



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 07:15 PM UTC

PDB ID : 4KC5 / pdb_00004kc5
Title : Crystal structure of the C-terminal part of RhiE from Burkholderia rhizoxinica
Authors : Zocher, G.; Heim, J.B.; Stehle, T.
Deposited on : 2013-04-24
Resolution : 2.14 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

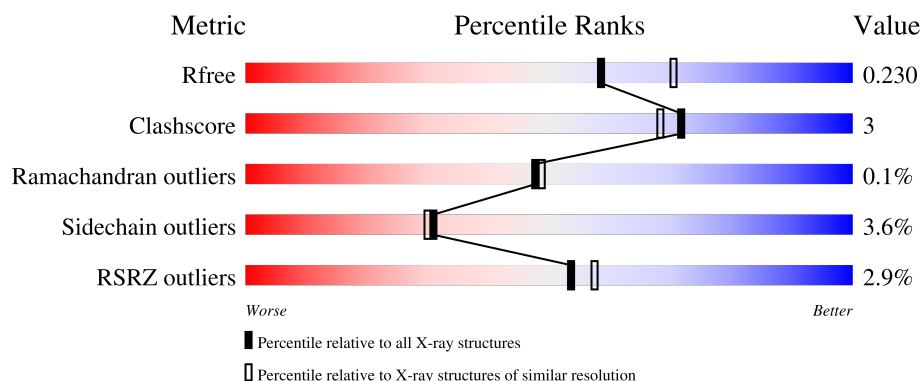
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.14 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}	180053	3689 (2.16-2.12)
Clashscore	190562	3812 (2.16-2.12)
Ramachandran outliers	187476	3773 (2.16-2.12)
Sidechain outliers	187428	3772 (2.16-2.12)
RSRZ outliers	180081	3691 (2.16-2.12)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	923	0% 90% 8% ..
1	B	923	4% 89% 9% .
1	C	923	3% 86% 11% .
1	D	923	3% 86% 11% ..

2 Entry composition [i](#)

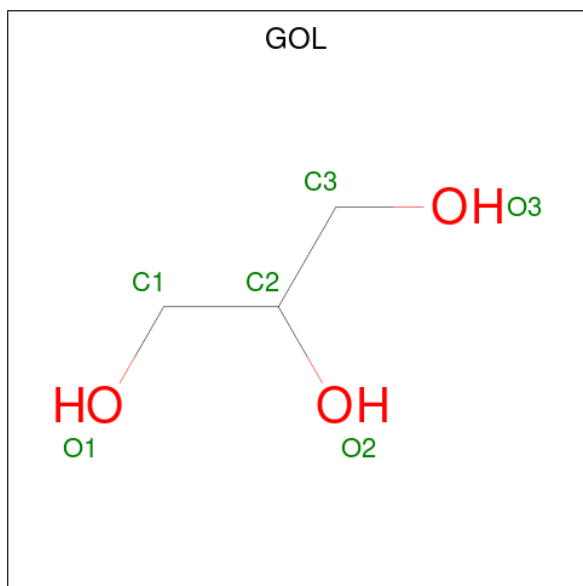
There are 3 unique types of molecules in this entry. The entry contains 29207 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 RhiE protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	914	Total	C	N	O	S	0	1	0
			7111	4506	1218	1356	31			
1	B	907	Total	C	N	O	S	0	0	0
			7035	4458	1205	1341	31			
1	C	901	Total	C	N	O	S	0	0	0
			6971	4419	1189	1332	31			
1	D	910	Total	C	N	O	S	0	1	0
			7068	4478	1215	1344	31			

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		

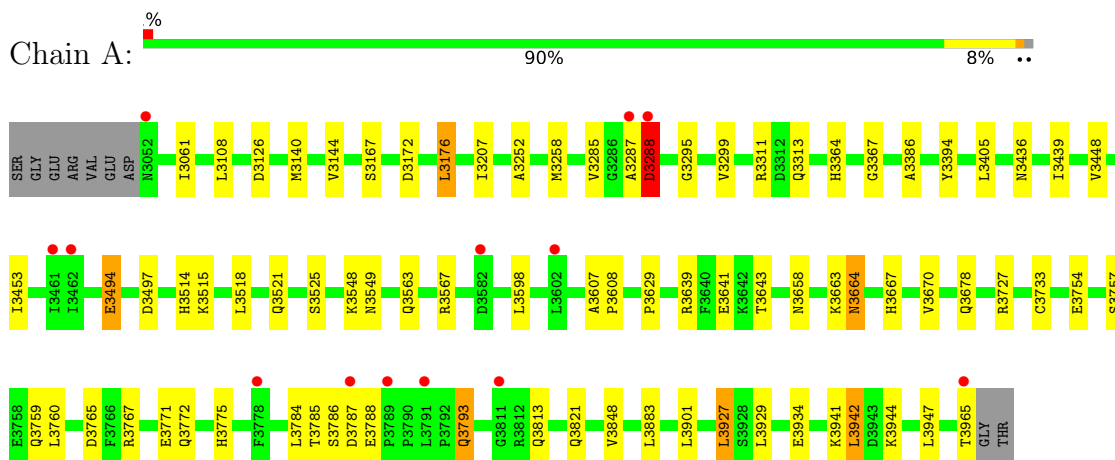
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	345	Total 345	O 345	0	0
3	B	207	Total 207	O 207	0	0
3	C	177	Total 177	O 177	0	0
3	D	287	Total 287	O 287	0	0

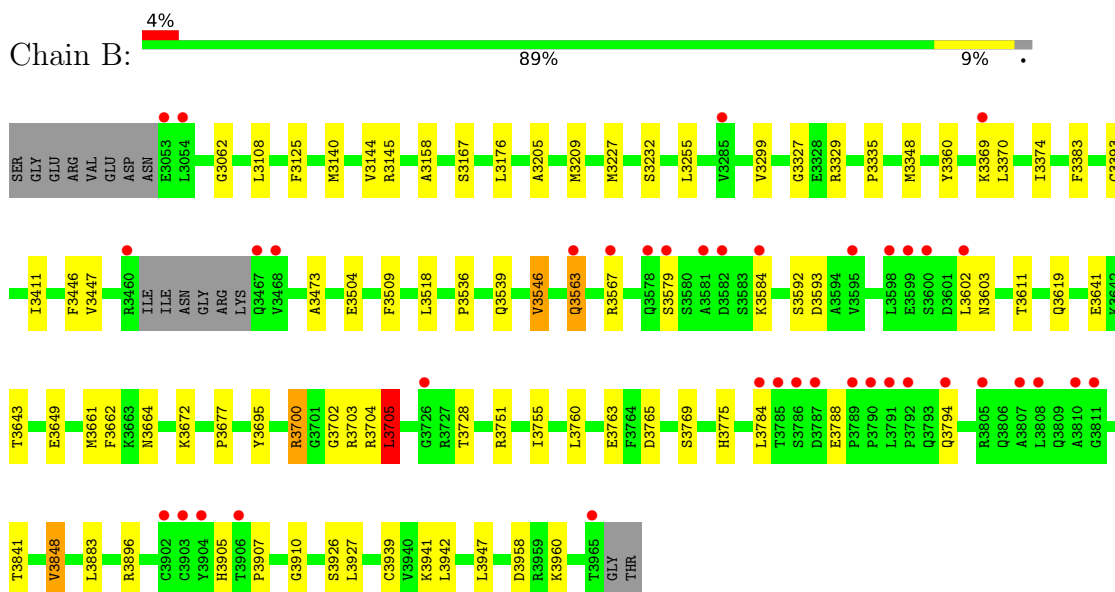
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

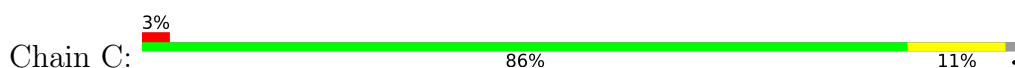
• Molecule 1: RhiE protein

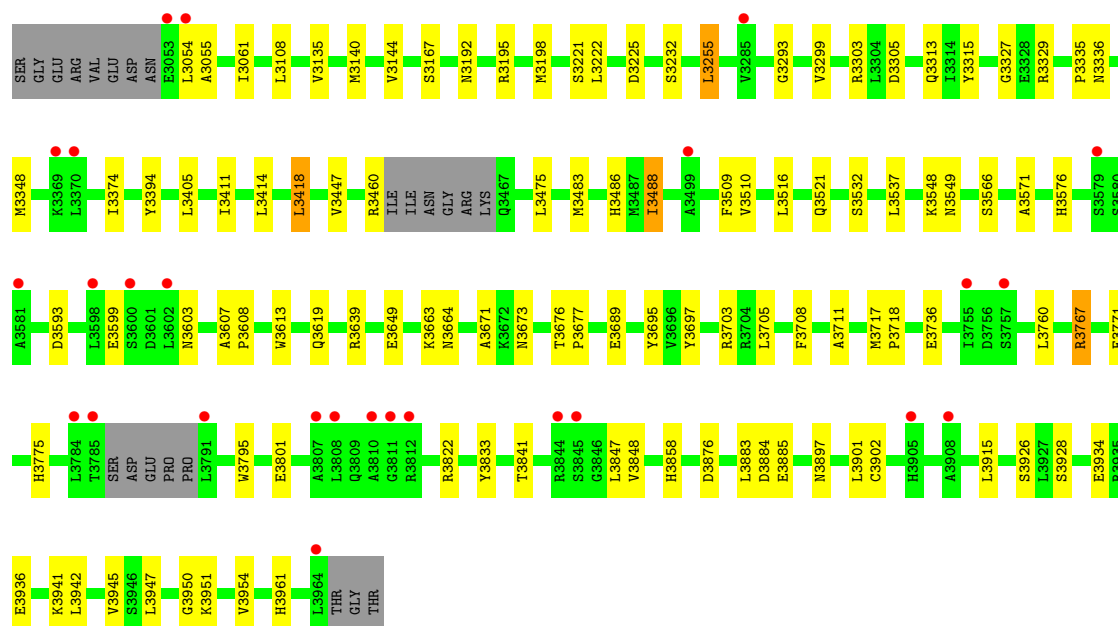


• Molecule 1: RhiE protein

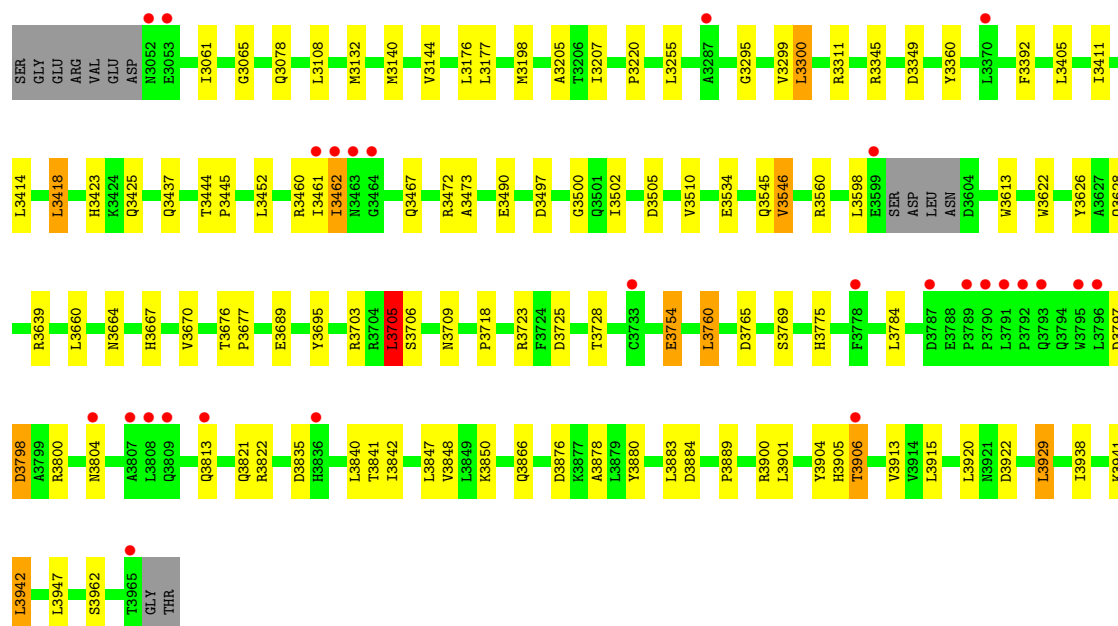
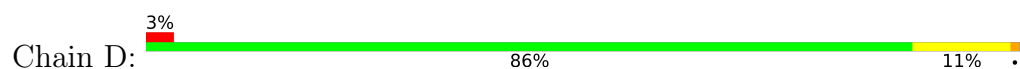


• Molecule 1: RhiE protein





• Molecule 1: RhiE protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	125.51Å 144.13Å 131.30Å 90.00° 96.65° 90.00°	Depositor
Resolution (Å)	48.35 – 2.14 48.35 – 2.14	Depositor EDS
% Data completeness (in resolution range)	99.2 (48.35-2.14) 99.2 (48.35-2.14)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.35 (at 2.14Å)	Xtriage
Refinement program	REFMAC 5.7.0027	Depositor
R, R_{free}	0.181 , 0.227 0.186 , 0.230	Depositor DCC
R_{free} test set	7585 reflections (3.00%)	wwPDB-VP
Wilson B-factor (Å ²)	33.0	Xtriage
Anisotropy	0.236	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 43.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.038 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	29207	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.76% 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:
GOL

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	1.00	3/7275 (0.0%)	1.00	10/9881 (0.1%)
1	B	0.85	0/7194	0.92	4/9774 (0.0%)
1	C	0.82	0/7127	0.90	2/9684 (0.0%)
1	D	0.97	3/7231 (0.0%)	0.98	7/9821 (0.1%)
All	All	0.91	6/28827 (0.0%)	0.95	23/39160 (0.1%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	3452	LEU	C-O	-5.91	1.17	1.24
1	A	3288	ASP	N-CA	5.60	1.52	1.46
1	D	3444	THR	C-O	-5.34	1.19	1.24
1	D	3462	ILE	CA-CB	5.25	1.61	1.54
1	A	3448	VAL	N-CA	-5.11	1.42	1.46
1	A	3386	ALA	CA-CB	-5.03	1.46	1.54

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	3705	LEU	CA-CB-CG	6.21	138.04	116.30
1	D	3835	ASP	N-CA-C	6.10	119.92	112.23
1	B	3546	VAL	CB-CA-C	6.04	116.57	110.65
1	D	3546	VAL	N-CA-CB	-5.89	104.16	112.12
1	D	3132	MET	CA-C-N	-5.85	113.94	119.85
1	D	3132	MET	C-N-CA	-5.85	113.94	119.85
1	D	3065	GLY	N-CA-C	5.62	118.62	111.37
1	A	3759	GLN	N-CA-C	5.56	118.53	108.69
1	A	3629	PRO	CA-C-N	-5.44	114.65	120.03
1	A	3629	PRO	C-N-CA	-5.44	114.65	120.03
1	D	3705	LEU	CA-CB-CG	5.35	135.01	116.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3207	ILE	CA-C-N	-5.25	113.12	118.85
1	A	3207	ILE	C-N-CA	-5.25	113.12	118.85
1	B	3546	VAL	N-CA-CB	-5.21	105.09	112.12
1	A	3494	GLU	CA-C-N	-5.17	114.46	119.78
1	A	3494	GLU	C-N-CA	-5.17	114.46	119.78
1	B	3702	GLY	N-CA-C	5.11	117.63	110.38
1	C	3054	LEU	N-CA-C	5.10	117.62	111.40
1	C	3671	ALA	N-CA-C	5.07	116.50	110.97
1	A	3678	GLN	CA-C-N	5.06	125.05	119.89
1	A	3678	GLN	C-N-CA	5.06	125.05	119.89
1	A	3364	HIS	N-CA-C	-5.03	105.48	110.97
1	D	3938	ILE	N-CA-C	5.02	114.84	108.12

There are no chirality outliers.

There are no planarity outliers.

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	7111	0	6932	37	0
1	B	7035	0	6852	41	0
1	C	6971	0	6754	56	0
1	D	7068	0	6883	55	0
2	A	6	0	8	0	0
3	A	345	0	0	3	0
3	B	207	0	0	3	0
3	C	177	0	0	2	0
3	D	287	0	0	2	0
All	All	29207	0	27429	183	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 3.

All (183) 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:B:3700:ARG:O	1:B:3704:ARG:NH2	2.17	0.78
1:A:3288:ASP:OD1	1:A:3288:ASP:C	2.30	0.75
1:D:3140:MET:HE3	1:D:3144:VAL:CG1	2.18	0.74
1:A:3140:MET:HE3	1:A:3144:VAL:CG1	2.21	0.71
1:A:3664:ASN:HD21	1:B:3664:ASN:HD21	1.41	0.67
1:C:3599:GLU:CB	3:C:4014:HOH:O	2.43	0.67
1:A:3765:ASP:OD1	1:A:3775:HIS:ND1	2.28	0.66
1:C:3847:LEU:HD11	1:C:3915:LEU:HD12	1.78	0.65
1:D:3472:ARG:HD3	1:D:3490:GLU:OE2	1.97	0.65
1:A:3311:ARG:NH2	1:A:3497:ASP:OD1	2.30	0.64
1:B:3751:ARG:NH2	1:B:3765:ASP:OD2	2.30	0.64
1:D:3840:LEU:HD11	1:D:3847:LEU:HD13	1.80	0.62
1:D:3295:GLY:HA3	1:D:3405:LEU:HD13	1.81	0.62
1:B:3728:THR:O	1:B:3784:LEU:HB2	1.99	0.62
1:A:3172:ASP:OD2	3:A:4297:HOH:O	2.16	0.61
1:B:3641:GLU:HG2	1:B:3643:THR:HG23	1.82	0.61
1:C:3885:GLU:OE2	1:C:3961:HIS:NE2	2.31	0.60
1:D:3639:ARG:HD2	3:D:4241:HOH:O	2.01	0.60
1:D:3311:ARG:NH2	1:D:3497:ASP:OD1	2.34	0.60
1:A:3140:MET:HE3	1:A:3144:VAL:HG11	1.83	0.59
1:B:3140:MET:HE3	1:B:3144:VAL:HG11	1.85	0.59
1:B:3140:MET:HE3	1:B:3144:VAL:CG1	2.33	0.58
1:C:3509:PHE:CZ	1:C:3537:LEU:HD22	2.38	0.57
1:A:3785:THR:OG1	1:A:3787:ASP:HB2	2.05	0.57
1:D:3462:ILE:HD11	1:D:3467:GLN:OE1	2.03	0.57
1:A:3901:LEU:HD12	1:A:3942:LEU:HD22	1.85	0.57
1:C:3483:MET:HE1	1:D:3220:PRO:HA	1.86	0.57
1:C:3901:LEU:HD23	1:C:3902:CYS:N	2.20	0.57
1:A:3667:HIS:HB3	1:A:3670:VAL:HB	1.86	0.57
1:A:3607:ALA:HB3	1:A:3608:PRO:HD3	1.88	0.56
1:D:3061:ILE:HD11	1:D:3300:LEU:HD13	1.88	0.55
1:A:3436:ASN:HB3	1:A:3439:ILE:HD12	1.89	0.55
1:D:3345:ARG:O	1:D:3349:ASP:HB2	2.07	0.55
1:C:3695:TYR:HB3	1:C:3705:LEU:HD21	1.88	0.55
1:D:3140:MET:HE3	1:D:3144:VAL:HG12	1.89	0.55
1:D:3705:LEU:HD13	1:D:3709:ASN:HD22	1.72	0.55
1:D:3822:ARG:HD3	1:D:3884:ASP:OD2	2.07	0.55
1:D:3689:GLU:OE1	1:D:3703:ARG:HD3	2.07	0.54
1:D:3177:LEU:HD21	1:D:3207:ILE:HG22	1.90	0.54
1:C:3521:GLN:CG	1:C:3639:ARG:HD2	2.38	0.53
1:A:3287:ALA:HB1	1:A:3367:GLY:O	2.09	0.53
1:D:3728:THR:HG22	1:D:3784:LEU:HD22	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3348:MET:HE1	1:B:3383:PHE:CE1	2.44	0.52
1:D:3676:THR:HB	1:D:3677:PRO:HD2	1.91	0.52
1:D:3505:ASP:OD1	1:D:3560:ARG:NH1	2.43	0.52
1:C:3140:MET:HE3	1:C:3144:VAL:CG1	2.39	0.52
1:A:3658:ASN:O	1:A:3663:LYS:HE2	2.09	0.52
1:D:3078:GLN:NE2	3:D:4083:HOH:O	2.30	0.52
1:C:3695:TYR:HB3	1:C:3705:LEU:CD2	2.40	0.51
1:C:3303:ARG:HD2	1:C:3305:ASP:OD1	2.11	0.51
1:B:3728:THR:O	1:B:3784:LEU:CB	2.59	0.50
1:C:3901:LEU:HD23	1:C:3901:LEU:C	2.36	0.50
1:B:3695:TYR:HB3	1:B:3705:LEU:HD22	1.93	0.50
1:D:3461:ILE:N	1:D:3461:ILE:HD12	2.27	0.50
1:C:3822:ARG:HD3	1:C:3884:ASP:OD2	2.12	0.50
1:D:3392:PHE:CE1	1:D:3445:PRO:HB3	2.47	0.50
1:B:3062:GLY:HA3	1:B:3158:ALA:HB2	1.93	0.49
1:C:3192:ASN:HA	1:C:3195:ARG:O	2.12	0.49
1:A:3754:GLU:HG3	1:B:3677:PRO:HB2	1.94	0.49
1:D:3765:ASP:OD1	1:D:3775:HIS:HA	2.12	0.49
1:A:3793:GLN:HE21	1:A:3793:GLN:HA	1.78	0.49
1:B:3751:ARG:NH2	1:B:3765:ASP:CG	2.70	0.49
1:C:3135:VAL:HG23	3:C:4121:HOH:O	2.12	0.49
1:D:3723:ARG:NE	1:D:3754:GLU:OE2	2.45	0.49
1:D:3797:ASP:O	1:D:3800:ARG:N	2.45	0.49
1:B:3841:THR:HB	1:B:3848:VAL:HG13	1.95	0.49
1:D:3299:VAL:HG13	1:D:3411:ILE:HD11	1.93	0.49
1:D:3140:MET:HE3	1:D:3144:VAL:HG11	1.93	0.49
1:D:3598:LEU:H	1:D:3598:LEU:HD23	1.77	0.49
1:C:3689:GLU:OE1	1:C:3703:ARG:HD3	2.13	0.49
1:D:3878:ALA:HB1	1:D:3915:LEU:HD11	1.93	0.49
1:C:3950:GLY:O	1:C:3954:VAL:HG23	2.13	0.48
1:D:3695:TYR:HB3	1:D:3705:LEU:HD22	1.94	0.48
1:A:3295:GLY:HA3	1:A:3405:LEU:HD13	1.95	0.48
1:C:3942:LEU:HD21	1:C:3945:VAL:HG22	1.96	0.48
1:A:3521:GLN:HE21	1:A:3639:ARG:NH2	2.12	0.47
1:B:3536:PRO:HD2	1:B:3539:GLN:OE1	2.14	0.47
1:D:3510:VAL:HB	1:D:3613:TRP:CH2	2.49	0.47
1:C:3847:LEU:C	1:C:3847:LEU:HD12	2.39	0.47
1:D:3177:LEU:C	1:D:3177:LEU:HD12	2.40	0.47
1:D:3660:LEU:O	1:D:3664:ASN:HB2	2.15	0.47
1:B:3370:LEU:O	1:B:3374:ILE:HD12	2.14	0.47
1:D:3414:LEU:HG	1:D:3418:LEU:HD22	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:3866:GLN:O	1:D:3906:THR:HG23	2.14	0.47
1:B:3905:HIS:O	1:B:3939:CYS:HB3	2.15	0.47
1:D:3880:TYR:OH	1:D:3889:PRO:O	2.31	0.47
1:A:3927:LEU:O	1:A:3944:LYS:HA	2.16	0.46
1:B:3299:VAL:HG13	1:B:3411:ILE:HD11	1.96	0.46
1:A:3518:LEU:HD11	1:A:3641:GLU:HB2	1.97	0.46
1:C:3676:THR:HB	1:C:3677:PRO:CD	2.46	0.46
1:C:3140:MET:HE3	1:C:3144:VAL:HG11	1.98	0.46
1:D:3705:LEU:HD13	1:D:3709:ASN:ND2	2.30	0.46
3:A:4295:HOH:O	1:B:3227:MET:HE2	2.16	0.45
1:D:3901:LEU:HD12	1:D:3942:LEU:HD22	1.97	0.45
1:A:3525:SER:HB2	1:A:3639:ARG:NH1	2.31	0.45
1:D:3929:LEU:C	1:D:3929:LEU:HD23	2.41	0.45
1:C:3394:TYR:CD1	1:C:3447:VAL:HG13	2.51	0.45
1:D:3797:ASP:O	1:D:3798:ASP:C	2.60	0.45
1:B:3958:ASP:OD1	1:B:3960:LYS:HB3	2.17	0.45
1:B:3509:PHE:HA	3:B:4093:HOH:O	2.16	0.45
1:B:3703:ARG:NH2	3:B:4184:HOH:O	2.49	0.45
1:C:3255:LEU:N	1:C:3255:LEU:HD23	2.32	0.45
1:C:3603:ASN:N	1:C:3603:ASN:OD1	2.49	0.45
1:A:3929:LEU:C	1:A:3929:LEU:HD23	2.42	0.45
1:C:3736:GLU:HG3	1:C:3775:HIS:CD2	2.51	0.45
1:C:3833:TYR:CE2	1:C:3858:HIS:HB2	2.52	0.45
1:C:3335:PRO:HG2	1:C:3374:ILE:HD13	1.99	0.44
1:D:3847:LEU:C	1:D:3847:LEU:HD12	2.42	0.44
1:A:3126:ASP:OD2	1:A:3514[B]:HIS:CE1	2.70	0.44
1:D:3502:ILE:HD12	1:D:3626:TYR:CE2	2.52	0.44
1:A:3176:LEU:O	1:A:3252:ALA:HA	2.18	0.44
1:D:3676:THR:HB	1:D:3677:PRO:CD	2.47	0.44
1:D:3706:SER:HB2	1:D:3876:ASP:OD2	2.18	0.44
1:D:3754:GLU:HA	1:D:3760:LEU:HD12	2.00	0.44
1:B:3751:ARG:HH22	1:B:3765:ASP:CG	2.25	0.44
1:A:3786:SER:C	1:A:3788:GLU:H	2.24	0.44
1:B:3205:ALA:HB1	1:B:3209:MET:HE3	2.00	0.44
1:B:3370:LEU:N	3:B:4094:HOH:O	2.35	0.44
1:B:3393:CYS:O	1:B:3446:PHE:HA	2.18	0.44
1:B:3140:MET:CE	1:B:3144:VAL:CG1	2.95	0.43
1:B:3661:MET:HE3	1:B:3662:PHE:CZ	2.52	0.43
1:C:3607:ALA:HB3	1:C:3608:PRO:HD3	2.00	0.43
1:C:3767:ARG:NH1	1:C:3771:GLU:O	2.51	0.43
1:D:3667:HIS:HB3	1:D:3670:VAL:HB	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3641:GLU:HG2	1:A:3643:THR:HG23	2.01	0.43
1:C:3293:GLY:C	1:C:3405:LEU:HD22	2.44	0.43
1:B:3167:SER:OG	1:B:3619:GLN:OE1	2.37	0.43
1:C:3934:GLU:C	1:C:3936:GLU:H	2.25	0.43
1:B:3518:LEU:HD11	1:B:3641:GLU:HB2	2.01	0.43
1:B:3751:ARG:NH1	1:B:3763:GLU:OE1	2.44	0.43
1:B:3927:LEU:HD12	1:B:3927:LEU:C	2.43	0.43
1:A:3563:GLN:HG2	1:A:3567:ARG:NH2	2.33	0.43
1:C:3571:ALA:O	1:C:3576:HIS:O	2.37	0.42
1:C:3795:TRP:CZ2	1:C:3928:SER:HB3	2.53	0.42
1:C:3548:LYS:O	1:C:3549:ASN:C	2.62	0.42
1:C:3717:MET:O	1:C:3718:PRO:C	2.62	0.42
1:B:3907:PRO:HG3	1:B:3939:CYS:SG	2.59	0.42
1:C:3055:ALA:HA	1:C:3303:ARG:HD3	2.02	0.42
1:D:3295:GLY:HA3	1:D:3405:LEU:CD1	2.49	0.42
1:D:3545:GLN:HB3	1:D:3622:TRP:CG	2.54	0.42
1:D:3904:TYR:O	1:D:3905:HIS:HB3	2.19	0.42
1:D:3848:VAL:HA	1:D:3913:VAL:O	2.19	0.42
1:A:3140:MET:HE3	1:A:3144:VAL:HG12	1.99	0.42
1:C:3225:ASP:CG	1:D:3205:ALA:HB2	2.45	0.42
1:C:3475:LEU:O	1:C:3486:HIS:HA	2.19	0.42
1:D:3423:HIS:O	1:D:3425:GLN:HG3	2.19	0.42
1:C:3315:TYR:HB3	1:C:3418:LEU:HG	2.02	0.41
1:A:3548:LYS:O	1:A:3549:ASN:C	2.61	0.41
1:B:3125:PHE:CD1	1:B:3145:ARG:HB3	2.55	0.41
1:B:3563:GLN:HE21	1:B:3563:GLN:H	1.68	0.41
1:C:3414:LEU:HG	1:C:3418:LEU:HD22	2.02	0.41
1:D:3500:GLY:HA2	1:D:3628:GLN:OE1	2.20	0.41
1:A:3641:GLU:OE1	1:A:3643:THR:HG21	2.21	0.41
1:C:3510:VAL:HB	1:C:3613:TRP:CH2	2.55	0.41
1:C:3516:LEU:HD23	1:C:3516:LEU:HA	1.94	0.41
1:C:3061:ILE:HA	1:C:3313:GLN:O	2.20	0.41
1:C:3708:PHE:O	1:C:3711:ALA:HB3	2.20	0.41
1:A:3061:ILE:HA	1:A:3313:GLN:O	2.20	0.41
1:A:3515:LYS:NZ	3:A:4316:HOH:O	2.54	0.41
1:A:3767:ARG:NH1	1:A:3771:GLU:O	2.54	0.41
1:C:3521:GLN:HG2	1:C:3639:ARG:HD2	2.03	0.41
1:D:3360:TYR:O	1:D:3473:ALA:HA	2.21	0.41
1:A:3664:ASN:HD21	1:B:3664:ASN:ND2	2.14	0.41
1:A:3394:TYR:CE2	1:A:3453:ILE:HD11	2.56	0.41
1:A:3525:SER:HB2	1:A:3639:ARG:HH11	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3327:GLY:O	1:B:3329:ARG:HD3	2.20	0.41
1:C:3327:GLY:O	1:C:3329:ARG:HD3	2.21	0.41
1:C:3336:ASN:OD1	1:C:3336:ASN:C	2.64	0.41
1:C:3483:MET:CE	1:D:3220:PRO:HA	2.48	0.41
1:C:3697:TYR:OH	1:C:3876:ASP:OD2	2.32	0.41
1:A:3641:GLU:OE1	1:A:3643:THR:CG2	2.69	0.40
1:B:3592:SER:O	1:B:3593:ASP:HB2	2.20	0.40
1:C:3348:MET:HA	1:C:3488:ILE:HD13	2.03	0.40
1:B:3335:PRO:HG2	1:B:3374:ILE:HD13	2.04	0.40
1:B:3765:ASP:OD1	1:B:3775:HIS:HD2	2.04	0.40
1:C:3167:SER:OG	1:C:3619:GLN:OE1	2.39	0.40
1:C:3299:VAL:HG13	1:C:3411:ILE:HD11	2.04	0.40
1:D:3841:THR:HB	1:D:3848:VAL:HG13	2.03	0.40
1:C:3221:SER:C	1:C:3222:LEU:HD12	2.46	0.40
1:C:3673:ASN:OD1	1:C:3673:ASN:C	2.63	0.40
1:C:3676:THR:HB	1:C:3677:PRO:HD2	2.04	0.40
1:C:3841:THR:HB	1:C:3848:VAL:HG13	2.02	0.40
1:B:3360:TYR:O	1:B:3473:ALA:HA	2.21	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	913/923 (99%)	898 (98%)	14 (2%)	1 (0%)	48	49
1	B	903/923 (98%)	880 (98%)	22 (2%)	1 (0%)	48	49
1	C	895/923 (97%)	874 (98%)	21 (2%)	0	100	100
1	D	907/923 (98%)	873 (96%)	32 (4%)	2 (0%)	43	42
All	All	3618/3692 (98%)	3525 (97%)	89 (2%)	4 (0%)	48	49

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	3798	ASP
1	A	3757	SER
1	B	3910	GLY
1	D	3900	ARG

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	762/778 (98%)	736 (97%)	26 (3%)	32	32
1	B	754/778 (97%)	723 (96%)	31 (4%)	27	24
1	C	742/778 (95%)	720 (97%)	22 (3%)	36	37
1	D	755/778 (97%)	725 (96%)	30 (4%)	28	25
All	All	3013/3112 (97%)	2904 (96%)	109 (4%)	31	30

All (109) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3108	LEU
1	A	3167	SER
1	A	3176	LEU
1	A	3258	MET
1	A	3285	VAL
1	A	3288	ASP
1	A	3299	VAL
1	A	3494	GLU
1	A	3598	LEU
1	A	3664	ASN
1	A	3727	ARG
1	A	3733	CYS
1	A	3760	LEU
1	A	3772	GLN
1	A	3784	LEU
1	A	3793	GLN
1	A	3813	GLN
1	A	3821	GLN

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Mol	Chain	Res	Type
1	A	3848	VAL
1	A	3883	LEU
1	A	3927	LEU
1	A	3934	GLU
1	A	3941	LYS
1	A	3942	LEU
1	A	3947	LEU
1	A	3965	THR
1	B	3108	LEU
1	B	3176	LEU
1	B	3232	SER
1	B	3255	LEU
1	B	3369	LYS
1	B	3447	VAL
1	B	3504	GLU
1	B	3546	VAL
1	B	3563	GLN
1	B	3567	ARG
1	B	3579	SER
1	B	3584	LYS
1	B	3602	LEU
1	B	3603	ASN
1	B	3611	THR
1	B	3649	GLU
1	B	3672	LYS
1	B	3700	ARG
1	B	3705	LEU
1	B	3755	ILE
1	B	3760	LEU
1	B	3769	SER
1	B	3788	GLU
1	B	3794	GLN
1	B	3848	VAL
1	B	3883	LEU
1	B	3896	ARG
1	B	3926	SER
1	B	3941	LYS
1	B	3942	LEU
1	B	3947	LEU
1	C	3108	LEU
1	C	3198	MET
1	C	3232	SER

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Mol	Chain	Res	Type
1	C	3255	LEU
1	C	3418	LEU
1	C	3460	ARG
1	C	3488	ILE
1	C	3532	SER
1	C	3566	SER
1	C	3593	ASP
1	C	3649	GLU
1	C	3663	LYS
1	C	3664	ASN
1	C	3760	LEU
1	C	3767	ARG
1	C	3801	GLU
1	C	3883	LEU
1	C	3897	ASN
1	C	3926	SER
1	C	3941	LYS
1	C	3947	LEU
1	C	3951	LYS
1	D	3108	LEU
1	D	3176	LEU
1	D	3198	MET
1	D	3255	LEU
1	D	3300	LEU
1	D	3418	LEU
1	D	3437	GLN
1	D	3460	ARG
1	D	3534	GLU
1	D	3546	VAL
1	D	3705	LEU
1	D	3718	PRO
1	D	3725	ASP
1	D	3754	GLU
1	D	3760	LEU
1	D	3769	SER
1	D	3804	ASN
1	D	3813	GLN
1	D	3821	GLN
1	D	3842	ILE
1	D	3850	LYS
1	D	3883	LEU
1	D	3906	THR

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Mol	Chain	Res	Type
1	D	3920	LEU
1	D	3922	ASP
1	D	3929	LEU
1	D	3941	LYS
1	D	3942	LEU
1	D	3947	LEU
1	D	3962	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3149	GLN
1	A	3333	ASN
1	A	3423	HIS
1	A	3434	GLN
1	A	3467	GLN
1	A	3521	GLN
1	A	3793	GLN
1	B	3185	HIS
1	B	3325	ASN
1	B	3423	HIS
1	B	3425	GLN
1	B	3563	GLN
1	B	3612	GLN
1	B	3615	ASN
1	B	3664	ASN
1	B	3775	HIS
1	B	3813	GLN
1	B	3952	GLN
1	C	3149	GLN
1	C	3313	GLN
1	C	3325	ASN
1	C	3401	ASN
1	C	3484	ASN
1	C	3545	GLN
1	C	3612	GLN
1	C	3678	GLN
1	C	3737	HIS
1	C	3772	GLN
1	C	3813	GLN
1	C	3921	ASN
1	D	3244	HIS

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Mol	Chain	Res	Type
1	D	3313	GLN
1	D	3325	ASN
1	D	3450	GLN
1	D	3484	ASN
1	D	3709	ASN
1	D	3806	GLN
1	D	3813	GLN
1	D	3866	GLN
1	D	3905	HIS

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 oligosaccharides 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	GOL	A	4001	-	5,5,5	0.82	0	5,5,5	0.98	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	GOL	A	4001	-	-	0/4/4/4	-

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 ⓘ

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	914/923 (99%)	-0.23	13 (1%)	73	77	18, 35, 62, 89	1 (0%)
1	B	907/923 (98%)	0.19	39 (4%)	40	45	27, 48, 79, 118	0
1	C	901/923 (97%)	0.16	26 (2%)	53	57	29, 48, 77, 109	0
1	D	910/923 (98%)	0.00	27 (2%)	52	56	19, 39, 76, 113	1 (0%)
All	All	3632/3692 (98%)	0.03	105 (2%)	53	57	18, 42, 76, 118	2 (0%)

All (105) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	3786	SER	5.7
1	D	3461	ILE	5.4
1	D	3790	PRO	5.1
1	D	3462	ILE	4.7
1	B	3790	PRO	4.5
1	B	3810	ALA	4.3
1	B	3599	GLU	4.2
1	A	3052	ASN	4.1
1	B	3807	ALA	4.1
1	D	3809	GLN	4.1
1	D	3052	ASN	4.0
1	C	3600	SER	4.0
1	C	3785	THR	4.0
1	B	3789	PRO	4.0
1	C	3810	ALA	3.9
1	B	3602	LEU	3.6
1	D	3463	ASN	3.6
1	B	3904	TYR	3.5
1	D	3733	CYS	3.4
1	B	3965	THR	3.4
1	B	3791	LEU	3.4

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Mol	Chain	Res	Type	RSRZ
1	D	3965	THR	3.3
1	D	3796	LEU	3.3
1	D	3599	GLU	3.3
1	D	3778	PHE	3.2
1	C	3791	LEU	3.1
1	A	3965	THR	3.1
1	C	3808	LEU	3.1
1	A	3778	PHE	3.0
1	D	3791	LEU	2.9
1	A	3462	ILE	2.9
1	B	3600	SER	2.9
1	B	3054	LEU	2.9
1	B	3285	VAL	2.8
1	D	3792	PRO	2.8
1	B	3805	ARG	2.8
1	B	3598	LEU	2.8
1	B	3053	GLU	2.8
1	A	3288	ASP	2.8
1	D	3053	GLU	2.8
1	B	3808	LEU	2.8
1	B	3726	GLY	2.8
1	D	3287	ALA	2.7
1	B	3784	LEU	2.7
1	D	3795	TRP	2.7
1	C	3369	LYS	2.7
1	D	3804	ASN	2.7
1	B	3792	PRO	2.6
1	C	3285	VAL	2.6
1	C	3964	LEU	2.5
1	D	3836	HIS	2.5
1	B	3785	THR	2.5
1	C	3054	LEU	2.5
1	B	3579	SER	2.4
1	A	3602	LEU	2.4
1	C	3811	GLY	2.4
1	C	3908	ALA	2.4
1	C	3905	HIS	2.4
1	B	3467	GLN	2.4
1	B	3595	VAL	2.4
1	B	3903	CYS	2.4
1	C	3784	LEU	2.3
1	B	3582	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	3787	ASP	2.3
1	B	3468	VAL	2.3
1	D	3789	PRO	2.3
1	C	3807	ALA	2.3
1	D	3808	LEU	2.3
1	A	3461	ILE	2.3
1	B	3906	THR	2.3
1	B	3902	CYS	2.3
1	A	3787	ASP	2.3
1	B	3787	ASP	2.3
1	C	3602	LEU	2.3
1	D	3370	LEU	2.3
1	D	3464	GLY	2.3
1	C	3579	SER	2.3
1	B	3460	ARG	2.3
1	B	3369	LYS	2.3
1	A	3287	ALA	2.2
1	B	3811	GLY	2.2
1	D	3807	ALA	2.2
1	C	3598	LEU	2.2
1	B	3563	GLN	2.2
1	C	3845	SER	2.2
1	D	3793	GLN	2.1
1	D	3813	GLN	2.1
1	C	3581	ALA	2.1
1	C	3053	GLU	2.1
1	D	3906	THR	2.1
1	B	3567	ARG	2.1
1	C	3499	ALA	2.1
1	B	3578	GLN	2.1
1	C	3812	ARG	2.1
1	C	3844	ARG	2.1
1	C	3370	LEU	2.1
1	C	3757	SER	2.1
1	A	3582	ASP	2.1
1	C	3755	ILE	2.1
1	B	3581	ALA	2.1
1	A	3791	LEU	2.0
1	B	3794	GLN	2.0
1	B	3584	LYS	2.0
1	A	3789	PRO	2.0
1	A	3811	GLY	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 oligosaccharides 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. 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	B-factors($\text{\AA}^2$)	Q<0.9
2	GOL	A	4001	6/6	0.89	0.11	31,34,37,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.