



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 01:33 AM GMT

PDB ID : 1S1T
Title : Crystal structure of L100I mutant HIV-1 reverse transcriptase in complex with UC-781
Authors : Ren, J.; Nichols, C.E.; Chamberlain, P.P.; Stammers, D.K.
Deposited on : 2004-01-07
Resolution : 2.40 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

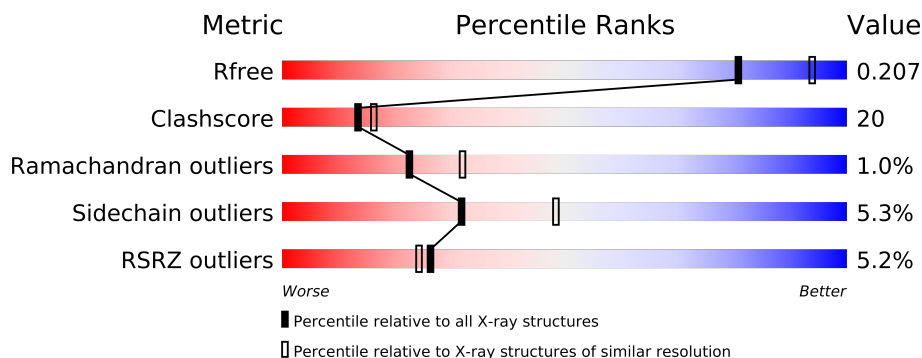
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance


The reported resolution of this entry is 2.40 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}	66092	2207 (2.40-2.40)
Clashscore	79885	2789 (2.40-2.40)
Ramachandran outliers	78287	2736 (2.40-2.40)
Sidechain outliers	78261	2737 (2.40-2.40)
RSRZ outliers	66119	2210 (2.40-2.40)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	560	
2	B	440	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8012 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	534	Total	C	N	O	S	0	0	0
			4364	2825	727	804	8			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	100	ILE	LEU	ENGINEERED	UNP P04585
A	280	CSD	CYS	MODIFIED RESIDUE	UNP P04585

- Molecule 2 is a protein called Reverse transcriptase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	416	Total	C	N	O	S	0	0	0
			3432	2232	569	624	7			

There is a discrepancy between the modelled and reference sequences:

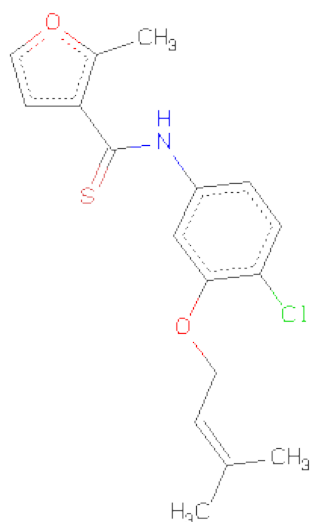
Chain	Residue	Modelled	Actual	Comment	Reference
B	100	ILE	LEU	ENGINEERED	UNP P04585

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



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

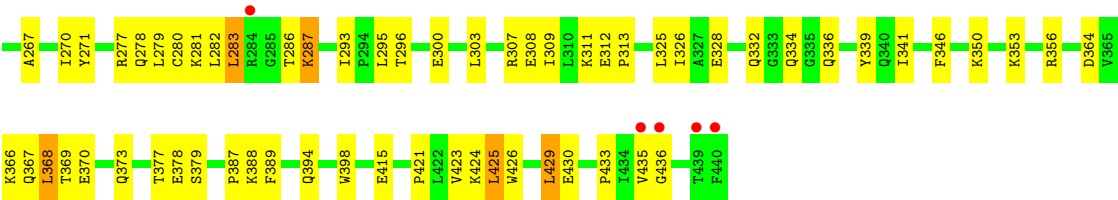
- Molecule 4 is 2-METHYL-FURAN-3-CARBOTHIOICACID [4-CHLORO-3-(3-METHYL-BUT-2-ENYLOXY)-PHENYL]-AMIDE (three-letter code: UC1) (formula: C₁₇H₁₈ClNO₂S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	Cl	N	O	S	0	0
			22	17	1	1	2	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	110	Total 110	O 110	0	0
5	B	74	Total 74	O 74	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	137.51Å 109.38Å 72.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.42 – 2.40 29.42 – 2.41	Depositor EDS
% Data completeness (in resolution range)	96.5 (29.42-2.40) 96.7 (29.42-2.41)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 2.42Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.206 , 0.274 0.201 , 0.207	Depositor DCC
R_{free} test set	2086 reflections (5.02%)	DCC
Wilson B-factor (Å ²)	44.3	Xtriage
Anisotropy	0.514	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 48.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 41526 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8012	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.61% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CSD, PO4, UC1

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	0.38	0/4470	0.62	0/6074
2	B	0.39	0/3528	0.63	0/4790
All	All	0.38	0/7998	0.63	0/10864

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4364	0	4402	191	0
2	B	3432	0	3465	138	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	22	0	18	1	0
5	A	110	0	0	3	0
5	B	74	0	0	11	0
All	All	8012	0	7885	319	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including

hydrogens) of the entry. The overall clashscore for this entry is 20.

All (319) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:492:GLU:HG2	1:A:530:LYS:HB2	1.39	1.04
2:B:114:ALA:HB2	2:B:214:LEU:HD21	1.46	0.94
1:A:112:GLY:HA2	1:A:185:ASP:HB3	1.52	0.92
1:A:114:ALA:HB1	1:A:214:LEU:HD22	1.54	0.88
2:B:163:SER:O	2:B:167:ILE:HG23	1.75	0.86
1:A:448:ARG:NH1	1:A:473:THR:HB	1.90	0.85
1:A:101:LYS:N	1:A:101:LYS:HE3	1.92	0.85
1:A:380:ILE:HD11	1:A:386:THR:HG22	1.61	0.82
2:B:5:ILE:HG22	2:B:6:GLU:H	1.44	0.81
2:B:242:GLN:NE2	2:B:243:PRO:HD2	1.95	0.80
2:B:5:ILE:HG22	2:B:6:GLU:N	2.01	0.76
2:B:241:VAL:HG12	5:B:1124:HOH:O	1.84	0.76
1:A:241:VAL:HG21	1:A:270:ILE:HG21	1.68	0.75
1:A:108:VAL:CG1	1:A:223:LYS:HB2	2.16	0.75
1:A:94:ILE:H	1:A:94:ILE:HD13	1.50	0.74
1:A:17:ASP:O	1:A:83:ARG:HD3	1.88	0.73
2:B:161:GLN:O	2:B:165:THR:HG22	1.87	0.73
2:B:242:GLN:HE21	2:B:243:PRO:HD2	1.52	0.72
1:A:64:LYS:H	1:A:64:LYS:HD2	1.54	0.72
1:A:28:GLU:HB3	1:A:135:ILE:HD11	1.70	0.72
1:A:239:TRP:CE2	1:A:316:GLY:HA3	2.25	0.71
2:B:366:LYS:O	2:B:370:GLU:HG3	1.90	0.71
2:B:64:LYS:HE2	2:B:71:TRP:CE2	2.26	0.71
2:B:169:GLU:HB2	2:B:170:PRO:HD3	1.73	0.70
1:A:64:LYS:HE3	1:A:71:TRP:CZ3	2.25	0.70
1:A:386:THR:HG21	5:B:1047:HOH:O	1.91	0.70
1:A:108:VAL:HG11	1:A:223:LYS:HB2	1.74	0.70
1:A:238:LYS:HB2	1:A:316:GLY:O	1.92	0.69
2:B:244:ILE:HG23	2:B:429:LEU:HB3	1.74	0.69
1:A:71:TRP:HA	1:A:71:TRP:CE3	2.26	0.69
2:B:169:GLU:O	2:B:173:LYS:HD3	1.93	0.69
1:A:257:ILE:O	1:A:261:VAL:HG23	1.92	0.68
1:A:169:GLU:HB3	1:A:170:PRO:HD3	1.75	0.68
1:A:114:ALA:HA	1:A:117:SER:OG	1.94	0.68
1:A:104:LYS:HB2	1:A:192:ASP:HA	1.75	0.67
2:B:63:ILE:HD13	2:B:74:LEU:HD22	1.77	0.67
2:B:279:LEU:HA	2:B:282:LEU:HD12	1.75	0.66
2:B:56:TYR:HE2	2:B:126:LYS:HE2	1.60	0.66
1:A:71:TRP:HA	1:A:71:TRP:HE3	1.61	0.66
1:A:73:LYS:HE3	1:A:75:VAL:HG23	1.76	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:254:VAL:O	2:B:258:GLN:HG3	1.96	0.65
2:B:175:ASN:ND2	2:B:201:LYS:HD2	2.10	0.65
2:B:161:GLN:HE22	2:B:182:GLN:NE2	1.95	0.65
1:A:46:LYS:HE2	1:A:116:PHE:HB3	1.78	0.65
1:A:357:MET:HB2	1:A:367:GLN:NE2	2.11	0.64
1:A:112:GLY:CA	1:A:185:ASP:HB3	2.26	0.64
1:A:114:ALA:CB	1:A:214:LEU:HD22	2.28	0.64
2:B:421:PRO:O	2:B:425:LEU:HD22	1.98	0.64
1:A:448:ARG:HH12	1:A:473:THR:HB	1.61	0.64
1:A:29:GLU:HG2	1:A:71:TRP:HE1	1.61	0.64
2:B:250:ASP:OD2	2:B:250:ASP:N	2.31	0.63
1:A:7:THR:HG22	1:A:119:PRO:HB2	1.80	0.62
2:B:332:GLN:NE2	2:B:424:LYS:HE2	2.13	0.62
1:A:356:ARG:CZ	1:A:358:ARG:HD3	2.29	0.62
2:B:169:GLU:HG2	2:B:173:LYS:HZ3	1.64	0.62
2:B:195:ILE:HG13	2:B:199:ARG:HE	1.64	0.62
1:A:373:GLN:HG2	5:B:1042:HOH:O	2.00	0.62
1:A:90:VAL:HG12	1:A:158:ALA:HB2	1.80	0.62
1:A:38:CYS:HB3	1:A:144:TYR:CE1	2.35	0.62
2:B:35:VAL:O	2:B:39:THR:HG23	2.00	0.62
1:A:33:ALA:O	1:A:36:GLU:HB3	2.00	0.61
2:B:169:GLU:HA	2:B:173:LYS:HZ2	1.65	0.61
2:B:161:GLN:HE22	2:B:182:GLN:HE22	1.48	0.61
2:B:84:THR:HB	2:B:154:LYS:HE2	1.82	0.61
1:A:540:LYS:HB2	1:A:542:ILE:HG13	1.81	0.61
2:B:388:LYS:HE2	2:B:415:GLU:HB3	1.82	0.61
2:B:379:SER:CB	2:B:387:PRO:HD3	2.31	0.61
1:A:409:THR:O	2:B:364:ASP:HB2	2.01	0.61
2:B:379:SER:OG	2:B:387:PRO:HD3	2.01	0.60
1:A:378:GLU:O	1:A:382:ILE:HG12	2.01	0.60
1:A:268:SER:HB3	1:A:353:LYS:HE2	1.82	0.60
1:A:293:ILE:HD12	1:A:293:ILE:N	2.16	0.60
1:A:376:THR:O	1:A:380:ILE:HG12	2.02	0.59
1:A:380:ILE:CD1	1:A:386:THR:HG22	2.31	0.59
1:A:90:VAL:O	1:A:91:GLN:C	2.41	0.59
1:A:21:VAL:HG13	1:A:59:PRO:HD3	1.84	0.59
2:B:114:ALA:CB	2:B:214:LEU:HD21	2.26	0.59
1:A:239:TRP:CZ2	1:A:316:GLY:HA3	2.37	0.59
2:B:103:LYS:HE2	2:B:179:VAL:HG23	1.85	0.59
1:A:23:GLN:HE22	1:A:60:VAL:H	1.51	0.59
1:A:73:LYS:HE3	1:A:75:VAL:CG2	2.33	0.59
2:B:426:TRP:O	2:B:429:LEU:HB2	2.03	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:395:LYS:HD3	1:A:414:TRP:CZ2	2.38	0.59
2:B:423:VAL:HG21	5:B:1140:HOH:O	2.02	0.58
1:A:413:GLU:HG3	5:A:1063:HOH:O	2.03	0.58
1:A:317:VAL:HG12	1:A:318:TYR:N	2.16	0.58
2:B:287:LYS:HE2	2:B:293:ILE:HD11	1.86	0.58
2:B:5:ILE:CG2	2:B:6:GLU:H	2.15	0.58
2:B:7:THR:HG22	2:B:119:PRO:HG2	1.85	0.58
1:A:116:PHE:CZ	1:A:151:GLN:HB2	2.39	0.58
1:A:38:CYS:SG	1:A:132:ILE:HD11	2.44	0.57
1:A:118:VAL:HB	1:A:149:LEU:HD22	1.85	0.57
1:A:228:LEU:HD22	1:A:242:GLN:CD	2.24	0.57
1:A:72:ARG:HG3	1:A:72:ARG:HH11	1.70	0.57
1:A:340:GLN:HB3	1:A:351:THR:HG22	1.86	0.57
1:A:90:VAL:CG1	1:A:158:ALA:HB2	2.34	0.57
1:A:206:ARG:HG3	1:A:216:THR:CG2	2.34	0.57
1:A:516:GLU:O	1:A:520:GLN:HG3	2.05	0.56
2:B:65:LYS:HE3	2:B:110:ASP:OD1	2.05	0.56
1:A:183:TYR:CD1	1:A:184:MET:HB2	2.40	0.56
1:A:356:ARG:HG3	1:A:356:ARG:HH11	1.70	0.56
2:B:111:VAL:HG11	2:B:187:LEU:HD22	1.87	0.56
1:A:279:LEU:HD23	1:A:302:GLU:OE1	2.05	0.56
1:A:101:LYS:HE3	1:A:101:LYS:H	1.69	0.55
2:B:244:ILE:HG13	2:B:426:TRP:CZ2	2.42	0.55
1:A:536:VAL:HG12	2:B:258:GLN:HB3	1.88	0.55
1:A:270:ILE:CG2	1:A:314:VAL:HG11	2.36	0.55
2:B:170:PRO:O	2:B:174:GLN:HG3	2.06	0.55
2:B:46:LYS:HE2	2:B:116:PHE:CD1	2.41	0.55
2:B:203:GLU:HA	2:B:206:ARG:HG3	1.89	0.55
1:A:210:LEU:CD1	1:A:215:THR:HG22	2.37	0.55
1:A:253:THR:O	1:A:257:ILE:HG13	2.06	0.55
2:B:60:VAL:HG23	2:B:75:VAL:HG22	1.90	0.54
1:A:244:ILE:CG2	1:A:310:LEU:HD22	2.37	0.54
1:A:260:LEU:O	1:A:264:LEU:HD23	2.07	0.54
1:A:301:LEU:O	1:A:304:ALA:HB3	2.07	0.54
1:A:122:GLU:CD	1:A:122:GLU:H	2.10	0.54
1:A:143:ARG:HH11	1:A:143:ARG:HG2	1.73	0.54
1:A:49:LYS:HA	1:A:144:TYR:HD2	1.73	0.54
1:A:248:GLU:HA	1:A:307:ARG:NH2	2.22	0.53
1:A:330:GLN:HB2	1:A:338:THR:OG1	2.08	0.53
1:A:112:GLY:HA2	1:A:185:ASP:CB	2.33	0.53
2:B:206:ARG:O	2:B:210:LEU:N	2.34	0.53
2:B:88:TRP:HZ3	2:B:93:GLY:N	2.06	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:271:TYR:HB3	2:B:309:ILE:HG21	1.89	0.53
1:A:511:ASP:OD1	1:A:512:GLN:HG2	2.08	0.53
2:B:241:VAL:HG13	5:B:1123:HOH:O	2.08	0.53
1:A:57:ASN:ND2	1:A:131:THR:OG1	2.42	0.53
1:A:37:ILE:HD11	1:A:71:TRP:O	2.09	0.53
1:A:46:LYS:HE2	1:A:116:PHE:CB	2.38	0.52
1:A:182:GLN:HG3	5:A:1018:HOH:O	2.08	0.52
1:A:434:ILE:CD1	1:A:530:LYS:HB3	2.40	0.52
2:B:56:TYR:CE2	2:B:126:LYS:HE2	2.42	0.52
1:A:250:ASP:N	1:A:250:ASP:OD2	2.43	0.52
2:B:195:ILE:HG13	2:B:199:ARG:NE	2.25	0.52
2:B:241:VAL:HG22	5:B:1123:HOH:O	2.09	0.52
1:A:135:ILE:HG23	1:A:136:ASN:CG	2.30	0.52
2:B:98:ALA:O	2:B:101:LYS:HG2	2.09	0.52
2:B:239:TRP:CH2	2:B:378:GLU:HG2	2.45	0.52
2:B:241:VAL:HA	5:B:1123:HOH:O	2.10	0.51
1:A:9:PRO:HG2	2:B:53:GLU:HG3	1.92	0.51
2:B:169:GLU:HG2	2:B:173:LYS:NZ	2.25	0.51
1:A:539:HIS:O	1:A:540:LYS:HD2	2.10	0.51
2:B:252:TRP:CZ3	2:B:260:LEU:HD22	2.45	0.51
1:A:361:HIS:CD2	1:A:361:HIS:N	2.79	0.51
2:B:169:GLU:CG	2:B:173:LYS:HZ3	2.24	0.51
2:B:31:ILE:O	2:B:35:VAL:HG23	2.11	0.51
1:A:143:ARG:NH1	1:A:143:ARG:HG2	2.25	0.51
1:A:366:LYS:HZ1	2:B:394:GLN:HE21	1.57	0.51
1:A:335:GLY:HA2	1:A:367:GLN:OE1	2.11	0.50
1:A:244:ILE:HD11	1:A:263:LYS:HB3	1.93	0.50
2:B:61:PHE:CZ	2:B:74:LEU:HD23	2.47	0.50
1:A:244:ILE:HG23	1:A:310:LEU:HD13	1.93	0.50
1:A:108:VAL:HG13	1:A:223:LYS:HB2	1.91	0.50
1:A:53:GLU:HG3	1:A:53:GLU:O	2.11	0.50
1:A:317:VAL:HG21	1:A:347:LYS:HB3	1.93	0.50
1:A:452:LEU:HD11	1:A:470:THR:HG22	1.94	0.50
1:A:452:LEU:CD1	1:A:470:THR:HG22	2.42	0.50
2:B:208:HIS:O	2:B:211:ARG:HG3	2.12	0.49
1:A:31:ILE:HG12	1:A:133:PRO:HG2	1.93	0.49
1:A:21:VAL:CG1	1:A:59:PRO:HD3	2.42	0.49
1:A:23:GLN:HG2	1:A:131:THR:O	2.11	0.49
1:A:90:VAL:O	1:A:90:VAL:HG23	2.11	0.49
2:B:73:LYS:HE2	2:B:146:TYR:OH	2.12	0.49
2:B:287:LYS:HE2	2:B:293:ILE:CD1	2.43	0.49
2:B:207:GLN:O	2:B:210:LEU:HB3	2.13	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:523:GLU:O	1:A:527:LYS:HG3	2.13	0.49
1:A:539:HIS:C	1:A:540:LYS:HD2	2.33	0.49
2:B:387:PRO:HG2	2:B:389:PHE:CE1	2.47	0.49
2:B:125:ARG:HB3	2:B:145:GLN:NE2	2.28	0.48
1:A:49:LYS:HA	1:A:144:TYR:CD2	2.48	0.48
2:B:433:PRO:HB2	2:B:436:GLY:HA2	1.95	0.48
2:B:239:TRP:CZ3	2:B:378:GLU:HG2	2.49	0.48
2:B:267:ALA:HB2	2:B:426:TRP:CZ3	2.49	0.48
2:B:270:ILE:HG12	2:B:346:PHE:HB3	1.95	0.48
1:A:3:SER:HB3	1:A:4:PRO:HD2	1.96	0.48
1:A:58:THR:HG23	1:A:76:ASP:O	2.13	0.48
2:B:40:GLU:O	2:B:44:GLU:HG3	2.13	0.48
1:A:270:ILE:HG22	1:A:314:VAL:HG11	1.95	0.48
1:A:317:VAL:CG1	1:A:318:TYR:N	2.77	0.47
1:A:447:ASN:HB3	1:A:450:THR:OG1	2.13	0.47
1:A:206:ARG:HG3	1:A:216:THR:HG23	1.95	0.47
1:A:126:LYS:HG2	5:A:1015:HOH:O	2.13	0.47
1:A:57:ASN:HA	1:A:129:ALA:O	2.14	0.47
1:A:460:ASN:HA	2:B:286:THR:O	2.14	0.47
2:B:373:GLN:O	2:B:377:THR:HG23	2.13	0.47
2:B:64:LYS:HE2	2:B:71:TRP:CZ2	2.48	0.47
2:B:350:LYS:HG3	5:B:1123:HOH:O	2.14	0.47
1:A:94:ILE:H	1:A:94:ILE:CD1	2.23	0.47
2:B:152:GLY:HA2	2:B:184:MET:HE3	1.95	0.47
2:B:161:GLN:HA	2:B:161:GLN:NE2	2.29	0.47
1:A:366:LYS:NZ	2:B:394:GLN:NE2	2.63	0.47
1:A:53:GLU:OE2	1:A:53:GLU:HA	2.15	0.47
1:A:502:ALA:O	1:A:506:ILE:HG13	2.15	0.47
2:B:57:ASN:HD22	2:B:143:ARG:NH1	2.12	0.47
1:A:434:ILE:HD13	1:A:530:LYS:HB3	1.97	0.47
1:A:23:GLN:NE2	1:A:60:VAL:H	2.12	0.47
2:B:162:SER:O	2:B:165:THR:HG23	2.14	0.46
1:A:235:HIS:HB2	1:A:238:LYS:O	2.15	0.46
2:B:332:GLN:HE22	2:B:424:LYS:HD3	1.80	0.46
2:B:67:ASP:O	2:B:67:ASP:CG	2.54	0.46
1:A:111:VAL:O	1:A:114:ALA:HB3	2.15	0.46
2:B:332:GLN:NE2	2:B:424:LYS:CE	2.79	0.46
1:A:377:THR:O	1:A:381:VAL:HG23	2.15	0.46
1:A:63:ILE:O	1:A:63:ILE:HD12	2.15	0.46
1:A:226:PRO:HA	1:A:234:LEU:O	2.15	0.46
2:B:277:ARG:O	2:B:281:LYS:HG3	2.16	0.46
1:A:433:PRO:HA	1:A:532:TYR:CD2	2.50	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:242:GLN:HB2	5:B:1125:HOH:O	2.15	0.46
1:A:235:HIS:HB2	1:A:238:LYS:HD3	1.98	0.46
2:B:51:GLY:HA3	2:B:53:GLU:OE1	2.15	0.46
2:B:171:PHE:CG	2:B:205:LEU:HD23	2.51	0.46
1:A:125:ARG:HD3	1:A:147:ASN:HA	1.96	0.46
1:A:120:LEU:O	1:A:121:ASP:C	2.53	0.46
1:A:101:LYS:NZ	2:B:138:GLU:OE1	2.49	0.46
1:A:329:ILE:O	1:A:392:PRO:HD3	2.16	0.46
1:A:503:LEU:HD13	1:A:535:TRP:CG	2.51	0.46
1:A:24:TRP:CD1	1:A:25:PRO:HD2	2.51	0.46
1:A:340:GLN:CB	1:A:351:THR:HG22	2.45	0.45
1:A:371:ALA:O	1:A:375:ILE:HG13	2.16	0.45
1:A:254:VAL:HG22	1:A:286:THR:HG21	1.96	0.45
2:B:308:GLU:O	2:B:311:LYS:HB2	2.16	0.45
2:B:328:GLU:O	2:B:339:TYR:HA	2.16	0.45
1:A:226:PRO:HB3	1:A:235:HIS:CE1	2.51	0.45
2:B:334:GLN:O	2:B:336:GLN:OE1	2.34	0.45
1:A:53:GLU:O	1:A:53:GLU:CG	2.65	0.45
2:B:353:LYS:NZ	2:B:430:GLU:HB2	2.31	0.45
2:B:97:PRO:O	2:B:99:GLY:N	2.50	0.45
1:A:308:GLU:HA	1:A:311:LYS:HE2	1.98	0.45
1:A:541:GLY:H	2:B:280:CYS:HB3	1.81	0.45
2:B:175:ASN:HD22	2:B:201:LYS:NZ	2.14	0.45
1:A:11:LYS:O	1:A:85:GLN:HB3	2.16	0.45
1:A:27:THR:O	1:A:31:ILE:HG13	2.17	0.45
2:B:205:LEU:HD13	2:B:205:LEU:C	2.37	0.45
2:B:195:ILE:HG23	2:B:196:GLY:N	2.32	0.45
2:B:116:PHE:C	2:B:116:PHE:CD1	2.90	0.45
1:A:206:ARG:NH2	1:A:217:PRO:C	2.70	0.45
2:B:356:ARG:HB2	2:B:367:GLN:HG2	1.97	0.45
2:B:295:LEU:HB2	2:B:300:GLU:OE1	2.17	0.45
2:B:202:ILE:O	2:B:205:LEU:HB3	2.16	0.44
1:A:156:SER:HB2	1:A:157:PRO:HD3	1.98	0.44
1:A:8:VAL:O	1:A:121:ASP:HB2	2.17	0.44
1:A:366:LYS:NZ	2:B:394:GLN:HE21	2.15	0.44
1:A:7:THR:CG2	1:A:119:PRO:HB2	2.45	0.44
2:B:326:ILE:O	2:B:341:ILE:HA	2.18	0.44
2:B:98:ALA:O	2:B:101:LYS:CG	2.66	0.44
1:A:356:ARG:NE	1:A:358:ARG:HD3	2.33	0.43
1:A:536:VAL:HB	1:A:542:ILE:HD13	1.99	0.43
1:A:379:SER:CB	1:A:387:PRO:HD3	2.48	0.43
2:B:278:GLN:HA	2:B:278:GLN:NE2	2.33	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:540:LYS:C	1:A:542:ILE:H	2.20	0.43
1:A:401:TRP:CZ3	1:A:409:THR:HG21	2.53	0.43
1:A:64:LYS:HE3	1:A:71:TRP:CH2	2.53	0.43
1:A:96:HIS:ND1	1:A:230:MET:HE1	2.34	0.43
2:B:421:PRO:O	2:B:425:LEU:CD2	2.63	0.43
1:A:155:GLY:O	1:A:159:ILE:HG13	2.19	0.43
2:B:236:PRO:C	2:B:238:LYS:H	2.22	0.43
1:A:360:ALA:HB3	1:A:361:HIS:HD2	1.84	0.43
1:A:383:TRP:O	1:A:385:LYS:HG3	2.18	0.43
4:A:999:UC1:H2	4:A:999:UC1:C9	2.48	0.43
2:B:160:PHE:CD1	2:B:160:PHE:O	2.72	0.43
1:A:90:VAL:HG12	1:A:158:ALA:CB	2.47	0.43
1:A:23:GLN:OE1	1:A:59:PRO:HA	2.19	0.43
2:B:260:LEU:HD21	2:B:303:LEU:HD21	2.00	0.43
1:A:28:GLU:HB3	1:A:135:ILE:CD1	2.43	0.43
1:A:56:TYR:O	1:A:143:ARG:NH2	2.51	0.43
1:A:136:ASN:OD1	1:A:138:GLU:HB2	2.18	0.43
2:B:111:VAL:HG21	2:B:164:MET:CE	2.49	0.43
1:A:255:ASN:HD22	1:A:255:ASN:HA	1.62	0.43
1:A:100:ILE:C	1:A:101:LYS:HE3	2.40	0.42
1:A:469:LEU:HD12	1:A:477:THR:HG22	2.01	0.42
2:B:350:LYS:HE2	2:B:378:GLU:OE1	2.19	0.42
1:A:540:LYS:HB3	2:B:280:CYS:SG	2.59	0.42
2:B:433:PRO:CB	2:B:436:GLY:HA2	2.49	0.42
2:B:115:TYR:HB3	2:B:149:LEU:HB2	2.00	0.42
2:B:435:VAL:HG23	2:B:436:GLY:N	2.34	0.42
1:A:246:LEU:HA	1:A:247:PRO:HD2	1.86	0.42
1:A:542:ILE:HG12	2:B:283:LEU:HD23	2.02	0.42
2:B:303:LEU:O	2:B:307:ARG:HG3	2.20	0.42
2:B:369:THR:O	2:B:373:GLN:HG3	2.20	0.42
1:A:92:LEU:O	1:A:92:LEU:HD13	2.20	0.42
2:B:149:LEU:HA	2:B:150:PRO:HD3	1.79	0.42
1:A:64:LYS:HB3	1:A:71:TRP:CE3	2.54	0.42
1:A:225:PRO:HA	1:A:226:PRO:C	2.40	0.42
2:B:282:LEU:HD21	2:B:296:THR:HG23	2.00	0.42
1:A:399:GLU:OE2	1:A:402:TRP:HZ3	2.03	0.42
1:A:99:GLY:O	1:A:101:LYS:HE2	2.20	0.42
2:B:100:ILE:HG23	2:B:101:LYS:N	2.35	0.42
2:B:183:TYR:HB3	2:B:188:TYR:HE1	1.83	0.42
1:A:184:MET:HB3	1:A:185:ASP:H	1.50	0.41
2:B:173:LYS:N	2:B:173:LYS:HD2	2.34	0.41
2:B:175:ASN:HD21	2:B:201:LYS:HD2	1.83	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:246:LEU:HD22	1:A:260:LEU:HD11	2.01	0.41
1:A:254:VAL:CG2	1:A:286:THR:HG21	2.50	0.41
2:B:295:LEU:HG	5:B:1136:HOH:O	2.20	0.41
1:A:271:TYR:HA	1:A:272:PRO:HD3	1.77	0.41
2:B:175:ASN:ND2	2:B:201:LYS:NZ	2.69	0.41
1:A:412:PRO:O	1:A:413:GLU:C	2.59	0.41
1:A:440:PHE:CE1	1:A:489:SER:HB3	2.56	0.41
1:A:323:LYS:NZ	1:A:344:GLU:OE2	2.53	0.41
1:A:58:THR:HG23	1:A:59:PRO:HD2	2.01	0.41
1:A:298:GLU:H	1:A:298:GLU:CD	2.15	0.41
1:A:486:LEU:HB3	1:A:524:GLN:HB3	2.00	0.41
2:B:114:ALA:HB1	2:B:160:PHE:CZ	2.55	0.41
1:A:234:LEU:HD23	1:A:239:TRP:HB3	2.02	0.41
1:A:298:GLU:OE2	1:A:298:GLU:N	2.36	0.41
2:B:9:PRO:HA	2:B:121:ASP:OD2	2.21	0.41
2:B:368:LEU:HD13	2:B:398:TRP:CZ3	2.56	0.41
2:B:312:GLU:HA	2:B:313:PRO:HD3	1.93	0.41
1:A:43:LYS:O	1:A:43:LYS:HD3	2.21	0.41
1:A:492:GLU:HA	1:A:530:LYS:O	2.22	0.40
1:A:253:THR:HA	1:A:291:GLU:O	2.21	0.40
2:B:66:LYS:O	2:B:67:ASP:HB3	2.21	0.40
2:B:97:PRO:O	2:B:98:ALA:C	2.59	0.40
2:B:73:LYS:HB3	2:B:73:LYS:NZ	2.36	0.40
1:A:79:GLU:HA	1:A:82:LYS:HG2	2.03	0.40
1:A:534:ALA:HB1	5:B:1098:HOH:O	2.21	0.40
2:B:151:GLN:HB3	2:B:185:ASP:OD1	2.22	0.40
1:A:324:ASP:O	1:A:343:GLN:HG2	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	527/560 (94%)	487 (92%)	35 (7%)	5 (1%)	25	35

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	410/440 (93%)	384 (94%)	22 (5%)	4 (1%)	22	32
All	All	937/1000 (94%)	871 (93%)	57 (6%)	9 (1%)	22	32

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	85	GLN
2	B	85	GLN
1	A	91	GLN
2	B	98	ALA
1	A	247	PRO
1	A	133	PRO
2	B	237	ASP
1	A	14	PRO
2	B	213	GLY

5.3.2 Protein sidechains ⓘ

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	476/499 (95%)	444 (93%)	32 (7%)	23	35
2	B	377/400 (94%)	364 (97%)	13 (3%)	49	70
All	All	853/899 (95%)	808 (95%)	45 (5%)	32	48

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	TRP
1	A	43	LYS
1	A	64	LYS
1	A	71	TRP
1	A	72	ARG
1	A	73	LYS
1	A	89	GLU
1	A	92	LEU
1	A	94	ILE

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Mol	Chain	Res	Type
1	A	101	LYS
1	A	109	LEU
1	A	113	ASP
1	A	115	TYR
1	A	120	LEU
1	A	151	GLN
1	A	182	GLN
1	A	184	MET
1	A	205	LEU
1	A	238	LYS
1	A	255	ASN
1	A	283	LEU
1	A	322	SER
1	A	340	GLN
1	A	356	ARG
1	A	361	HIS
1	A	368	LEU
1	A	402	TRP
1	A	404	GLU
1	A	423	VAL
1	A	475	GLN
1	A	496	VAL
1	A	517	LEU
2	B	40	GLU
2	B	73	LYS
2	B	116	PHE
2	B	165	THR
2	B	215	THR
2	B	243	PRO
2	B	250	ASP
2	B	283	LEU
2	B	287	LYS
2	B	325	LEU
2	B	368	LEU
2	B	425	LEU
2	B	429	LEU

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	57	ASN
1	A	147	ASN

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Mol	Chain	Res	Type
1	A	174	GLN
1	A	242	GLN
1	A	255	ASN
1	A	278	GLN
1	A	332	GLN
1	A	361	HIS
1	A	475	GLN
1	A	500	GLN
2	B	57	ASN
2	B	175	ASN
2	B	182	GLN
2	B	197	GLN
2	B	208	HIS
2	B	235	HIS
2	B	242	GLN
2	B	269	GLN
2	B	278	GLN
2	B	332	GLN
2	B	394	GLN
2	B	407	GLN
2	B	428	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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	7,7,8	6.71	2 (28%)	6,8,10	5.96	4 (66%)

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	-	1/3/6/8	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	280	CSD	O-C	17.42	1.23	1.11
1	A	280	CSD	CA-C	2.66	1.53	1.48

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	280	CSD	CA-CB-SG	12.62	128.82	110.82
1	A	280	CSD	OD2-SG-OD1	4.36	116.63	109.39
1	A	280	CSD	OD2-SG-CB	4.16	114.16	97.42
1	A	280	CSD	C-CA-N	-3.70	110.13	113.83

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	280	CSD	CA-CB-SG-OD1

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

3 ligands 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	$\# Z > 2$
3	PO4	A	2001	-	4,4,4	0.75	0	6,6,6	0.31	0
4	UC1	A	999	-	23,23,23	1.46	3 (13%)	28,31,31	1.49	5 (17%)
3	PO4	B	1000	-	4,4,4	0.91	0	6,6,6	0.31	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	2001	-	-	0/0/0/0	0/0/0/0
4	UC1	A	999	-	-	1/11/14/14	0/2/2/2
3	PO4	B	1000	-	-	0/0/0/0	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	999	UC1	CA-C8	3.39	1.53	1.48
4	A	999	UC1	C-N	2.67	1.40	1.35
4	A	999	UC1	O7-C11	2.14	1.39	1.35

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	999	UC1	C9-C-N	3.69	118.77	114.10
4	A	999	UC1	S-C-N	-3.46	118.39	124.48
4	A	999	UC1	OB-C3-C4	3.19	120.61	116.33
4	A	999	UC1	C3-C4-CL	2.36	122.53	119.45
4	A	999	UC1	CA-C8-C9	2.01	133.63	128.69

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	999	UC1	S-C-N-C1

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	534/560 (95%)	-0.14	24 (4%) 32 30	22, 46, 98, 138	0
2	B	416/440 (94%)	0.03	26 (6%) 19 18	22, 47, 101, 146	0
All	All	950/1000 (95%)	-0.07	50 (5%) 26 23	22, 47, 101, 146	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	88	TRP	7.0
2	B	67	ASP	6.1
2	B	65	LYS	5.3
2	B	69	THR	5.3
1	A	543	GLY	4.7
1	A	541	GLY	4.5
2	B	440	PHE	4.4
1	A	221	HIS	4.3
1	A	52	PRO	4.1
2	B	240	THR	4.0
2	B	5	ILE	3.9
2	B	195	ILE	3.8
2	B	4	PRO	3.7
1	A	542	ILE	3.6
2	B	435	VAL	3.6
1	A	135	ILE	3.5
2	B	68	SER	3.4
2	B	213	GLY	3.2
2	B	214	LEU	3.2
1	A	71	TRP	3.1
1	A	90	VAL	3.0
1	A	53	GLU	3.0
1	A	64	LYS	3.0
1	A	91	GLN	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	136	ASN	3.0
2	B	116	PHE	2.9
1	A	63	ILE	2.8
1	A	220	LYS	2.7
1	A	24	TRP	2.6
2	B	177	ASP	2.6
2	B	95	PRO	2.6
2	B	66	LYS	2.5
2	B	241	VAL	2.5
1	A	115	TYR	2.5
2	B	439	THR	2.4
1	A	72	ARG	2.4
1	A	116	PHE	2.4
1	A	358	ARG	2.4
2	B	184	MET	2.4
1	A	92	LEU	2.4
1	A	244	ILE	2.4
2	B	436	GLY	2.4
1	A	245	VAL	2.3
2	B	284	ARG	2.3
2	B	174	GLN	2.3
2	B	94	ILE	2.3
1	A	62	ALA	2.2
2	B	199	ARG	2.2
2	B	6	GLU	2.2
1	A	3	SER	2.1

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
1	CSD	A	280	8/9	0.11	-0.71	42,50,73,77	0

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	PO4	A	2001	5/5	0.15	0.96	106,109,116,126	0
4	UC1	A	999	22/22	0.12	0.14	26,35,43,47	0
3	PO4	B	1000	5/5	0.13	-0.83	102,105,111,114	0

6.5 Other polymers

There are no such residues in this entry.