



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:59 PM GMT

PDB ID : 1N0U
Title : Crystal structure of yeast elongation factor 2 in complex with sordarin
Authors : Joergensen, R.; Ortiz, P.A.; Carr-Schmid, A.; Nissen, P.; Kinzy, T.G.; Andersen, G.R.
Deposited on : 2002-10-15
Resolution : 2.12 Å(reported)

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

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

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

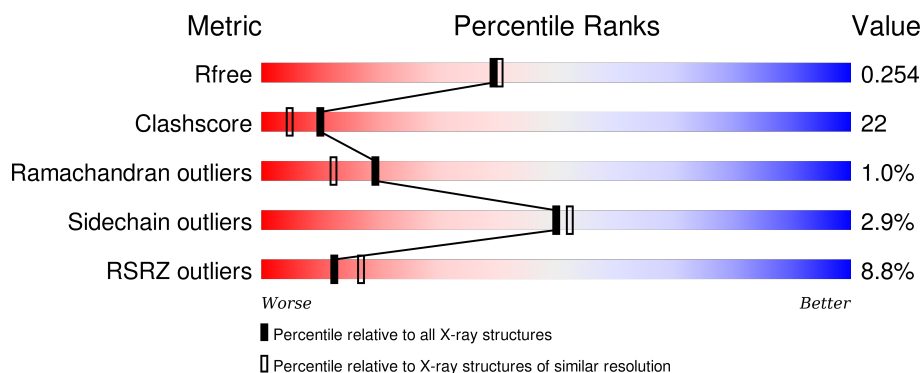
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.12 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	4587 (2.14-2.10)
Clashscore	102246	5132 (2.14-2.10)
Ramachandran outliers	100387	5080 (2.14-2.10)
Sidechain outliers	100360	5081 (2.14-2.10)
RSRZ outliers	91569	4597 (2.14-2.10)

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	842	<div> <div>9%</div> <div>62%</div> <div>33%</div> <div>••</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
2	SO1	A	843	X	-	-	-

2 Entry composition [i](#)

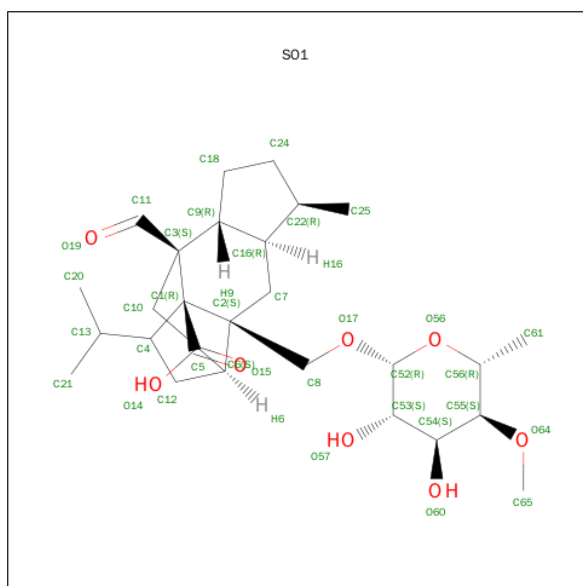
There are 3 unique types of molecules in this entry. The entry contains 6904 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Elongation factor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	819	6375	4057	1086	1202	30	0	0	0

- Molecule 2 is [1R-(1.ALPHA.,3A.BETA.,4.BETA.,4A.BETA.,7.BETA.,7A.ALPHA.,8A.B.ETA.)]8A-[(6-DEOXY-4-O-METHYL-BETA-D-ALTROPYRANOSYLOXY)METHYL]-4-FORMYL-4,4A,5,6,7,7A,8,8A-OCTAHYDRO-7-METHYL-3-(1-METHYLETHYL)-1,4-METHANO-S-INDACENE-3A(1H)-CARBOXYLIC ACID (three-letter code: SO1) (formula: C₂₇H₄₂O₈).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	35	27	8	0	0

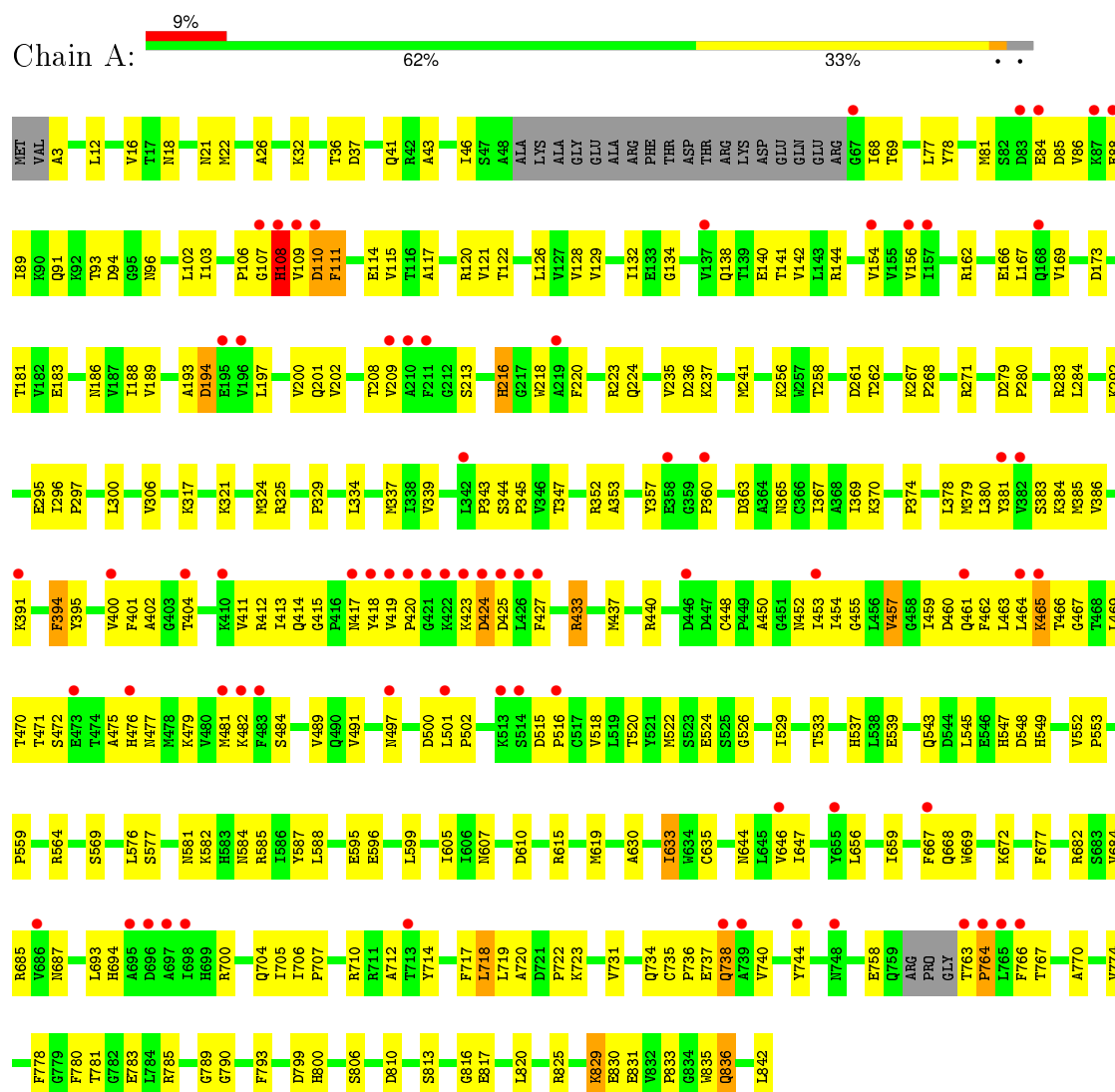
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	494	Total 494	O 494	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: Elongation factor 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	119.96 Å 150.83 Å 65.07 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.00 – 2.12 29.99 – 2.12	Depositor EDS
% Data completeness (in resolution range)	98.0 (31.00-2.12) 98.0 (29.99-2.12)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.12 Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.236 , 0.254 0.236 , 0.254	Depositor DCC
R_{free} test set	1953 reflections (2.94%)	DCC
Wilson B-factor (Å ²)	34.7	Xtriage
Anisotropy	0.130	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 51.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	2 of 66839 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6904	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.21% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO1

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	0/6497	0.62	1/8797 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	110	ASP	N-CA-C	-5.38	96.46	111.00

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	6375	0	6441	284	0
2	A	35	0	40	2	0
3	A	494	0	0	48	0
All	All	6904	0	6481	284	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 22.

All (284) 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:463:LEU:HD21	1:A:467:GLY:HA3	1.46	0.97
1:A:126:LEU:HD11	1:A:156:VAL:HG23	1.50	0.93
1:A:667:PHE:HB3	3:A:1142:HOH:O	1.69	0.91
1:A:109:VAL:HG11	1:A:142:VAL:HG22	1.52	0.88
1:A:132:ILE:HD12	1:A:162:ARG:HD3	1.55	0.87
1:A:186:ASN:HB3	1:A:201:GLN:HE21	1.40	0.86
1:A:685:ARG:HE	1:A:687:ASN:HD21	1.20	0.85
1:A:103:ILE:HD12	1:A:122:THR:HG22	1.59	0.85
1:A:533:THR:H	1:A:537:HIS:HD2	1.26	0.84
1:A:109:VAL:HG22	1:A:138:GLN:HG3	1.60	0.82
1:A:216:HIS:HA	3:A:1026:HOH:O	1.80	0.81
1:A:694:HIS:O	1:A:700:ARG:HD3	1.81	0.80
1:A:18:ASN:HD21	1:A:94:ASP:H	1.27	0.79
1:A:829:LYS:HE2	3:A:905:HOH:O	1.83	0.78
1:A:91:GLN:NE2	1:A:344:SER:H	1.81	0.78
1:A:91:GLN:HE22	1:A:344:SER:H	1.32	0.78
1:A:284:LEU:HD13	1:A:324:MET:HE3	1.64	0.78
1:A:109:VAL:HG21	1:A:142:VAL:HG23	1.65	0.77
1:A:734:GLN:HE21	1:A:767:THR:HG22	1.50	0.77
1:A:433:ARG:HB3	1:A:457:VAL:CG1	2.17	0.75
1:A:378:LEU:H	1:A:471:THR:HG22	1.52	0.74
1:A:780:PHE:HA	3:A:1144:HOH:O	1.88	0.74
1:A:693:LEU:HB3	1:A:700:ARG:HD2	1.69	0.74
1:A:126:LEU:HD11	1:A:156:VAL:CG2	2.18	0.73
1:A:718:LEU:HB3	1:A:835:TRP:HB3	1.70	0.73
1:A:829:LYS:HE3	1:A:830:GLU:H	1.50	0.73
1:A:799:ASP:OD1	1:A:800:HIS:HD2	1.72	0.72
1:A:763:THR:N	1:A:764:PRO:HD3	2.04	0.72
1:A:466:THR:HB	3:A:943:HOH:O	1.89	0.71
1:A:132:ILE:HD12	1:A:162:ARG:CD	2.20	0.71
1:A:533:THR:H	1:A:537:HIS:CD2	2.09	0.70
1:A:630:ALA:O	1:A:633:ILE:HG23	1.91	0.70
1:A:194:ASP:HB2	1:A:197:LEU:HD13	1.73	0.70
1:A:202:VAL:HG12	1:A:209:VAL:CG2	2.23	0.68
1:A:189:VAL:CG1	1:A:200:VAL:HG13	2.24	0.68
1:A:103:ILE:HD11	1:A:453:ILE:HD11	1.76	0.68
1:A:836:GLN:H	1:A:836:GLN:NE2	1.90	0.67
1:A:482:LYS:HB2	1:A:793:PHE:CZ	2.29	0.67
1:A:91:GLN:HE22	1:A:343:PRO:HA	1.59	0.67
1:A:424:ASP:O	1:A:425:ASP:HB2	1.92	0.67
1:A:386:VAL:HG12	1:A:395:TYR:O	1.94	0.67
1:A:417:ASN:HB2	1:A:425:ASP:OD2	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:500:ASP:HB3	1:A:552:VAL:HG11	1.78	0.66
1:A:734:GLN:HE21	1:A:767:THR:CG2	2.09	0.66
1:A:785:ARG:HG3	1:A:785:ARG:HH11	1.61	0.66
1:A:91:GLN:HE21	1:A:347:THR:CB	2.09	0.65
1:A:813:SER:O	1:A:817:GLU:HG3	1.97	0.65
1:A:374:PRO:O	1:A:404:THR:HG23	1.97	0.65
1:A:500:ASP:CB	1:A:552:VAL:HG11	2.26	0.65
1:A:378:LEU:N	1:A:471:THR:HG22	2.12	0.65
1:A:497:ASN:HB3	1:A:500:ASP:OD2	1.97	0.64
1:A:385:MET:HG2	3:A:1102:HOH:O	1.97	0.64
1:A:284:LEU:HD13	1:A:324:MET:CE	2.27	0.64
1:A:369:ILE:HD13	1:A:402:ALA:HB2	1.79	0.64
1:A:202:VAL:HG12	1:A:209:VAL:HG23	1.78	0.64
1:A:472:SER:HB3	1:A:475:ALA:HB2	1.80	0.64
1:A:213:SER:OG	1:A:216:HIS:HB2	1.97	0.63
1:A:464:LEU:O	1:A:465:LYS:HB2	1.99	0.63
1:A:783:GLU:HB2	3:A:1144:HOH:O	1.98	0.63
1:A:186:ASN:HB3	1:A:201:GLN:NE2	2.14	0.63
1:A:103:ILE:HD11	1:A:453:ILE:CD1	2.29	0.63
1:A:668:GLN:NE2	3:A:1142:HOH:O	2.32	0.62
1:A:384:LYS:HD2	3:A:1082:HOH:O	1.99	0.62
1:A:685:ARG:NE	1:A:687:ASN:HD21	1.95	0.62
1:A:644:ASN:HD22	1:A:684:VAL:H	1.45	0.62
1:A:81:MET:HG3	1:A:339:VAL:HG11	1.81	0.62
1:A:353:ALA:CB	1:A:370:LYS:HG2	2.29	0.62
1:A:365:ASN:O	1:A:369:ILE:HG12	1.99	0.62
1:A:109:VAL:CG2	1:A:138:GLN:HG3	2.28	0.61
1:A:685:ARG:HE	1:A:687:ASN:ND2	1.97	0.61
1:A:378:LEU:H	1:A:471:THR:CG2	2.12	0.60
1:A:731:VAL:HG12	1:A:770:ALA:O	2.02	0.60
1:A:223:ARG:HD2	3:A:1304:HOH:O	2.02	0.59
1:A:418:TYR:HA	1:A:424:ASP:O	2.02	0.59
1:A:831:GLU:HG3	3:A:905:HOH:O	2.01	0.59
1:A:545:LEU:HA	1:A:549:HIS:HB2	1.85	0.59
1:A:710:ARG:NH1	1:A:714:TYR:OH	2.36	0.59
1:A:321:LYS:HG2	3:A:1026:HOH:O	2.02	0.59
1:A:103:ILE:HD12	1:A:122:THR:CG2	2.31	0.58
1:A:829:LYS:HE3	1:A:830:GLU:N	2.18	0.58
1:A:292:LYS:HD3	1:A:295:GLU:OE2	2.03	0.58
1:A:140:GLU:HG3	1:A:188:ILE:HD13	1.85	0.58
1:A:413:ILE:HB	1:A:427:PHE:HB2	1.83	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:836:GLN:H	1:A:836:GLN:HE21	1.50	0.58
1:A:353:ALA:HB3	1:A:370:LYS:HG2	1.86	0.57
1:A:296:ILE:O	1:A:300:LEU:HD13	2.04	0.57
1:A:585:ARG:NH1	1:A:842:LEU:HD23	2.19	0.57
1:A:415:GLY:H	1:A:425:ASP:HB3	1.70	0.57
1:A:705:ILE:HD12	3:A:977:HOH:O	2.05	0.56
1:A:810:ASP:O	1:A:816:GLY:HA3	2.05	0.56
1:A:369:ILE:HD12	1:A:401:PHE:HB3	1.87	0.56
1:A:706:ILE:HB	1:A:707:PRO:HD3	1.86	0.56
1:A:581:ASN:O	1:A:582:LYS:HB2	2.06	0.56
1:A:117:ALA:HB1	3:A:968:HOH:O	2.05	0.55
1:A:482:LYS:HB2	1:A:793:PHE:HZ	1.70	0.55
1:A:237:LYS:O	1:A:241:MET:HG2	2.06	0.55
1:A:156:VAL:HG21	1:A:334:LEU:HD22	1.89	0.55
1:A:279:ASP:HB3	1:A:280:PRO:HD3	1.88	0.54
1:A:296:ILE:HB	1:A:297:PRO:HD3	1.89	0.54
1:A:412:ARG:HD2	3:A:1010:HOH:O	2.07	0.54
1:A:734:GLN:HG3	1:A:767:THR:HG22	1.89	0.54
1:A:423:LYS:O	1:A:423:LYS:HG2	2.08	0.54
1:A:501:LEU:HB2	1:A:502:PRO:HD3	1.90	0.54
1:A:552:VAL:HG13	1:A:553:PRO:HD2	1.89	0.54
1:A:88:GLU:CD	1:A:223:ARG:HH21	2.12	0.54
1:A:200:VAL:HG12	3:A:1237:HOH:O	2.06	0.54
1:A:114:GLU:HB2	3:A:1037:HOH:O	2.07	0.54
1:A:88:GLU:OE2	1:A:223:ARG:NH2	2.42	0.53
1:A:829:LYS:HA	1:A:829:LYS:HE3	1.90	0.53
1:A:109:VAL:HG12	1:A:115:VAL:HG21	1.89	0.53
1:A:154:VAL:HG11	1:A:337:MET:HB3	1.91	0.53
1:A:615:ARG:HG2	1:A:619:MET:CE	2.39	0.53
1:A:646:VAL:C	1:A:647:ILE:HD12	2.29	0.53
1:A:461:GLN:HG2	3:A:904:HOH:O	2.09	0.53
1:A:3:ALA:HA	1:A:46:ILE:O	2.09	0.53
1:A:103:ILE:HD13	1:A:121:VAL:HG23	1.91	0.52
1:A:411:VAL:HG12	1:A:412:ARG:N	2.24	0.52
1:A:169:VAL:CG1	1:A:173:ASP:HB2	2.39	0.52
1:A:693:LEU:HB3	1:A:700:ARG:CD	2.39	0.52
1:A:91:GLN:HE22	1:A:344:SER:N	2.04	0.52
1:A:167:LEU:HD12	1:A:167:LEU:N	2.24	0.52
1:A:433:ARG:HB3	1:A:457:VAL:HG13	1.92	0.52
1:A:607:ASN:HB2	1:A:610:ASP:OD2	2.10	0.52
1:A:89:ILE:HG22	1:A:91:GLN:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:466:THR:HG22	3:A:968:HOH:O	2.09	0.52
1:A:193:ALA:CB	1:A:200:VAL:HG11	2.40	0.52
1:A:258:THR:HG21	3:A:1071:HOH:O	2.08	0.52
1:A:547:HIS:HD2	1:A:548:ASP:OD1	1.93	0.52
1:A:454:ILE:HG13	1:A:455:GLY:H	1.75	0.52
1:A:109:VAL:CG1	1:A:115:VAL:HG21	2.40	0.51
1:A:156:VAL:HG21	1:A:334:LEU:CD2	2.39	0.51
1:A:454:ILE:HG13	1:A:455:GLY:N	2.25	0.51
1:A:533:THR:N	1:A:537:HIS:HD2	2.03	0.51
1:A:569:SER:O	1:A:720:ALA:HB1	2.11	0.51
1:A:758:GLU:HG3	1:A:767:THR:OG1	2.10	0.51
1:A:457:VAL:HG23	3:A:973:HOH:O	2.09	0.51
1:A:120:ARG:NH1	1:A:481:MET:CE	2.74	0.51
1:A:806:SER:HB2	1:A:813:SER:HB2	1.92	0.50
1:A:615:ARG:HG2	1:A:619:MET:HE1	1.92	0.50
1:A:241:MET:HE1	3:A:1290:HOH:O	2.10	0.50
1:A:360:PRO:HD2	3:A:1019:HOH:O	2.11	0.50
1:A:736:PRO:HB2	1:A:738:GLN:OE1	2.11	0.49
1:A:576:LEU:HD21	1:A:585:ARG:HH11	1.77	0.49
1:A:120:ARG:HH12	1:A:481:MET:CE	2.25	0.49
1:A:202:VAL:CG1	1:A:209:VAL:CG2	2.90	0.49
1:A:107:GLY:O	1:A:109:VAL:HG13	2.13	0.49
1:A:605:ILE:N	1:A:605:ILE:HD12	2.28	0.49
1:A:216:HIS:HB3	1:A:218:TRP:CD1	2.48	0.49
1:A:644:ASN:ND2	1:A:684:VAL:H	2.09	0.49
1:A:433:ARG:HB3	1:A:457:VAL:HG11	1.93	0.49
1:A:588:LEU:HD12	1:A:588:LEU:C	2.33	0.48
1:A:400:VAL:HG12	1:A:450:ALA:HA	1.95	0.48
1:A:533:THR:HG22	3:A:1182:HOH:O	2.14	0.48
1:A:433:ARG:HD2	3:A:942:HOH:O	2.13	0.48
1:A:785:ARG:HG3	1:A:785:ARG:NH1	2.27	0.48
1:A:386:VAL:HG11	1:A:437:MET:CE	2.43	0.48
1:A:737:GLU:HB2	1:A:766:PHE:CE2	2.49	0.48
1:A:86:VAL:HG13	1:A:93:THR:HG21	1.95	0.48
1:A:559:PRO:HG2	1:A:778:PHE:CE1	2.48	0.48
1:A:576:LEU:HD13	1:A:587:TYR:CE1	2.48	0.48
1:A:419:VAL:HG12	3:A:1063:HOH:O	2.14	0.48
1:A:37:ASP:O	1:A:41:GLN:HG3	2.13	0.48
1:A:414:GLN:HB3	1:A:418:TYR:CD2	2.48	0.48
1:A:202:VAL:CG1	1:A:209:VAL:HG22	2.42	0.48
1:A:107:GLY:O	1:A:109:VAL:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:16:VAL:O	1:A:345:PRO:HD2	2.13	0.48
1:A:306:VAL:HG22	3:A:1111:HOH:O	2.14	0.48
1:A:520:THR:HA	1:A:529:ILE:O	2.13	0.48
1:A:200:VAL:HG22	1:A:200:VAL:O	2.13	0.47
1:A:129:VAL:HG13	1:A:134:GLY:O	2.14	0.47
1:A:820:LEU:CB	3:A:1118:HOH:O	2.61	0.47
1:A:820:LEU:HB3	3:A:1118:HOH:O	2.13	0.47
1:A:564:ARG:HG3	1:A:682:ARG:HB2	1.95	0.47
1:A:440:ARG:HD2	3:A:1056:HOH:O	2.14	0.47
1:A:833:PRO:HA	3:A:1095:HOH:O	2.13	0.47
1:A:110:ASP:O	1:A:111:PHE:HB2	2.14	0.47
1:A:26:ALA:HB2	1:A:128:VAL:HB	1.97	0.47
1:A:258:THR:HB	3:A:1028:HOH:O	2.14	0.47
1:A:110:ASP:HB3	1:A:785:ARG:NH1	2.30	0.47
1:A:111:PHE:CD2	1:A:789:GLY:HA2	2.49	0.47
1:A:394:PHE:N	1:A:394:PHE:HD2	2.13	0.47
1:A:394:PHE:N	1:A:394:PHE:CD2	2.83	0.47
1:A:584:ASN:HD22	1:A:693:LEU:HA	1.80	0.47
1:A:117:ALA:N	3:A:1057:HOH:O	2.48	0.47
1:A:279:ASP:OD2	1:A:283:ARG:CZ	2.63	0.47
1:A:84:GLU:HG3	1:A:85:ASP:N	2.30	0.47
1:A:718:LEU:HA	1:A:722:PRO:HG3	1.96	0.46
1:A:162:ARG:HG3	1:A:166:GLU:OE2	2.14	0.46
1:A:817:GLU:HA	3:A:1118:HOH:O	2.16	0.46
1:A:515:ASP:O	1:A:518:VAL:HG12	2.15	0.46
1:A:584:ASN:HD21	1:A:700:ARG:HG2	1.79	0.46
1:A:108:HIS:O	1:A:108:HIS:CG	2.69	0.46
1:A:357:TYR:CZ	1:A:476:HIS:HB3	2.50	0.46
1:A:633:ILE:HG13	1:A:633:ILE:O	2.16	0.45
1:A:737:GLU:HB2	1:A:766:PHE:HE2	1.80	0.45
1:A:774:VAL:HG11	2:A:843:SO1:H121	1.98	0.45
1:A:825:ARG:NE	3:A:1032:HOH:O	2.30	0.45
1:A:109:VAL:HG21	1:A:142:VAL:CG2	2.43	0.45
1:A:552:VAL:CG1	1:A:553:PRO:HD2	2.46	0.45
1:A:411:VAL:HG11	1:A:469:LEU:HB3	1.98	0.45
1:A:381:TYR:CZ	3:A:943:HOH:O	2.63	0.45
1:A:491:VAL:HA	1:A:559:PRO:HD3	1.98	0.45
1:A:197:LEU:N	1:A:197:LEU:HD12	2.31	0.45
1:A:108:HIS:CE1	3:A:1037:HOH:O	2.69	0.45
1:A:539:GLU:O	1:A:543:GLN:HG3	2.16	0.45
1:A:420:PRO:HB2	3:A:1063:HOH:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:379:MET:HB2	1:A:402:ALA:HB3	2.00	0.44
1:A:129:VAL:HG11	1:A:181:THR:HG23	2.00	0.44
1:A:321:LYS:HE2	3:A:1026:HOH:O	2.17	0.44
1:A:325:ARG:O	1:A:329:PRO:HG3	2.18	0.44
1:A:740:VAL:HG12	1:A:744:TYR:CE2	2.53	0.44
1:A:669:TRP:CD1	1:A:710:ARG:NH1	2.85	0.44
1:A:21:ASN:ND2	1:A:345:PRO:HG3	2.33	0.44
1:A:633:ILE:HD12	1:A:635:CYS:N	2.32	0.44
1:A:306:VAL:HG23	1:A:306:VAL:O	2.17	0.44
1:A:722:PRO:O	1:A:723:LYS:HD2	2.18	0.44
1:A:524:GLU:HG3	3:A:1156:HOH:O	2.17	0.43
1:A:216:HIS:HB3	1:A:218:TRP:HD1	1.84	0.43
1:A:114:GLU:CG	3:A:1037:HOH:O	2.66	0.43
1:A:459:ILE:HG22	1:A:459:ILE:O	2.18	0.43
1:A:32:LYS:O	1:A:36:THR:HG23	2.18	0.43
1:A:220:PHE:HA	1:A:224:GLN:OE1	2.19	0.43
1:A:500:ASP:CG	1:A:552:VAL:HG11	2.38	0.43
1:A:647:ILE:N	1:A:647:ILE:HD12	2.34	0.43
1:A:81:MET:O	1:A:96:ASN:HB3	2.19	0.43
1:A:261:ASP:OD1	1:A:262:THR:HG23	2.18	0.43
1:A:386:VAL:HG11	1:A:437:MET:HE3	2.01	0.43
1:A:581:ASN:ND2	1:A:704:GLN:HG3	2.34	0.43
1:A:559:PRO:HB2	2:A:843:SO1:H201	2.01	0.43
1:A:18:ASN:N	1:A:18:ASN:HD22	2.17	0.43
1:A:380:LEU:C	1:A:380:LEU:HD23	2.39	0.43
1:A:352:ARG:HH11	1:A:352:ARG:HG2	1.84	0.42
1:A:522:MET:HE2	1:A:526:GLY:O	2.18	0.42
1:A:484:SER:O	1:A:533:THR:HG21	2.19	0.42
1:A:738:GLN:OE1	1:A:738:GLN:N	2.51	0.42
1:A:16:VAL:HG11	1:A:450:ALA:O	2.19	0.42
1:A:462:PHE:HE2	3:A:1286:HOH:O	2.02	0.42
1:A:763:THR:N	1:A:764:PRO:CD	2.78	0.42
1:A:292:LYS:HD3	1:A:295:GLU:CD	2.39	0.42
1:A:108:HIS:O	1:A:108:HIS:CD2	2.72	0.42
1:A:22:MET:SD	1:A:102:LEU:HD12	2.59	0.42
1:A:126:LEU:CD1	1:A:156:VAL:HG23	2.36	0.42
1:A:140:GLU:HG3	1:A:188:ILE:CD1	2.49	0.42
1:A:515:ASP:OD2	1:A:537:HIS:HE1	2.02	0.42
1:A:489:VAL:HG22	1:A:781:THR:HG21	2.02	0.42
1:A:633:ILE:HD12	1:A:633:ILE:C	2.40	0.42
1:A:470:THR:HG21	1:A:475:ALA:HB1	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:ALA:CB	1:A:128:VAL:HB	2.50	0.42
1:A:718:LEU:HD12	1:A:718:LEU:HA	1.92	0.42
1:A:383:SER:O	1:A:384:LYS:HB3	2.20	0.42
1:A:659:ILE:CG2	1:A:705:ILE:HD13	2.50	0.42
1:A:448:CYS:SG	1:A:452:ASN:HB2	2.60	0.42
1:A:785:ARG:HB2	1:A:790:GLY:HA2	2.01	0.41
1:A:734:GLN:O	1:A:735:CYS:HB3	2.21	0.41
1:A:267:LYS:HA	1:A:268:PRO:HD3	1.86	0.41
1:A:202:VAL:CG1	1:A:208:THR:O	2.67	0.41
1:A:91:GLN:HG3	1:A:347:THR:OG1	2.21	0.41
1:A:717:PHE:HD2	1:A:718:LEU:HD13	1.86	0.41
1:A:785:ARG:O	1:A:790:GLY:N	2.46	0.41
1:A:577:SER:HB2	1:A:712:ALA:HB2	2.03	0.41
1:A:672:LYS:NZ	3:A:1226:HOH:O	2.52	0.41
1:A:515:ASP:HA	1:A:516:PRO:HD3	1.87	0.41
1:A:317:LYS:O	1:A:321:LYS:HG3	2.21	0.41
1:A:829:LYS:CA	1:A:829:LYS:HE3	2.51	0.41
1:A:719:LEU:HD21	1:A:835:TRP:CD2	2.56	0.41
1:A:656:LEU:O	1:A:659:ILE:HG12	2.20	0.41
1:A:169:VAL:HG12	1:A:173:ASP:HB2	2.02	0.41
1:A:256:LYS:NZ	3:A:1120:HOH:O	2.53	0.41
1:A:360:PRO:HB2	1:A:363:ASP:HB2	2.03	0.40
1:A:419:VAL:HG13	1:A:420:PRO:HD2	2.02	0.40
1:A:68:ILE:HG22	1:A:69:THR:N	2.36	0.40
1:A:235:VAL:HG21	3:A:1045:HOH:O	2.21	0.40
1:A:202:VAL:HG11	1:A:209:VAL:HG22	2.03	0.40
1:A:370:LYS:HD3	3:A:1291:HOH:O	2.21	0.40
1:A:120:ARG:HH12	1:A:481:MET:HE1	1.86	0.40
1:A:235:VAL:HG12	1:A:236:ASP:N	2.36	0.40
1:A:43:ALA:HB1	1:A:78:TYR:O	2.21	0.40
1:A:522:MET:CE	1:A:526:GLY:C	2.89	0.40
1:A:268:PRO:HG3	3:A:1335:HOH:O	2.21	0.40
1:A:111:PHE:CE1	1:A:141:THR:HG23	2.56	0.40
1:A:547:HIS:CD2	1:A:548:ASP:OD1	2.73	0.40
1:A:363:ASP:O	1:A:367:ILE:HG12	2.21	0.40
1:A:271:ARG:HB2	3:A:926:HOH:O	2.22	0.40
1:A:111:PHE:CE2	1:A:144:ARG:HD3	2.57	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	813/842 (97%)	780 (96%)	25 (3%)	8 (1%)	19	12

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	106	PRO
1	A	108	HIS
1	A	460	ASP
1	A	111	PHE
1	A	391	LYS
1	A	465	LYS
1	A	764	PRO
1	A	479	LYS

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	697/715 (98%)	677 (97%)	20 (3%)	50	52

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	LEU
1	A	77	LEU
1	A	108	HIS

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Mol	Chain	Res	Type
1	A	183	GLU
1	A	194	ASP
1	A	216	HIS
1	A	394	PHE
1	A	424	ASP
1	A	433	ARG
1	A	457	VAL
1	A	477	ASN
1	A	595	GLU
1	A	596	GLU
1	A	599	LEU
1	A	633	ILE
1	A	677	PHE
1	A	718	LEU
1	A	738	GLN
1	A	829	LYS
1	A	836	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	ASN
1	A	91	GLN
1	A	101	ASN
1	A	108	HIS
1	A	138	GLN
1	A	201	GLN
1	A	290	ASN
1	A	371	ASN
1	A	414	GLN
1	A	452	ASN
1	A	476	HIS
1	A	537	HIS
1	A	547	HIS
1	A	584	ASN
1	A	644	ASN
1	A	687	ASN
1	A	699	HIS
1	A	734	GLN
1	A	753	GLN
1	A	759	GLN
1	A	800	HIS

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Mol	Chain	Res	Type
1	A	836	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](#)

1 ligand 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	$\# Z > 2$
2	SO1	A	843	-	35,39,39	1.86	5 (14%)	35,64,64	2.23	5 (14%)

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	SO1	A	843	-	1/1/15/16	0/14/104/104	0/2/5/5

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	843	SO1	C12-C4	-6.59	1.38	1.54
2	A	843	SO1	C55-C56	2.29	1.56	1.52
2	A	843	SO1	C3-C1	3.56	1.63	1.57
2	A	843	SO1	C1-C5	3.73	1.57	1.50
2	A	843	SO1	C7-C2	4.23	1.60	1.54

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	843	SO1	C7-C2-C8	-4.02	102.42	109.94
2	A	843	SO1	C18-C9-C16	-3.91	97.96	103.60
2	A	843	SO1	O17-C52-C53	4.46	113.67	108.04
2	A	843	SO1	C12-C4-C13	6.93	128.22	112.53
2	A	843	SO1	C1-C4-C13	7.72	127.15	118.53

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	843	SO1	C4

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	843	SO1	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	819/842 (97%)	0.50	72 (8%) 12 17	19, 37, 64, 82	0

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	763	THR	7.7
1	A	110	ASP	7.4
1	A	107	GLY	6.2
1	A	109	VAL	5.8
1	A	420	PRO	5.3
1	A	422	LYS	5.2
1	A	483	PHE	5.2
1	A	698	ILE	5.0
1	A	108	HIS	4.8
1	A	764	PRO	4.7
1	A	424	ASP	4.5
1	A	421	GLY	4.3
1	A	67	GLY	4.2
1	A	419	VAL	4.2
1	A	427	PHE	4.2
1	A	418	TYR	4.2
1	A	195	GLU	3.7
1	A	417	ASN	3.7
1	A	426	LEU	3.7
1	A	461	GLN	3.7
1	A	655	TYR	3.6
1	A	464	LEU	3.6
1	A	425	ASP	3.5
1	A	168	GLN	3.4
1	A	391	LYS	3.3
1	A	360	PRO	3.3
1	A	465	LYS	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	156	VAL	3.2
1	A	453	ILE	3.1
1	A	696	ASP	3.1
1	A	211	PHE	3.1
1	A	695	ALA	3.0
1	A	83	ASP	3.0
1	A	516	PRO	2.9
1	A	423	LYS	2.9
1	A	501	LEU	2.8
1	A	686	VAL	2.8
1	A	513	LYS	2.8
1	A	210	ALA	2.8
1	A	84	GLU	2.7
1	A	410	LYS	2.7
1	A	157	ILE	2.6
1	A	497	ASN	2.6
1	A	154	VAL	2.6
1	A	476	HIS	2.6
1	A	342	LEU	2.6
1	A	446	ASP	2.6
1	A	473	GLU	2.5
1	A	88	GLU	2.4
1	A	739	ALA	2.4
1	A	482	LYS	2.4
1	A	738	GLN	2.4
1	A	196	VAL	2.4
1	A	219	ALA	2.3
1	A	209	VAL	2.3
1	A	514	SER	2.3
1	A	404	THR	2.3
1	A	766	PHE	2.3
1	A	400	VAL	2.3
1	A	667	PHE	2.3
1	A	137	VAL	2.3
1	A	382	VAL	2.3
1	A	646	VAL	2.2
1	A	744	TYR	2.2
1	A	748	ASN	2.2
1	A	358	GLU	2.2
1	A	381	TYR	2.1
1	A	713	THR	2.1
1	A	87	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	765	LEU	2.1
1	A	481	MET	2.1
1	A	697	ALA	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(\AA^2)	Q<0.9
2	SO1	A	843	35/35	0.94	0.13	0.80	21,26,31,38	0

6.5 Other polymers [i](#)

There are no such residues in this entry.