYS:HE3	1:A:284:ARG:NH2	2.30	0.47
2:B:242:GLN:HE22	2:B:353:LYS:HD3	1.80	0.47
2:B:242:GLN:OE1	2:B:353:LYS:HE2	2.14	0.47
2:B:242:GLN:HE21	2:B:242:GLN:HB3	1.53	0.47
1:A:35:VAL:O	1:A:39:THR:HB	2.15	0.47
1:A:31:ILE:O	1:A:35:VAL:HG23	2.15	0.47
2:B:194:GLU:O	2:B:198:HIS:N	2.45	0.47
1:A:332:GLN:HG2	1:A:332:GLN:O	2.14	0.47
2:B:170:PRO:HG3	2:B:208:HIS:CE1	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:164:MET:C	2:B:167:ILE:HG12	2.36	0.46
2:B:236:PRO:HA	2:B:239:TRP:CE2	2.50	0.46
2:B:115:TYR:C	2:B:117:SER:H	2.18	0.46
2:B:46:LYS:NZ	2:B:116:PHE:HD2	2.14	0.46
2:B:11:LYS:HB3	2:B:11:LYS:HE2	1.69	0.46
1:A:5:ILE:HG13	1:A:6:GLU:N	2.30	0.46
2:B:211:ARG:HH11	2:B:211:ARG:HG3	1.79	0.46
2:B:242:GLN:NE2	2:B:353:LYS:HD3	2.31	0.46
1:A:139:THR:HA	1:A:140:PRO:HD3	1.81	0.46
1:A:501:TYR:CE1	1:A:505:ILE:HD11	2.50	0.46
2:B:79:GLU:O	2:B:83:ARG:HG3	2.15	0.46
1:A:21:VAL:HB	1:A:59:PRO:HD3	1.97	0.46
1:A:409:THR:O	2:B:364:ASP:HB2	2.16	0.46
1:A:406:TRP:HH2	2:B:418:ASN:OD1	1.99	0.46
1:A:57:ASN:HA	1:A:129:ALA:O	2.16	0.46
1:A:391:LEU:C	1:A:417:VAL:HG12	2.36	0.45
2:B:365:VAL:O	2:B:369:THR:HG23	2.16	0.45
1:A:208:HIS:O	1:A:212:TRP:HD1	1.98	0.45
2:B:175:ASN:C	2:B:177:ASP:H	2.19	0.45
1:A:12:LEU:HD11	1:A:127:TYR:CE1	2.51	0.45
2:B:178:ILE:HG22	2:B:191:SER:CB	2.46	0.45
2:B:175:ASN:ND2	2:B:201:LYS:HE3	2.31	0.45
2:B:66:LYS:HE3	2:B:230:MET:HA	1.99	0.45
1:A:31:ILE:CG2	1:A:135:ILE:HG23	2.46	0.45
2:B:186:ASP:OD1	2:B:228:LEU:HD12	2.17	0.45
2:B:156:SER:N	2:B:157:PRO:HD2	2.31	0.45
2:B:420:PRO:HG2	2:B:423:VAL:CG1	2.46	0.45
2:B:295:LEU:H	2:B:295:LEU:CD1	2.25	0.45
2:B:238:LYS:HD2	2:B:238:LYS:H	1.81	0.45
1:A:507:GLN:NE2	2:B:421:PRO:HB3	2.27	0.45
2:B:270:ILE:HG12	2:B:346:PHE:HB3	1.98	0.45
2:B:427:TYR:O	2:B:428:GLN:CB	2.63	0.45
1:A:376:THR:HG23	1:A:386:THR:CG2	2.47	0.45
1:A:8:VAL:HA	1:A:9:PRO:HD3	1.78	0.44
1:A:108:VAL:HG12	1:A:227:PHE:CE1	2.52	0.44
1:A:58:THR:HG21	1:A:77:PHE:CD2	2.53	0.44
2:B:423:VAL:CG1	2:B:424:LYS:N	2.79	0.44
1:A:90:VAL:HG12	1:A:91:GLN:H	1.83	0.44
1:A:522:ILE:O	1:A:526:ILE:HG13	2.16	0.44
1:A:114:ALA:HB1	1:A:160:PHE:CE2	2.53	0.44
1:A:180:ILE:HG12	1:A:189:VAL:HG13	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:331:LYS:HB2	2:B:337:TRP:CZ3	2.52	0.44
1:A:275:LYS:HE2	1:A:332:GLN:NE2	2.33	0.44
2:B:276:VAL:O	2:B:279:LEU:N	2.51	0.44
2:B:241:VAL:O	2:B:243:PRO:HD3	2.18	0.44
2:B:171:PHE:HE2	2:B:178:ILE:CD1	2.29	0.44
1:A:100:LEU:O	1:A:318:TYR:HB3	2.16	0.44
1:A:177:ASP:N	1:A:177:ASP:OD2	2.51	0.44
2:B:66:LYS:HE3	2:B:230:MET:H	1.83	0.44
2:B:422:LEU:HB3	2:B:426:TRP:CH2	2.53	0.44
2:B:350:LYS:HG2	2:B:351:THR:N	2.32	0.43
2:B:282:LEU:CD2	2:B:296:THR:HG23	2.48	0.43
1:A:357:MET:CE	1:A:512:GLN:NE2	2.81	0.43
2:B:326:ILE:O	2:B:341:ILE:HA	2.18	0.43
1:A:182:GLN:HB3	6:A:1018:HOH:O	2.16	0.43
1:A:408:ALA:HB1	2:B:364:ASP:HB3	2.00	0.43
2:B:195:ILE:HD13	2:B:195:ILE:H	1.82	0.43
2:B:342:TYR:HB3	2:B:348:ASN:HA	1.99	0.43
2:B:376:THR:HB	2:B:410:TRP:CH2	2.54	0.43
2:B:24:TRP:CG	2:B:25:PRO:HD2	2.53	0.43
2:B:154:LYS:O	2:B:157:PRO:HD2	2.19	0.43
2:B:116:PHE:CD1	2:B:116:PHE:N	2.87	0.43
1:A:246:LEU:HD13	1:A:303:LEU:HD12	1.99	0.43
2:B:380:ILE:O	2:B:384:GLY:N	2.51	0.43
1:A:56:TYR:O	1:A:143:ARG:NH2	2.44	0.43
1:A:390:LYS:HD3	1:A:415:GLU:HG2	2.00	0.43
1:A:505:ILE:O	1:A:510:PRO:HD3	2.19	0.43
1:A:150:PRO:HG2	1:A:153:TRP:CB	2.48	0.43
2:B:164:MET:CA	2:B:167:ILE:HG12	2.49	0.42
2:B:112:GLY:HA3	2:B:151:GLN:HE21	1.83	0.42
1:A:10:VAL:HG11	1:A:153:TRP:HZ2	1.83	0.42
2:B:66:LYS:CD	2:B:230:MET:H	2.32	0.42
1:A:434:ILE:HB	1:A:437:ALA:CB	2.49	0.42
2:B:96:HIS:HA	2:B:97:PRO:HD3	1.82	0.42
2:B:27:THR:OG1	2:B:30:LYS:HG2	2.18	0.42
2:B:345:PRO:C	2:B:347:LYS:H	2.21	0.42
2:B:372:VAL:HG13	2:B:389:PHE:CE2	2.53	0.42
2:B:252:TRP:CZ3	2:B:260:LEU:HD22	2.55	0.42
2:B:227:PHE:HB2	2:B:231:GLY:HA2	1.96	0.42
2:B:195:ILE:CD1	2:B:195:ILE:H	2.33	0.42
2:B:160:PHE:CD1	2:B:160:PHE:O	2.72	0.42
1:A:457:TYR:C	1:A:457:TYR:CD1	2.93	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:164:MET:HA	2:B:167:ILE:HD11	2.01	0.42
1:A:350:LYS:HE2	1:A:350:LYS:HB2	1.73	0.42
1:A:368:LEU:O	1:A:368:LEU:HD12	2.20	0.42
1:A:343:GLN:HG3	1:A:349:LEU:HD11	2.01	0.42
1:A:61:PHE:C	1:A:61:PHE:CD1	2.94	0.42
1:A:244:ILE:O	1:A:244:ILE:HG23	2.20	0.42
2:B:306:ASN:O	2:B:310:LEU:HG	2.19	0.41
2:B:13:LYS:HB2	2:B:16:MET:SD	2.60	0.41
2:B:260:LEU:O	2:B:264:LEU:HG	2.21	0.41
2:B:178:ILE:O	2:B:178:ILE:HG13	2.20	0.41
2:B:201:LYS:HD3	2:B:201:LYS:HA	1.87	0.41
1:A:475:GLN:HB2	1:A:501:TYR:CE2	2.56	0.41
1:A:210:LEU:HA	1:A:210:LEU:HD12	1.91	0.41
2:B:106:VAL:CG1	2:B:234:LEU:HB2	2.50	0.41
2:B:210:LEU:HD12	2:B:224:GLU:CG	2.51	0.41
1:A:398:TRP:NE1	1:A:411:ILE:HD12	2.35	0.41
2:B:66:LYS:O	2:B:67:ASP:HB2	2.21	0.41
1:A:78:ARG:O	1:A:82:LYS:HG3	2.20	0.41
1:A:439:THR:HG22	1:A:441:TYR:CE1	2.56	0.41
1:A:399:GLU:HA	1:A:402:TRP:HE3	1.86	0.41
1:A:516:GLU:O	1:A:517:LEU:C	2.58	0.41
2:B:164:MET:HA	2:B:167:ILE:CG1	2.51	0.41
1:A:411:ILE:O	1:A:412:PRO:O	2.38	0.41
1:A:208:HIS:O	1:A:212:TRP:CD1	2.73	0.41
2:B:328:GLU:O	2:B:339:TYR:HA	2.20	0.41
1:A:113:ASP:HB3	1:A:116:PHE:HB2	2.02	0.41
2:B:175:ASN:N	2:B:176:PRO:HD3	2.35	0.41
2:B:187:LEU:HA	2:B:187:LEU:HD12	1.88	0.41
1:A:328:GLU:HG2	1:A:330:GLN:HE21	1.85	0.41
2:B:366:LYS:HE2	2:B:370:GLU:OE1	2.22	0.40
2:B:193:LEU:HD12	2:B:193:LEU:N	2.35	0.40
2:B:116:PHE:N	2:B:116:PHE:HD1	2.19	0.40
1:A:358:ARG:HD3	1:A:370:GLU:CD	2.41	0.40
2:B:374:LYS:O	2:B:378:GLU:HG3	2.21	0.40
2:B:323:LYS:HD3	2:B:323:LYS:HA	1.75	0.40
1:A:480:GLN:HE22	1:A:484:LEU:HG	1.86	0.40
2:B:211:ARG:NH1	2:B:211:ARG:HG3	2.36	0.40
1:A:435:VAL:HG22	2:B:290:THR:HG21	2.03	0.40
2:B:257:ILE:CG2	2:B:283:LEU:HD11	2.52	0.40
2:B:77:PHE:CE1	2:B:150:PRO:HB2	2.56	0.40
2:B:30:LYS:HG3	6:B:1041:HOH:O	2.20	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	518/534 (97%)	479 (92%)	34 (7%)	5 (1%)	19	34
2	B	393/422 (93%)	359 (91%)	32 (8%)	2 (0%)	34	55
All	All	911/956 (95%)	838 (92%)	66 (7%)	7 (1%)	24	41

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	66	LYS
1	A	412	PRO
1	A	91	GLN
2	B	116	PHE
2	B	239	TRP
1	A	195	ILE
1	A	345	PRO

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	472/479 (98%)	451 (96%)	21 (4%)	35	60
2	B	367/384 (96%)	354 (96%)	13 (4%)	43	70
All	All	839/863 (97%)	805 (96%)	34 (4%)	37	63

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	THR
1	A	24	TRP
1	A	28	GLU
1	A	39	THR
1	A	135	ILE
1	A	137	ASN
1	A	169	GLU
1	A	244	ILE
1	A	250	ASP
1	A	255	ASN
1	A	312	GLU
1	A	350	LYS
1	A	400	THR
1	A	402	TRP
1	A	443	ASP
1	A	459	THR
1	A	473	THR
1	A	477	THR
1	A	480	GLN
1	A	517	LEU
1	A	523	GLU
2	B	55	PRO
2	B	66	LYS
2	B	122	GLU
2	B	195	ILE
2	B	238	LYS
2	B	242	GLN
2	B	250	ASP
2	B	289	LEU
2	B	290	THR
2	B	295	LEU
2	B	303	LEU
2	B	374	LYS
2	B	414	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	GLN
1	A	91	GLN
1	A	151	GLN

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Mol	Chain	Res	Type
1	A	222	GLN
1	A	255	ASN
1	A	265	ASN
1	A	278	GLN
1	A	332	GLN
1	A	336	GLN
1	A	428	GLN
1	A	475	GLN
1	A	480	GLN
1	A	507	GLN
1	A	509	GLN
1	A	512	GLN
1	A	520	GLN
2	B	147	ASN
2	B	151	GLN
2	B	175	ASN
2	B	269	GLN
2	B	278	GLN
2	B	348	ASN
2	B	407	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	CSD	A	280	1	3,7,8	0.85	0	3,8,10	1.54	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
1	CSD	A	280	1	-	0/2/6/8	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 1 is 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	$\#|Z| > 2$
3	PO4	A	1300	-	4,4,4	1.01	0	6,6,6	0.27	0
3	PO4	A	1301	-	4,4,4	1.08	0	6,6,6	0.27	0
3	PO4	A	1302	-	4,4,4	1.08	0	6,6,6	0.27	0
5	NVP	A	999	-	18,23,23	1.00	0	18,34,34	1.03	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
3	PO4	A	1300	-	-	0/0/0/0	0/0/0/0
3	PO4	A	1301	-	-	0/0/0/0	0/0/0/0
3	PO4	A	1302	-	-	0/0/0/0	0/0/0/0
5	NVP	A	999	-	-	0/0/6/6	0/2/4/4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å²)	Q<0.9
1	A	522/534 (97%)	0.00	27 (5%)	31	35	30, 57, 105, 150	0
2	B	401/422 (95%)	0.14	35 (8%)	13	13	30, 62, 123, 138	0
All	All	923/956 (96%)	0.06	62 (6%)	21	23	30, 58, 117, 150	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	88	TRP	7.6
2	B	230	MET	7.3
1	A	470	THR	6.4
2	B	232	TYR	5.4
2	B	421	PRO	5.3
1	A	66	LYS	5.2
1	A	67	ASP	5.0
1	A	65	LYS	5.0
1	A	68	SER	4.9
1	A	69	THR	4.8
1	A	469	LEU	4.8
2	B	173	LYS	4.4
1	A	468	THR	4.2
1	A	70	LYS	4.1
1	A	139	THR	4.1
1	A	72	ARG	3.8
2	B	67	ASP	3.7
1	A	91	GLN	3.5
2	B	189	VAL	3.4
2	B	66	LYS	3.3
2	B	102	LYS	3.3
2	B	212	TRP	3.3
2	B	210	LEU	3.1
2	B	65	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
2	B	224	GLU	3.0
1	A	52	PRO	3.0
2	B	195	ILE	3.0
2	B	424	LYS	2.9
2	B	237	ASP	2.8
2	B	362	THR	2.7
2	B	419	THR	2.7
2	B	334	GLN	2.7
1	A	53	GLU	2.6
1	A	346	PHE	2.6
1	A	467	VAL	2.6
2	B	188	TYR	2.5
1	A	471	ASP	2.5
1	A	130	PHE	2.5
2	B	223	LYS	2.4
1	A	140	PRO	2.4
1	A	64	LYS	2.4
2	B	238	LYS	2.4
2	B	240	THR	2.3
2	B	166	LYS	2.3
1	A	402	TRP	2.3
2	B	106	VAL	2.3
2	B	95	PRO	2.3
1	A	491	LEU	2.3
2	B	211	ARG	2.2
2	B	104	LYS	2.2
1	A	495	ILE	2.1
1	A	128	THR	2.1
2	B	107	THR	2.1
2	B	174	GLN	2.1
1	A	61	PHE	2.1
2	B	202	ILE	2.1
2	B	229	TRP	2.0
2	B	284	ARG	2.0
1	A	129	ALA	2.0
2	B	420	PRO	2.0
2	B	205	LEU	2.0
1	A	472	THR	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. 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($Å^2$)	Q<0.9
1	CSD	A	280	8/9	0.96	0.15	-	47,50,82,90	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($Å^2$)	Q<0.9
3	PO4	A	1302	5/5	0.82	0.24	2.23	147,150,150,150	0
3	PO4	A	1301	5/5	0.95	0.15	0.40	126,126,127,129	0
5	NVP	A	999	20/20	0.98	0.15	0.31	28,38,43,46	0
4	MG	A	1303	1/1	0.74	0.14	-0.18	62,62,62,62	0
3	PO4	A	1300	5/5	0.64	0.21	-	148,148,150,150	0

6.5 Other polymers (i)

There are no such residues in this entry.