



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 04:51 pm GMT

PDB ID : 3LAL
Title : Crystal structure of HIV-1 reverse transcriptase in complex with N1-ethyl pyrimidinedione non-nucleoside inhibitor
Authors : Lansdon, E.B.; Mitchell, M.L.
Deposited on : 2010-01-06
Resolution : 2.51 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

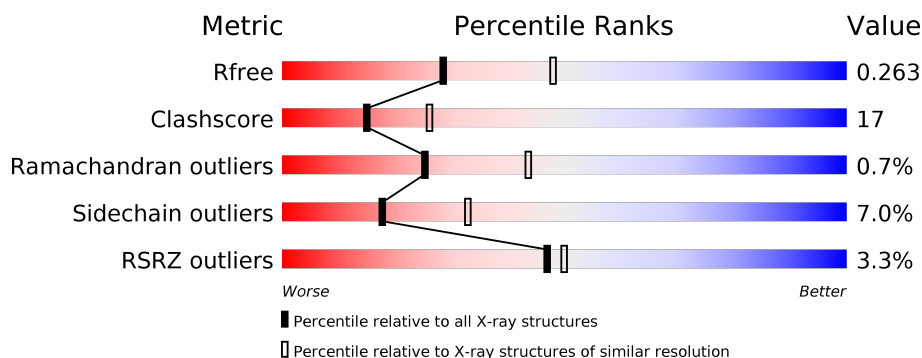
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.51 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}	100719	3846 (2.50-2.50)
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)
RSRZ outliers	101464	3876 (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 $\leq 5\%$. 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	560	<div> <div>3%</div> <div>61%</div> <div>34%</div> <div>• •</div> </div>
1	B	560	<div> <div>3%</div> <div>47%</div> <div>23%</div> <div>•</div> <div>28%</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
3	SO4	A	564	-	-	-	X



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

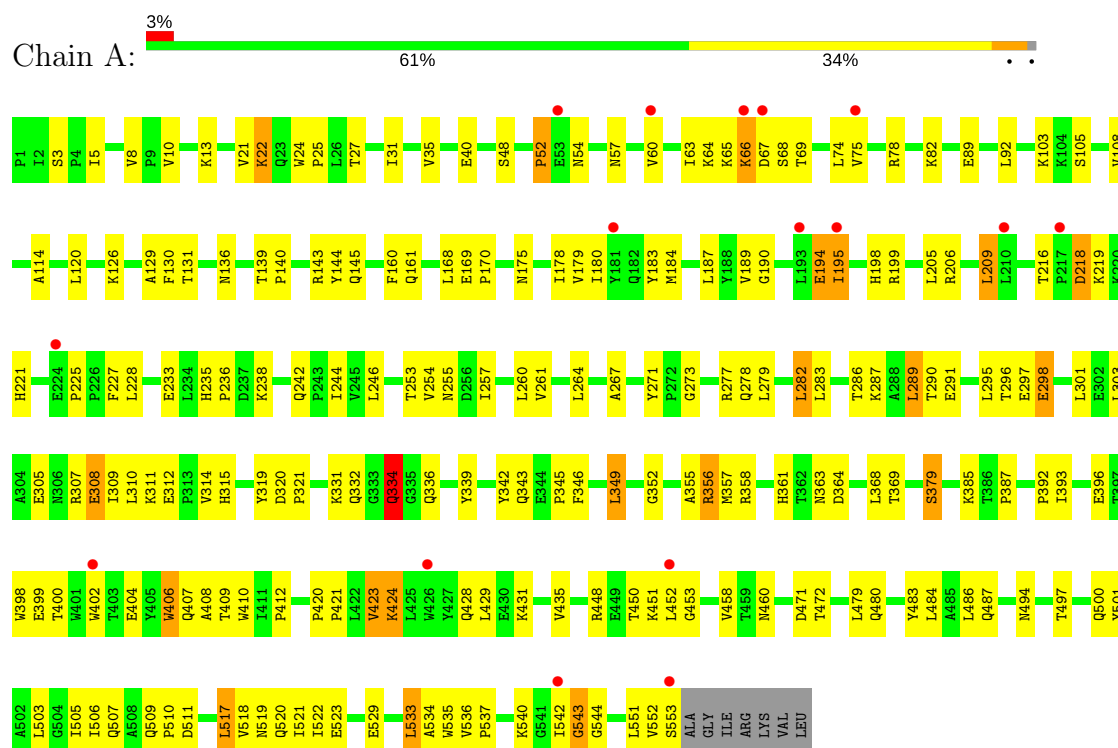
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	69	Total	O	0	0
			69	69		
4	B	53	Total	O	0	0
			53	53		

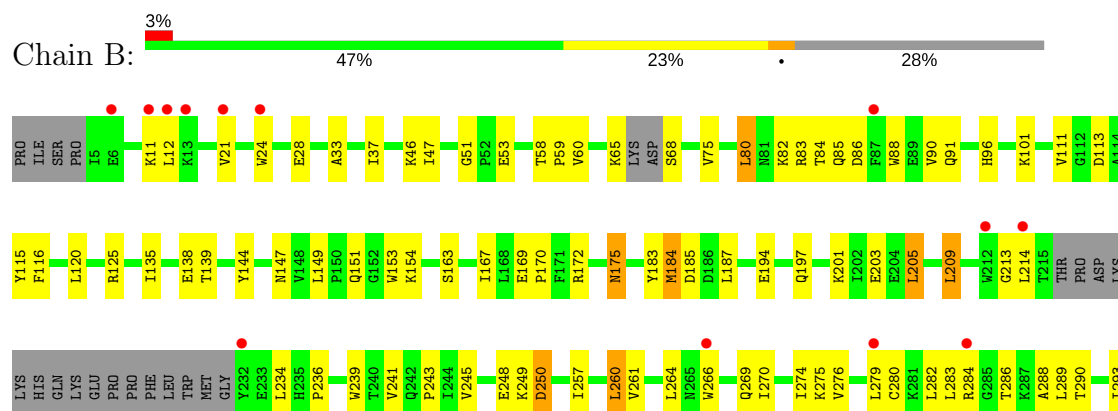
3 Residue-property plots

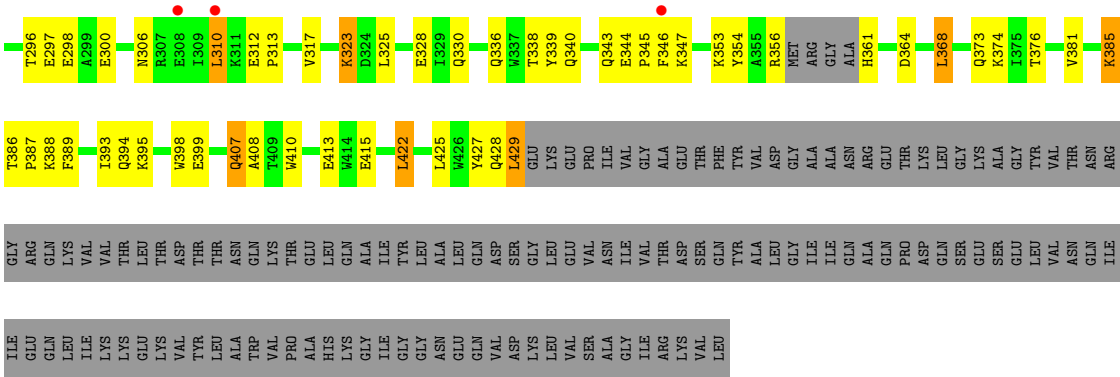
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

• Molecule 1: HIV Reverse transcriptase



• Molecule 1: HIV Reverse transcriptase





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	118.15Å 154.12Å 153.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.83 – 2.51 47.11 – 2.51	Depositor EDS
% Data completeness (in resolution range)	87.8 (29.83-2.51) 87.9 (47.11-2.51)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.19 (at 2.51Å)	Xtriage
Refinement program	CNX 2005	Depositor
R, R_{free}	0.218 , 0.267 0.209 , 0.263	Depositor DCC
R_{free} test set	2112 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	58.8	Xtriage
Anisotropy	0.359	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 42.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8013	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: KRV, SO4

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	0/4625	0.52	0/6284
1	B	0.38	0/3426	0.52	0/4655
All	All	0.38	0/8051	0.52	0/10939

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	52	PRO	Peptide
1	B	361	HIS	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4508	0	4558	167	0
1	B	3334	0	3365	113	0
2	A	24	0	19	0	0
3	A	20	0	0	0	0
3	B	5	0	0	0	0
4	A	69	0	0	3	0
4	B	53	0	0	4	0
All	All	8013	0	7942	268	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 17.

All (268) 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:131:THR:HG22	1:A:143:ARG:HG2	1.24	1.10
1:B:296:THR:HG22	1:B:298:GLU:H	1.28	0.95
1:A:510:PRO:HG3	4:A:568:HOH:O	1.68	0.91
1:B:373:GLN:HE22	1:B:407:GLN:H	1.17	0.90
1:A:393:ILE:HB	1:A:423:VAL:HG13	1.54	0.89
1:B:58:THR:HG23	4:B:563:HOH:O	1.75	0.86
1:A:131:THR:HG22	1:A:143:ARG:CG	2.05	0.85
1:A:65:LYS:O	1:A:66:LYS:HG3	1.76	0.85
1:A:131:THR:CG2	1:A:143:ARG:HH11	1.91	0.84
1:A:537:PRO:HB2	1:A:540:LYS:HG3	1.64	0.80
1:A:60:VAL:HG12	1:A:75:VAL:HG22	1.64	0.80
1:B:260:LEU:HD13	1:B:279:LEU:HD21	1.64	0.79
1:A:194:GLU:H	1:A:194:GLU:CD	1.87	0.76
1:B:376:THR:HG23	1:B:386:THR:HG23	1.68	0.76
1:B:65:LYS:HG3	1:B:68:SER:HB2	1.67	0.75
1:A:228:LEU:HB3	1:A:242:GLN:NE2	2.03	0.73
1:B:138:GLU:HG2	1:B:139:THR:HG23	1.69	0.73
1:A:297:GLU:O	1:A:301:LEU:HG	1.89	0.73
1:A:393:ILE:HB	1:A:423:VAL:CG1	2.21	0.70
1:A:277:ARG:HB2	1:A:336:GLN:NE2	2.07	0.70
1:B:373:GLN:NE2	1:B:407:GLN:H	1.88	0.70
1:B:395:LYS:O	1:B:399:GLU:HG2	1.92	0.69
1:A:114:ALA:HB1	1:A:160:PHE:CE1	2.28	0.69
1:A:199:ARG:HH11	1:A:219:LYS:HE2	1.58	0.68
1:B:241:VAL:HG23	1:B:243:PRO:HD3	1.75	0.68
1:A:66:LYS:HD3	1:A:67:ASP:H	1.59	0.68
1:A:278:GLN:HG3	1:A:298:GLU:HB2	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:520:GLN:O	1:A:523:GLU:HG2	1.94	0.68
1:A:277:ARG:NH1	1:A:334:GLN:HG3	2.10	0.67
1:B:393:ILE:HD13	1:B:398:TRP:HB2	1.77	0.66
1:B:194:GLU:HG3	1:B:197:GLN:HG3	1.76	0.66
1:B:345:PRO:O	1:B:346:PHE:HB2	1.94	0.66
1:A:542:ILE:HD11	1:B:261:VAL:HG11	1.77	0.66
1:B:24:TRP:HZ3	1:B:59:PRO:CG	2.07	0.66
1:A:27:THR:O	1:A:31:ILE:HG13	1.95	0.66
1:A:273:GLY:HA2	1:A:332:GLN:NE2	2.12	0.65
1:A:343:GLN:HG3	1:A:349:LEU:HD21	1.78	0.65
1:A:298:GLU:H	1:A:298:GLU:CD	1.99	0.65
1:A:368:LEU:HD22	1:A:423:VAL:HG11	1.79	0.65
1:B:24:TRP:HZ3	1:B:59:PRO:HG2	1.60	0.65
1:B:297:GLU:H	1:B:297:GLU:CD	2.00	0.65
1:B:60:VAL:HG12	1:B:75:VAL:HG22	1.78	0.64
1:A:480:GLN:HG2	1:A:517:LEU:HD11	1.79	0.64
1:A:199:ARG:NH1	1:A:219:LYS:HE2	2.12	0.64
1:A:305:GLU:O	1:A:309:ILE:HG13	1.98	0.64
1:B:205:LEU:HD22	1:B:209:LEU:HD22	1.80	0.64
1:B:33:ALA:O	1:B:37:ILE:HG13	1.98	0.63
1:A:356:ARG:CZ	1:A:358:ARG:HD3	2.29	0.63
1:B:86:ASP:O	1:B:90:VAL:HG22	1.99	0.62
1:A:408:ALA:HB1	1:B:364:ASP:HB3	1.80	0.62
1:B:175:ASN:HD21	1:B:201:LYS:NZ	1.98	0.62
1:A:257:ILE:O	1:A:261:VAL:HG23	2.00	0.62
1:A:544:GLY:HA2	1:B:286:THR:HG22	1.81	0.61
1:A:175:ASN:HB3	1:A:178:ILE:HD12	1.82	0.61
1:A:409:THR:O	1:B:364:ASP:HB2	2.01	0.61
1:A:334:GLN:H	1:A:334:GLN:CD	2.03	0.61
1:A:406:TRP:HE3	1:A:407:GLN:HE21	1.49	0.60
1:B:425:LEU:O	1:B:428:GLN:HG2	2.01	0.60
1:A:503:LEU:HD12	1:A:533:LEU:HD13	1.83	0.60
1:B:209:LEU:HD12	1:B:214:LEU:HD22	1.85	0.59
1:A:206:ARG:NH1	1:A:218:ASP:HA	2.17	0.59
1:A:379:SER:OG	1:A:387:PRO:HD3	2.02	0.58
1:B:312:GLU:HB3	1:B:313:PRO:HD2	1.85	0.58
1:A:168:LEU:HD11	1:A:187:LEU:HD21	1.86	0.58
1:A:238:LYS:HE2	1:A:315:HIS:CG	2.38	0.58
1:A:479:LEU:HB3	1:A:517:LEU:HD13	1.86	0.58
1:B:249:LYS:HG2	1:B:250:ASP:H	1.66	0.58
1:A:342:TYR:HA	1:A:349:LEU:HD23	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:254:VAL:HB	1:A:289:LEU:HA	1.86	0.58
1:B:296:THR:HG22	1:B:298:GLU:N	2.10	0.57
1:A:60:VAL:HG11	1:A:130:PHE:CD2	2.40	0.57
1:A:233:GLU:HG2	1:A:235:HIS:HE2	1.70	0.57
1:A:287:LYS:HB3	1:A:291:GLU:HG3	1.86	0.57
1:A:233:GLU:HG2	1:A:235:HIS:NE2	2.20	0.56
1:B:163:SER:O	1:B:167:ILE:HG13	2.04	0.56
1:A:65:LYS:HE2	1:A:66:LYS:HG2	1.88	0.56
1:B:169:GLU:HB3	1:B:170:PRO:HD3	1.87	0.56
1:B:317:VAL:HG22	1:B:347:LYS:HB3	1.87	0.56
1:A:358:ARG:NH2	1:B:394:GLN:HG3	2.20	0.56
1:B:175:ASN:HD21	1:B:201:LYS:HZ3	1.53	0.56
1:A:228:LEU:HB3	1:A:242:GLN:HE22	1.69	0.55
1:A:244:ILE:CD1	1:A:267:ALA:HB2	2.37	0.55
1:A:89:GLU:HG2	1:A:92:LEU:HD21	1.88	0.55
1:A:483:TYR:O	1:A:487:GLN:HG2	2.07	0.55
1:A:64:LYS:NZ	1:A:69:THR:HA	2.21	0.55
1:B:51:GLY:HA3	1:B:53:GLU:OE2	2.07	0.55
1:A:40:GLU:HA	1:A:40:GLU:OE2	2.06	0.55
1:A:406:TRP:CE3	1:A:407:GLN:HG2	2.42	0.54
1:A:57:ASN:OD1	1:A:131:THR:HG23	2.08	0.54
1:B:243:PRO:O	1:B:245:VAL:HG13	2.08	0.53
1:A:356:ARG:NH2	1:A:358:ARG:HD3	2.23	0.53
1:B:274:ILE:HA	1:B:306:ASN:HD21	1.72	0.53
1:A:358:ARG:HH21	1:B:394:GLN:HG3	1.73	0.53
1:A:319:TYR:OH	1:A:385:LYS:HE2	2.08	0.53
1:B:282:LEU:HB3	1:B:293:ILE:CD1	2.38	0.53
1:A:131:THR:HG23	1:A:143:ARG:HH11	1.73	0.53
1:A:169:GLU:HB3	1:A:170:PRO:HD3	1.90	0.53
1:A:228:LEU:N	1:A:228:LEU:HD12	2.24	0.53
1:B:151:GLN:HB3	1:B:185:ASP:OD2	2.08	0.53
1:A:31:ILE:O	1:A:35:VAL:HG23	2.07	0.52
1:B:46:LYS:HE2	1:B:116:PHE:CD1	2.43	0.52
1:B:429:LEU:HD12	1:B:429:LEU:N	2.23	0.52
1:A:363:ASN:HA	1:A:511:ASP:OD1	2.09	0.52
1:A:228:LEU:CG	1:A:242:GLN:HE21	2.22	0.52
1:B:101:LYS:HG2	4:B:574:HOH:O	2.09	0.52
1:B:28:GLU:HB2	1:B:135:ILE:HD11	1.91	0.52
1:A:246:LEU:HD12	1:A:307:ARG:HD3	1.92	0.52
1:A:450:THR:HG22	1:A:452:LEU:HB2	1.91	0.52
1:A:453:GLY:HA3	1:A:472:THR:HG21	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:282:LEU:HB3	1:B:293:ILE:HD13	1.90	0.52
1:A:289:LEU:CD2	1:A:289:LEU:H	2.21	0.52
1:A:279:LEU:O	1:A:282:LEU:HB2	2.10	0.52
1:B:306:ASN:O	1:B:310:LEU:HD22	2.10	0.51
1:A:369:THR:HG1	1:A:398:TRP:HZ3	1.56	0.51
1:A:273:GLY:HA2	1:A:332:GLN:HE22	1.75	0.51
1:A:536:VAL:HG13	1:A:537:PRO:HD2	1.92	0.51
1:A:225:PRO:HG3	1:A:227:PHE:CE2	2.46	0.51
1:A:66:LYS:HD3	1:A:68:SER:H	1.76	0.51
1:A:331:LYS:HE3	1:A:364:ASP:OD2	2.11	0.51
1:A:503:LEU:HD22	1:A:535:TRP:HB2	1.93	0.51
1:A:542:ILE:O	1:A:543:GLY:O	2.28	0.51
1:B:113:ASP:O	1:B:116:PHE:HD2	1.94	0.51
1:A:392:PRO:O	1:A:423:VAL:HG12	2.11	0.51
1:B:236:PRO:O	1:B:239:TRP:HB2	2.10	0.51
1:A:225:PRO:HG3	1:A:227:PHE:CZ	2.46	0.50
1:A:450:THR:CG2	1:A:452:LEU:HB2	2.41	0.50
1:B:213:GLY:C	1:B:214:LEU:HD12	2.31	0.50
1:A:105:SER:O	1:A:190:GLY:HA2	2.12	0.50
1:A:13:LYS:HE3	1:A:82:LYS:O	2.12	0.50
1:A:542:ILE:HD13	1:B:280:CYS:HB2	1.92	0.50
1:B:115:TYR:HB3	1:B:149:LEU:HB2	1.93	0.50
1:B:323:LYS:HB3	1:B:343:GLN:NE2	2.27	0.49
1:B:111:VAL:HG11	1:B:187:LEU:HD22	1.94	0.49
1:A:219:LYS:HB3	1:A:219:LYS:NZ	2.27	0.49
1:A:369:THR:OG1	1:A:398:TRP:HZ3	1.96	0.49
1:A:509:GLN:N	1:A:510:PRO:HD3	2.26	0.49
1:B:183:TYR:CE2	1:B:184:MET:HG3	2.47	0.49
1:A:400:THR:O	1:A:404:GLU:HG2	2.12	0.49
1:B:205:LEU:HD22	1:B:209:LEU:CD2	2.42	0.49
1:A:289:LEU:N	1:A:289:LEU:HD23	2.28	0.49
1:A:194:GLU:O	1:A:195:ILE:C	2.51	0.48
1:B:274:ILE:HA	1:B:306:ASN:ND2	2.27	0.48
1:B:373:GLN:NE2	1:B:408:ALA:H	2.11	0.48
1:A:161:GLN:NE2	1:A:184:MET:O	2.43	0.48
1:B:373:GLN:HE22	1:B:407:GLN:N	1.99	0.48
1:A:552:VAL:O	1:A:552:VAL:HG23	2.13	0.48
1:B:194:GLU:H	1:B:197:GLN:HE21	1.62	0.48
1:B:85:GLN:HA	1:B:88:TRP:NE1	2.28	0.48
1:B:28:GLU:CB	1:B:135:ILE:HD11	2.44	0.48
1:B:387:PRO:HG2	1:B:389:PHE:CE1	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:450:THR:O	1:A:451:LYS:HB2	2.14	0.47
1:A:451:LYS:HB3	1:A:471:ASP:HA	1.96	0.47
1:B:260:LEU:HD22	1:B:264:LEU:CD1	2.45	0.47
1:A:289:LEU:HD23	1:A:290:THR:H	1.78	0.47
1:A:21:VAL:O	1:A:57:ASN:HB3	2.15	0.47
1:B:422:LEU:HD12	1:B:422:LEU:HA	1.73	0.47
1:B:429:LEU:H	1:B:429:LEU:HD12	1.79	0.47
1:A:355:ALA:O	1:A:356:ARG:C	2.53	0.47
1:A:420:PRO:HA	1:A:421:PRO:C	2.34	0.47
1:A:183:TYR:CE2	1:A:184:MET:HG3	2.50	0.47
1:A:497:THR:O	1:A:535:TRP:HA	2.15	0.47
1:A:282:LEU:HD11	1:A:296:THR:HG23	1.97	0.47
1:B:96:HIS:HE1	1:B:381:VAL:O	1.98	0.47
1:A:255:ASN:HB2	1:A:289:LEU:HB2	1.97	0.46
1:A:345:PRO:HA	1:A:346:PHE:HA	1.58	0.46
1:B:340:GLN:NE2	4:B:580:HOH:O	2.42	0.46
1:A:228:LEU:HG	1:A:242:GLN:HE21	1.81	0.46
1:A:501:TYR:CE1	1:A:505:ILE:HD11	2.50	0.46
1:B:276:VAL:HG12	1:B:276:VAL:O	2.15	0.46
1:A:289:LEU:N	1:A:289:LEU:CD2	2.78	0.46
1:A:194:GLU:N	1:A:194:GLU:CD	2.61	0.46
1:A:52:PRO:HA	1:A:54:ASN:N	2.30	0.46
1:A:435:VAL:HA	1:B:290:THR:HG21	1.97	0.46
1:A:542:ILE:HG23	1:B:283:LEU:HD13	1.97	0.46
1:A:244:ILE:HD13	1:A:267:ALA:HB2	1.98	0.46
1:A:66:LYS:CD	1:A:67:ASP:H	2.25	0.46
1:A:228:LEU:CB	1:A:242:GLN:NE2	2.77	0.46
1:A:518:VAL:O	1:A:522:ILE:HG13	2.15	0.46
1:A:396:GLU:HA	1:A:399:GLU:HG2	1.98	0.46
1:A:64:LYS:HZ3	1:A:69:THR:HA	1.81	0.45
1:B:88:TRP:CZ2	1:B:154:LYS:HD3	2.51	0.45
1:B:373:GLN:HE21	1:B:408:ALA:H	1.64	0.45
1:A:552:VAL:O	1:A:553:SER:HB3	2.16	0.45
1:A:511:ASP:HB3	4:A:616:HOH:O	2.16	0.45
1:B:120:LEU:HD23	1:B:125:ARG:HG2	1.98	0.45
1:B:261:VAL:HG13	1:B:276:VAL:HG11	1.99	0.45
1:A:131:THR:HG22	1:A:143:ARG:HH11	1.76	0.45
1:A:131:THR:CG2	1:A:143:ARG:HG2	2.18	0.45
1:B:125:ARG:HD3	1:B:147:ASN:HA	1.99	0.44
1:A:542:ILE:O	1:A:543:GLY:C	2.56	0.44
1:B:249:LYS:CG	1:B:250:ASP:H	2.29	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:21:VAL:HG12	1:A:22:LYS:N	2.31	0.44
1:B:353:LYS:HD3	1:B:429:LEU:HD22	1.99	0.44
1:A:105:SER:HB2	1:A:198:HIS:ND1	2.33	0.44
1:A:129:ALA:HA	1:A:144:TYR:O	2.18	0.44
1:A:54:ASN:O	1:A:143:ARG:NH2	2.51	0.44
1:B:175:ASN:ND2	1:B:201:LYS:NZ	2.63	0.44
1:B:266:TRP:HZ2	1:B:427:TYR:HH	1.66	0.44
1:B:65:LYS:CG	1:B:68:SER:HB2	2.42	0.44
1:A:139:THR:HB	1:A:140:PRO:HD2	2.00	0.44
1:A:235:HIS:HB3	1:A:236:PRO:HD2	2.00	0.44
1:A:48:SER:O	1:A:144:TYR:HA	2.18	0.44
1:B:407:GLN:HB2	1:B:407:GLN:HE21	1.50	0.43
1:A:131:THR:HG23	1:A:143:ARG:NH1	2.32	0.43
1:B:328:GLU:O	1:B:339:TYR:HA	2.18	0.43
1:A:286:THR:HG23	1:A:286:THR:O	2.17	0.43
1:B:257:ILE:O	1:B:261:VAL:HG23	2.18	0.43
1:A:199:ARG:HD3	1:A:219:LYS:HE2	1.99	0.43
1:B:86:ASP:OD1	1:B:90:VAL:HG21	2.18	0.43
1:A:179:VAL:O	1:A:189:VAL:HA	2.19	0.43
1:B:47:ILE:HD12	1:B:144:TYR:CG	2.54	0.43
1:B:354:TYR:HD2	1:B:374:LYS:HD2	1.83	0.43
1:B:21:VAL:HB	1:B:59:PRO:HD3	2.01	0.43
1:A:246:LEU:HD22	1:A:260:LEU:CD1	2.49	0.43
1:A:406:TRP:CE3	1:A:407:GLN:NE2	2.86	0.43
1:B:24:TRP:CZ3	1:B:59:PRO:CG	2.97	0.43
1:A:486:LEU:CD1	1:A:521:ILE:HG23	2.49	0.43
1:B:269:GLN:HG2	1:B:269:GLN:H	1.65	0.43
1:A:195:ILE:HD12	1:A:199:ARG:NH2	2.34	0.43
1:A:65:LYS:C	1:A:66:LYS:HG3	2.35	0.43
1:B:388:LYS:HA	1:B:413:GLU:O	2.19	0.43
1:B:82:LYS:HE3	1:B:82:LYS:HB2	1.72	0.43
1:B:275:LYS:H	1:B:306:ASN:HD21	1.67	0.43
1:A:308:GLU:O	1:A:311:LYS:HB2	2.19	0.42
1:A:63:ILE:HG22	1:A:64:LYS:N	2.34	0.42
1:B:296:THR:HG22	1:B:297:GLU:N	2.33	0.42
1:B:330:GLN:HE21	1:B:338:THR:HG1	1.64	0.42
1:A:228:LEU:CB	1:A:242:GLN:HE21	2.32	0.42
1:A:534:ALA:HB1	4:A:594:HOH:O	2.18	0.42
1:B:175:ASN:ND2	1:B:201:LYS:HD2	2.34	0.42
1:A:180:ILE:CG2	1:A:187:LEU:HD22	2.49	0.42
1:A:494:ASN:HB3	1:B:289:LEU:HD12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:325:LEU:HD12	1:B:385:LYS:HB3	2.02	0.42
1:A:271:TYR:CE1	1:A:314:VAL:HG23	2.55	0.42
1:A:429:LEU:HD11	1:A:506:ILE:HG22	2.02	0.42
1:B:344:GLU:HA	1:B:345:PRO:HD3	1.95	0.42
1:B:12:LEU:HD23	1:B:84:THR:HG22	2.01	0.42
1:B:236:PRO:HA	1:B:239:TRP:CD2	2.54	0.42
1:A:298:GLU:CD	1:A:298:GLU:N	2.71	0.41
1:A:312:GLU:OE2	1:A:312:GLU:N	2.52	0.41
1:A:209:LEU:HD23	1:A:216:THR:HG21	2.01	0.41
1:B:249:LYS:HG2	1:B:250:ASP:N	2.32	0.41
1:A:458:VAL:HG11	1:B:286:THR:HG21	2.01	0.41
1:A:460:ASN:ND2	1:B:288:ALA:HB2	2.34	0.41
1:B:80:LEU:HD13	1:B:153:TRP:CD1	2.55	0.41
1:A:431:LYS:NZ	1:A:431:LYS:HB2	2.35	0.41
1:B:296:THR:O	1:B:300:GLU:HG3	2.20	0.41
1:A:108:VAL:O	1:A:108:VAL:HG13	2.20	0.41
1:A:253:THR:HA	1:A:291:GLU:O	2.21	0.41
1:B:245:VAL:HG23	1:B:245:VAL:O	2.21	0.41
1:B:388:LYS:HE2	1:B:415:GLU:OE1	2.21	0.41
1:A:424:LYS:HB3	1:A:424:LYS:HE3	1.77	0.41
1:A:103:LYS:HA	1:A:103:LYS:HD3	1.85	0.41
1:B:260:LEU:HD22	1:B:264:LEU:HD11	2.02	0.41
1:A:218:ASP:OD2	1:A:221:HIS:ND1	2.53	0.41
1:A:484:LEU:HA	1:A:484:LEU:HD12	1.83	0.41
1:A:339:TYR:CZ	1:A:352:GLY:HA3	2.56	0.41
1:B:172:ARG:HD2	4:B:564:HOH:O	2.20	0.41
1:A:126:LYS:HA	1:A:145:GLN:NE2	2.37	0.40
1:A:320:ASP:HA	1:A:321:PRO:HD3	1.84	0.40
1:A:8:VAL:O	1:A:10:VAL:HG23	2.21	0.40
1:B:270:ILE:HG12	1:B:346:PHE:O	2.21	0.40
1:A:3:SER:OG	1:A:5:ILE:HG22	2.21	0.40
1:B:338:THR:HG21	1:B:427:TYR:O	2.21	0.40
1:A:195:ILE:HG23	1:A:199:ARG:NE	2.37	0.40
1:A:209:LEU:HA	1:A:209:LEU:HD12	1.92	0.40
1:B:368:LEU:HD13	1:B:398:TRP:CZ3	2.56	0.40
1:A:24:TRP:CD2	1:A:25:PRO:HD2	2.57	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	551/560 (98%)	522 (95%)	22 (4%)	7 (1%)	14	25
1	B	395/560 (70%)	384 (97%)	11 (3%)	0	100	100
All	All	946/1120 (84%)	906 (96%)	33 (4%)	7 (1%)	25	43

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	195	ILE
1	A	543	GLY
1	A	334	GLN
1	A	410	TRP
1	A	136	ASN
1	A	356	ARG
1	A	412	PRO

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	495/500 (99%)	459 (93%)	36 (7%)	16	31
1	B	367/500 (73%)	343 (94%)	24 (6%)	20	37
All	All	862/1000 (86%)	802 (93%)	60 (7%)	18	33

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	LYS
1	A	66	LYS
1	A	74	LEU
1	A	78	ARG
1	A	120	LEU
1	A	194	GLU
1	A	205	LEU
1	A	209	LEU
1	A	218	ASP
1	A	264	LEU
1	A	282	LEU
1	A	283	LEU
1	A	289	LEU
1	A	295	LEU
1	A	298	GLU
1	A	303	LEU
1	A	308	GLU
1	A	310	LEU
1	A	334	GLN
1	A	349	LEU
1	A	357	MET
1	A	361	HIS
1	A	379	SER
1	A	402	TRP
1	A	406	TRP
1	A	423	VAL
1	A	424	LYS
1	A	428	GLN
1	A	448	ARG
1	A	500	GLN
1	A	507	GLN
1	A	517	LEU
1	A	519	ASN
1	A	529	GLU
1	A	533	LEU
1	A	551	LEU
1	B	11	LYS
1	B	80	LEU
1	B	83	ARG
1	B	91	GLN
1	B	175	ASN
1	B	184	MET
1	B	203	GLU

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Mol	Chain	Res	Type
1	B	205	LEU
1	B	209	LEU
1	B	234	LEU
1	B	248	GLU
1	B	250	ASP
1	B	260	LEU
1	B	284	ARG
1	B	310	LEU
1	B	323	LYS
1	B	336	GLN
1	B	356	ARG
1	B	368	LEU
1	B	385	LYS
1	B	407	GLN
1	B	410	TRP
1	B	422	LEU
1	B	429	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	145	GLN
1	A	242	GLN
1	A	258	GLN
1	A	332	GLN
1	A	336	GLN
1	A	348	ASN
1	A	407	GLN
1	A	428	GLN
1	A	487	GLN
1	A	500	GLN
1	A	519	ASN
1	A	524	GLN
1	A	545	ASN
1	B	85	GLN
1	B	175	ASN
1	B	197	GLN
1	B	258	GLN
1	B	306	ASN
1	B	330	GLN
1	B	336	GLN
1	B	340	GLN

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Mol	Chain	Res	Type
1	B	348	ASN
1	B	373	GLN
1	B	407	GLN
1	B	428	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

6 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	$\# Z > 2$
2	KRV	A	561	-	20,25,25	1.91	6 (30%)	22,36,36	3.14	5 (22%)
3	SO4	A	562	-	4,4,4	0.31	0	6,6,6	0.16	0
3	SO4	A	563	-	4,4,4	0.34	0	6,6,6	0.15	0
3	SO4	A	564	-	4,4,4	0.38	0	6,6,6	0.10	0
3	SO4	A	565	-	4,4,4	0.34	0	6,6,6	0.11	0
3	SO4	B	561	-	4,4,4	0.24	0	6,6,6	0.09	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical

component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	KRV	A	561	-	-	0/16/16/16	0/2/2/2
3	SO4	A	562	-	-	0/0/0/0	0/0/0/0
3	SO4	A	563	-	-	0/0/0/0	0/0/0/0
3	SO4	A	564	-	-	0/0/0/0	0/0/0/0
3	SO4	A	565	-	-	0/0/0/0	0/0/0/0
3	SO4	B	561	-	-	0/0/0/0	0/0/0/0

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	561	KRV	C11-N10	2.04	1.36	1.33
2	A	561	KRV	C17-C16	2.75	1.43	1.39
2	A	561	KRV	C23-C22	2.98	1.44	1.39
2	A	561	KRV	C23-C16	3.21	1.44	1.39
2	A	561	KRV	C21-C18	3.63	1.46	1.39
2	A	561	KRV	C21-C22	3.88	1.45	1.39

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	561	KRV	O15-C14-C13	-5.22	113.93	120.12
2	A	561	KRV	C13-C12-C25	2.63	125.25	122.34
2	A	561	KRV	C21-C18-C19	2.66	122.76	119.53
2	A	561	KRV	C16-C14-C13	6.94	127.39	119.46
2	A	561	KRV	C11-N10-C9	10.47	124.31	115.16

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

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	553/560 (98%)	0.31	16 (2%)	52	55	40, 62, 93, 117	0
1	B	403/560 (71%)	0.26	16 (3%)	39	41	36, 57, 93, 108	0
All	All	956/1120 (85%)	0.29	32 (3%)	47	50	36, 60, 93, 117	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	346	PHE	4.0
1	A	193	LEU	3.8
1	B	12	LEU	3.8
1	B	279	LEU	3.8
1	B	232	TYR	3.5
1	A	553	SER	3.4
1	A	195	ILE	3.3
1	A	426	TRP	2.9
1	B	13	LYS	2.9
1	A	181	TYR	2.9
1	A	66	LYS	2.8
1	B	284	ARG	2.6
1	A	402	TRP	2.6
1	B	24	TRP	2.6
1	B	212	TRP	2.4
1	A	542	ILE	2.4
1	B	11	LYS	2.4
1	A	452	LEU	2.4
1	B	266	TRP	2.4
1	B	214	LEU	2.3
1	B	87	PHE	2.3
1	A	217	PRO	2.3
1	A	53	GLU	2.2
1	A	60	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	67	ASP	2.2
1	A	224	GLU	2.2
1	B	308	GLU	2.2
1	A	210	LEU	2.2
1	B	6	GLU	2.1
1	A	75	VAL	2.1
1	B	310	LEU	2.1
1	B	21	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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(Å ²)	Q<0.9
3	SO4	A	564	5/5	0.85	0.45	12.61	121,121,121,121	0
2	KRV	A	561	24/24	0.93	0.23	0.87	55,59,66,67	0
3	SO4	A	562	5/5	0.94	0.16	0.39	77,78,80,82	0
3	SO4	B	561	5/5	0.94	0.13	-1.08	82,83,84,85	0
3	SO4	A	563	5/5	0.97	0.12	-1.15	76,77,78,79	0
3	SO4	A	565	5/5	0.84	0.14	-	120,120,121,121	0

6.5 Other polymers [i](#)

There are no such residues in this entry.