



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:02 PM UTC

PDB ID : 4RSI / pdb_00004rsi
Title : Yeast Smc2-Smc4 hinge domain with extended coiled coils
Authors : Soh, Y.M.; Shin, H.C.; Oh, B.H.
Deposited on : 2014-11-08
Resolution : 2.90 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

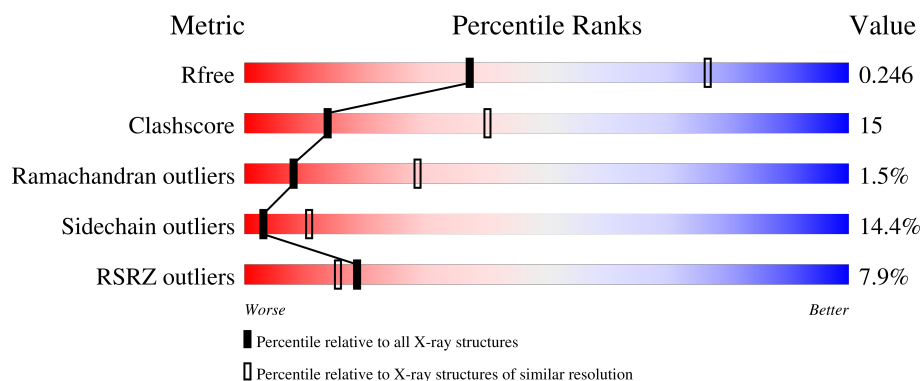
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	397	8% 48% 18% 5% 29%
2	B	397	6% 58% 31% 8%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5252 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.

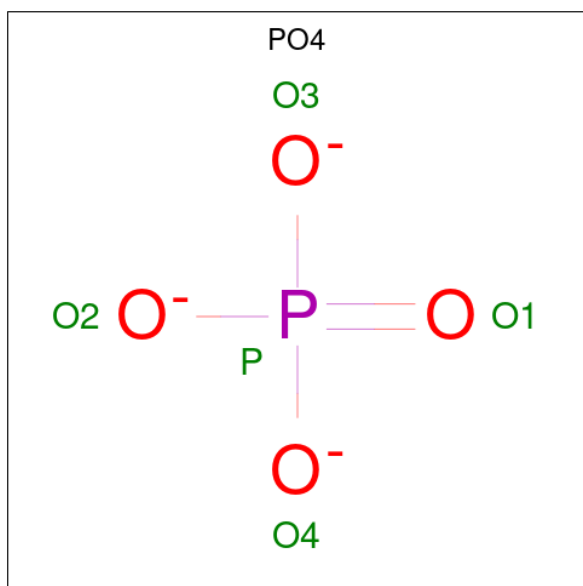
- Molecule 1 is a protein called Structural maintenance of chromosomes protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	283	Total	C	N	O	S	0	0	0
			2210	1396	390	419	5			

- Molecule 2 is a protein called Structural maintenance of chromosomes protein 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	386	Total	C	N	O	S	0	0	0
			3024	1884	537	592	11			

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



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

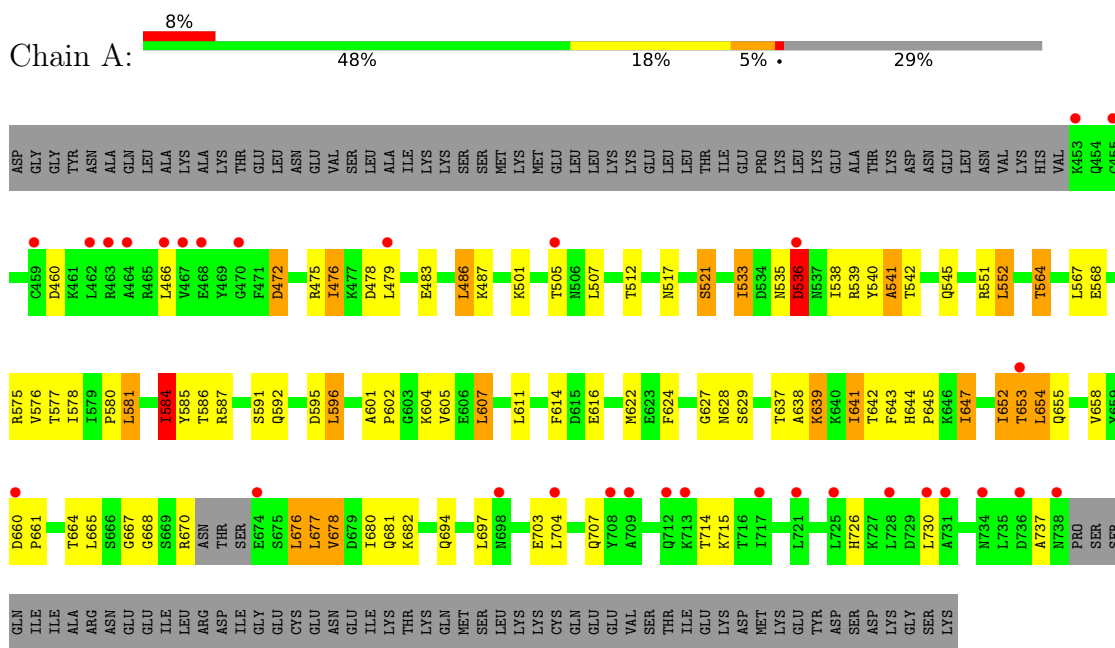
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	7	Total 7	O 7	0	0
4	B	1	Total 1	O 1	0	0

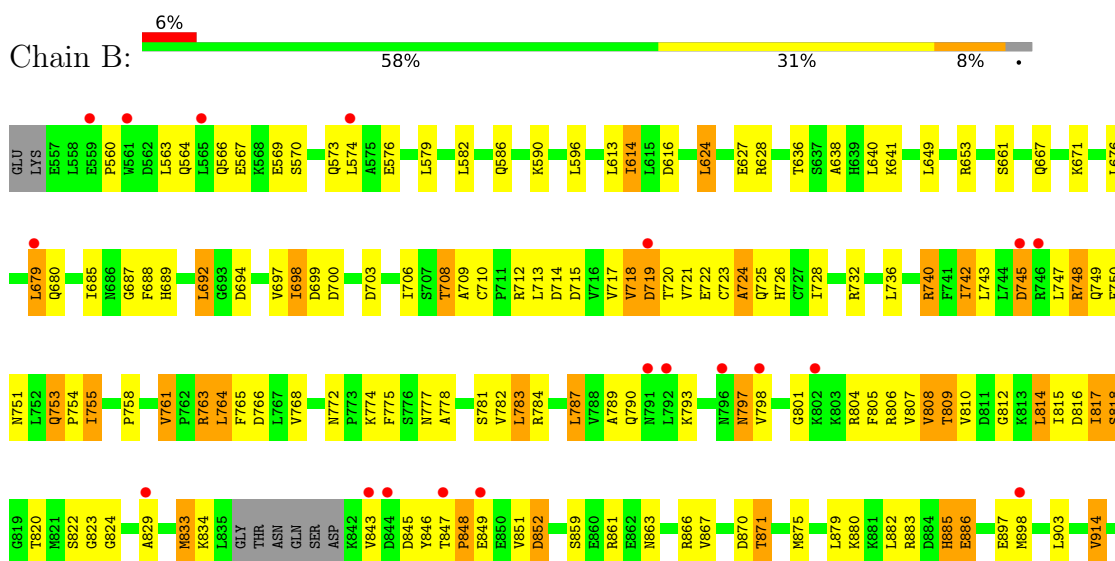
3 Residue-property plots [i](#)

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: Structural maintenance of chromosomes protein 2



• Molecule 2: Structural maintenance of chromosomes protein 4





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	185.26Å 49.71Å 154.28Å 90.00° 92.52° 90.00°	Depositor
Resolution (Å)	38.92 – 2.90 38.92 – 2.90	Depositor EDS
% Data completeness (in resolution range)	80.7 (38.92-2.90) 91.1 (38.92-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.22 (at 2.61Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.223 , 0.266 0.242 , 0.246	Depositor DCC
R_{free} test set	3653 reflections (9.98%)	wwPDB-VP
Wilson B-factor (Å ²)	47.6	Xtriage
Anisotropy	0.241	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 62.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.029 for -h,-k,l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5252	wwPDB-VP
Average B, all atoms (Å ²)	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.45% 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: PO4

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	0.69	0/2243	1.03	11/3034 (0.4%)
2	B	0.58	0/3057	0.93	3/4112 (0.1%)
All	All	0.63	0/5300	0.97	14/7146 (0.2%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	GLY	N-CA-C	-10.35	100.37	112.79
1	A	644	HIS	CA-C-N	6.38	127.82	119.84
1	A	644	HIS	C-N-CA	6.38	127.82	119.84
2	B	724	ALA	N-CA-C	-6.22	104.19	110.97
1	A	584	ILE	CB-CA-C	-6.19	101.86	111.26
1	A	737	ALA	N-CA-C	5.78	118.63	109.96
1	A	601	ALA	CA-C-N	5.73	125.67	119.76
1	A	601	ALA	C-N-CA	5.73	125.67	119.76
1	A	472	ASP	CA-C-N	5.60	125.44	119.28
1	A	472	ASP	C-N-CA	5.60	125.44	119.28
1	A	647	ILE	CB-CA-C	-5.48	105.24	111.59
1	A	576	VAL	N-CA-C	5.12	116.08	108.46
2	B	933	VAL	N-CA-C	5.10	115.24	110.30
1	A	678	VAL	CB-CA-C	-5.07	105.40	112.04

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	2210	0	2195	56	0
2	B	3024	0	3029	107	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	7	0	0	0	0
4	B	1	0	0	0	0
All	All	5252	0	5224	152	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 15.

All (152) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:787:LEU:HB2	2:B:807:VAL:HG22	1.45	0.98
2:B:706:ILE:HD13	2:B:833:MET:HG3	1.60	0.81
2:B:753:GLN:NE2	2:B:754:PRO:O	2.15	0.79
1:A:726:HIS:HE1	1:A:730:LEU:HD13	1.51	0.76
2:B:809:THR:HG22	2:B:812:GLY:H	1.50	0.76
2:B:806:ARG:HG3	2:B:816:ASP:HA	1.68	0.73
2:B:816:ASP:OD1	2:B:817:ILE:N	2.24	0.70
2:B:679:LEU:HD13	2:B:685:ILE:HD13	1.73	0.70
1:A:536:ASP:N	1:A:536:ASP:OD1	2.24	0.69
2:B:709:ALA:O	2:B:806:ARG:NH2	2.19	0.69
2:B:749:GLN:HA	2:B:777:ASN:HD21	1.59	0.67
1:A:637:THR:O	1:A:641:ILE:HG12	1.94	0.66
2:B:763:ARG:HE	2:B:765:PHE:HB3	1.61	0.66
1:A:726:HIS:CD2	2:B:898:MET:HG3	2.32	0.65
2:B:940:ARG:NH1	2:B:944:GLU:OE2	2.29	0.65
2:B:687:GLY:O	2:B:718:VAL:HG12	1.97	0.64
1:A:552:LEU:HD11	1:A:677:LEU:HD23	1.79	0.64
1:A:545:GLN:HB2	1:A:677:LEU:HB2	1.80	0.64
2:B:764:LEU:HB3	2:B:783:LEU:HD23	1.81	0.63
1:A:587:ARG:O	1:A:628:ASN:ND2	2.27	0.63
1:A:575:ARG:HA	2:B:824:GLY:HA2	1.82	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:789:ALA:HB1	2:B:793:LYS:HG3	1.81	0.61
2:B:863:ASN:O	2:B:866:ARG:N	2.35	0.60
1:A:584:ILE:HA	2:B:818:SER:O	2.01	0.60
1:A:660:ASP:HB3	1:A:664:THR:HB	1.83	0.59
2:B:708:THR:HG22	2:B:829:ALA:HB3	1.84	0.59
1:A:652:ILE:HD13	1:A:658:VAL:HG13	1.85	0.59
2:B:720:THR:HG22	2:B:722:GLU:H	1.68	0.59
2:B:694:ASP:HB3	2:B:834:LYS:NZ	2.18	0.58
1:A:507:LEU:HD11	1:A:680:ILE:HG23	1.85	0.58
1:A:643:PHE:HE1	1:A:661:PRO:HA	1.67	0.58
1:A:567:LEU:HD22	2:B:823:GLY:HA3	1.87	0.57
1:A:607:LEU:HD23	1:A:629:SER:O	2.04	0.57
1:A:726:HIS:HD2	2:B:898:MET:HG3	1.69	0.57
1:A:564:THR:O	1:A:568:GLU:HG2	2.04	0.57
1:A:676:LEU:HD22	1:A:680:ILE:HD11	1.86	0.56
1:A:653:THR:HG22	1:A:655:GLN:H	1.70	0.55
2:B:789:ALA:HA	2:B:793:LYS:HE3	1.88	0.55
1:A:726:HIS:CE1	1:A:730:LEU:HD13	2.38	0.55
2:B:706:ILE:HA	2:B:764:LEU:HD11	1.89	0.54
2:B:745:ASP:N	2:B:745:ASP:OD1	2.40	0.54
1:A:521:SER:O	1:A:521:SER:OG	2.20	0.54
2:B:628:ARG:HH21	2:B:883:ARG:HA	1.72	0.54
2:B:750:PHE:HB2	2:B:777:ASN:OD1	2.08	0.53
1:A:577:THR:HG23	2:B:822:SER:HB2	1.90	0.53
1:A:533:ILE:HD11	1:A:677:LEU:CD1	2.38	0.53
2:B:755:ILE:HD12	2:B:763:ARG:HD2	1.89	0.53
2:B:772:ASN:HD22	2:B:774:LYS:HE2	1.74	0.53
2:B:943:GLY:O	2:B:946:ASN:N	2.42	0.53
2:B:710:CYS:O	2:B:713:LEU:HD13	2.08	0.52
1:A:578:ILE:O	1:A:580:PRO:HD3	2.09	0.52
2:B:880:LYS:O	2:B:883:ARG:HB3	2.09	0.52
2:B:671:LYS:HE2	2:B:736:LEU:HA	1.92	0.52
2:B:560:PRO:O	2:B:564:GLN:HB2	2.08	0.52
2:B:942:ARG:O	2:B:946:ASN:HB2	2.10	0.52
1:A:539:ARG:NH2	1:A:540:TYR:OH	2.43	0.52
1:A:596:LEU:HD13	1:A:647:ILE:HG13	1.91	0.52
2:B:566:GLN:HA	2:B:569:GLU:HB3	1.92	0.51
1:A:501:LYS:HD3	2:B:653:ARG:HH22	1.75	0.51
1:A:641:ILE:HG22	1:A:647:ILE:HG21	1.92	0.51
2:B:717:VAL:HG22	2:B:742:ILE:HB	1.92	0.51
2:B:847:THR:O	2:B:849:GLU:N	2.43	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:596:LEU:HB3	2:B:914:VAL:HG23	1.93	0.51
2:B:570:SER:O	2:B:574:LEU:HG	2.11	0.51
2:B:847:THR:C	2:B:849:GLU:H	2.19	0.51
1:A:591:SER:OG	1:A:592:GLN:N	2.44	0.51
1:A:665:LEU:HD21	2:B:725:GLN:HG3	1.93	0.50
2:B:871:THR:O	2:B:875:MET:HG3	2.11	0.49
2:B:564:GLN:HA	2:B:567:GLU:CD	2.38	0.49
2:B:798:VAL:HG22	2:B:807:VAL:CG2	2.43	0.49
2:B:692:LEU:HD22	2:B:713:LEU:HA	1.95	0.49
2:B:698:ILE:HG12	2:B:699:ASP:N	2.28	0.49
2:B:687:GLY:HA3	2:B:719:ASP:OD1	2.13	0.48
1:A:472:ASP:O	1:A:476:ILE:HG13	2.14	0.48
1:A:667:GLY:HA3	2:B:728:ILE:HD13	1.95	0.48
1:A:668:GLY:N	2:B:728:ILE:HG23	2.29	0.48
1:A:535:ASN:OD1	1:A:538:ILE:HD11	2.14	0.48
1:A:476:ILE:HG12	1:A:707:GLN:HG3	1.96	0.47
2:B:712:ARG:HB2	2:B:782:VAL:HG13	1.95	0.47
1:A:653:THR:HG22	1:A:655:GLN:N	2.29	0.47
1:A:475:ARG:O	1:A:478:ASP:N	2.47	0.47
2:B:614:ILE:HD13	2:B:897:GLU:HG2	1.97	0.47
2:B:709:ALA:HB2	2:B:808:VAL:HG11	1.97	0.47
2:B:758:PRO:O	2:B:761:VAL:HG23	2.14	0.47
2:B:721:VAL:HG13	2:B:743:LEU:HD13	1.97	0.47
1:A:517:ASN:OD1	1:A:517:ASN:N	2.48	0.46
2:B:680:GLN:OE1	2:B:688:PHE:HB3	2.16	0.46
2:B:698:ILE:HG12	2:B:699:ASP:H	1.79	0.46
1:A:551:ARG:CZ	1:A:624:PHE:CZ	2.99	0.46
2:B:763:ARG:HD3	2:B:766:ASP:OD2	2.15	0.46
1:A:677:LEU:O	1:A:681:GLN:HG2	2.16	0.46
2:B:763:ARG:NH2	2:B:765:PHE:CD2	2.84	0.46
2:B:649:LEU:HD13	2:B:861:ARG:HG2	1.98	0.46
2:B:667:GLN:O	2:B:671:LYS:HB2	2.16	0.46
2:B:768:VAL:HG13	2:B:833:MET:HE1	1.99	0.45
1:A:535:ASN:O	1:A:536:ASP:C	2.59	0.45
2:B:846:TYR:HB3	2:B:851:VAL:HG23	1.98	0.45
2:B:867:VAL:O	2:B:870:ASP:N	2.48	0.45
1:A:602:PRO:O	1:A:604:LYS:HG3	2.16	0.45
2:B:689:HIS:HB2	2:B:717:VAL:O	2.16	0.45
1:A:665:LEU:CD2	2:B:725:GLN:HG3	2.47	0.45
2:B:778:ALA:O	2:B:781:SER:N	2.45	0.45
2:B:790:GLN:HB3	2:B:810:VAL:CG2	2.46	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:886:GLU:O	2:B:886:GLU:HG3	2.17	0.45
2:B:624:LEU:HD11	2:B:885:HIS:HB3	1.99	0.45
2:B:723:CYS:HA	2:B:726:HIS:HB2	1.99	0.45
2:B:748:ARG:HG3	2:B:749:GLN:N	2.31	0.45
1:A:614:PHE:CG	1:A:622:MET:HG3	2.52	0.44
1:A:637:THR:HG22	1:A:641:ILE:HD11	1.98	0.44
2:B:715:ASP:OD1	2:B:740:ARG:HD2	2.17	0.44
2:B:676:LEU:HB3	2:B:688:PHE:CZ	2.53	0.44
2:B:755:ILE:HG13	2:B:763:ARG:NH1	2.32	0.44
2:B:847:THR:C	2:B:849:GLU:N	2.75	0.44
2:B:586:GLN:NE2	2:B:925:VAL:HG22	2.33	0.44
2:B:790:GLN:HB3	2:B:810:VAL:HG23	1.99	0.44
2:B:774:LYS:HE3	2:B:775:PHE:CZ	2.53	0.44
2:B:782:VAL:HB	2:B:783:LEU:HD12	2.00	0.44
1:A:483:GLU:O	1:A:487:LYS:HG3	2.18	0.44
2:B:751:ASN:N	2:B:751:ASN:OD1	2.49	0.43
2:B:798:VAL:HG13	2:B:805:PHE:O	2.18	0.43
1:A:507:LEU:HD23	1:A:507:LEU:HA	1.87	0.43
1:A:643:PHE:CE1	1:A:661:PRO:HA	2.51	0.43
2:B:563:LEU:O	2:B:567:GLU:HG3	2.19	0.43
2:B:627:GLU:HG2	2:B:882:LEU:HD21	1.99	0.43
1:A:642:THR:HG22	1:A:643:PHE:CD1	2.54	0.43
2:B:720:THR:HG22	2:B:722:GLU:HB2	2.00	0.42
2:B:772:ASN:ND2	2:B:774:LYS:HE2	2.34	0.42
2:B:806:ARG:HB2	2:B:817:ILE:CD1	2.49	0.42
1:A:486:LEU:HD23	1:A:697:LEU:HA	2.00	0.42
2:B:720:THR:HB	2:B:723:CYS:HB3	2.01	0.42
2:B:789:ALA:O	2:B:810:VAL:HG23	2.20	0.42
2:B:724:ALA:O	2:B:728:ILE:HG13	2.19	0.42
1:A:541:ALA:O	1:A:542:THR:C	2.63	0.42
1:A:551:ARG:CZ	1:A:624:PHE:HZ	2.31	0.42
2:B:613:LEU:O	2:B:616:ASP:N	2.52	0.42
2:B:758:PRO:HG2	2:B:805:PHE:CE2	2.54	0.42
2:B:790:GLN:HG2	2:B:793:LYS:HE2	2.01	0.42
2:B:638:ALA:HA	2:B:641:LYS:HE3	2.02	0.41
2:B:694:ASP:HB3	2:B:834:LYS:HZ2	1.84	0.41
2:B:798:VAL:HG11	2:B:815:ILE:HB	2.02	0.41
2:B:712:ARG:C	2:B:714:ASP:N	2.77	0.41
1:A:479:LEU:CB	1:A:704:LEU:HD12	2.50	0.41
1:A:581:LEU:HA	1:A:581:LEU:HD23	1.84	0.41
2:B:763:ARG:NE	2:B:765:PHE:HB3	2.30	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:538:ILE:C	1:A:540:TYR:H	2.29	0.41
2:B:590:LYS:HB2	2:B:921:TYR:CE1	2.56	0.41
2:B:808:VAL:HG13	2:B:814:LEU:HG	2.03	0.41
2:B:797:ASN:OD1	2:B:807:VAL:HG21	2.21	0.41
2:B:573:GLN:HA	2:B:576:GLU:HB3	2.03	0.40
2:B:875:MET:O	2:B:879:LEU:HD13	2.21	0.40
1:A:638:ALA:O	1:A:639:LYS:C	2.64	0.40
2:B:848:PRO:O	2:B:852:ASP:HB2	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	279/397 (70%)	237 (85%)	35 (12%)	7 (2%)	4	17
2	B	382/397 (96%)	335 (88%)	44 (12%)	3 (1%)	16	44
All	All	661/794 (83%)	572 (86%)	79 (12%)	10 (2%)	8	28

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	654	LEU
2	B	700	ASP
1	A	541	ALA
1	A	581	LEU
2	B	848	PRO
1	A	639	LYS
1	A	645	PRO
1	A	536	ASP
1	A	627	GLY
2	B	614	ILE

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	236/359 (66%)	203 (86%)	33 (14%)	3	11
2	B	328/354 (93%)	280 (85%)	48 (15%)	3	10
All	All	564/713 (79%)	483 (86%)	81 (14%)	3	11

All (81) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	460	ASP
1	A	466	LEU
1	A	476	ILE
1	A	486	LEU
1	A	505	THR
1	A	512	THR
1	A	521	SER
1	A	533	ILE
1	A	536	ASP
1	A	552	LEU
1	A	564	THR
1	A	584	ILE
1	A	585	TYR
1	A	586	THR
1	A	595	ASP
1	A	596	LEU
1	A	605	VAL
1	A	607	LEU
1	A	611	LEU
1	A	616	GLU
1	A	641	ILE
1	A	652	ILE
1	A	653	THR
1	A	654	LEU
1	A	670	ARG
1	A	676	LEU
1	A	677	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	678	VAL
1	A	682	LYS
1	A	694	GLN
1	A	703	GLU
1	A	714	THR
1	A	715	LYS
2	B	579	LEU
2	B	582	LEU
2	B	624	LEU
2	B	636	THR
2	B	640	LEU
2	B	661	SER
2	B	679	LEU
2	B	692	LEU
2	B	697	VAL
2	B	698	ILE
2	B	703	ASP
2	B	708	THR
2	B	718	VAL
2	B	719	ASP
2	B	732	ARG
2	B	740	ARG
2	B	742	ILE
2	B	745	ASP
2	B	747	LEU
2	B	748	ARG
2	B	753	GLN
2	B	755	ILE
2	B	761	VAL
2	B	763	ARG
2	B	764	LEU
2	B	783	LEU
2	B	784	ARG
2	B	787	LEU
2	B	797	ASN
2	B	804	ARG
2	B	808	VAL
2	B	809	THR
2	B	814	LEU
2	B	817	ILE
2	B	818	SER
2	B	820	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	833	MET
2	B	843	VAL
2	B	845	ASP
2	B	852	ASP
2	B	859	SER
2	B	871	THR
2	B	885	HIS
2	B	886	GLU
2	B	903	LEU
2	B	914	VAL
2	B	936	LYS
2	B	948	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	565	GLN
1	A	694	GLN
1	A	726	HIS
2	B	564	GLN
2	B	586	GLN
2	B	753	GLN
2	B	772	ASN

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](#)

2 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	B	1001	-	4,4,4	0.85	0	6,6,6	0.63	0
3	PO4	A	801	-	4,4,4	0.76	0	6,6,6	0.45	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 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	283/397 (71%)	0.60	31 (10%) 10 9	37, 73, 145, 151	0
2	B	386/397 (97%)	0.67	22 (5%) 29 23	46, 86, 109, 128	0
All	All	669/794 (84%)	0.64	53 (7%) 18 15	37, 82, 136, 151	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	466	LEU	8.1
1	A	738	ASN	8.0
2	B	792	LEU	5.2
1	A	467	VAL	5.1
2	B	829	ALA	4.8
2	B	746	ARG	4.7
1	A	455	CYS	4.6
2	B	559	GLU	4.2
1	A	725	LEU	4.0
1	A	713	LYS	3.9
2	B	947	ASP	3.7
1	A	453	LYS	3.6
2	B	798	VAL	3.3
1	A	464	ALA	3.2
1	A	728	LEU	3.1
1	A	712	GLN	3.0
2	B	791	ASN	3.0
2	B	898	MET	3.0
2	B	948	LEU	2.9
2	B	796	ASN	2.8
1	A	536	ASP	2.7
2	B	745	ASP	2.7
2	B	561	TRP	2.7
2	B	844	ASP	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	731	ALA	2.6
1	A	730	LEU	2.6
1	A	463	ARG	2.6
1	A	704	LEU	2.5
1	A	734	ASN	2.5
1	A	462	LEU	2.5
1	A	709	ALA	2.4
2	B	843	VAL	2.4
1	A	736	ASP	2.4
1	A	660	ASP	2.3
1	A	708	TYR	2.3
1	A	717	ILE	2.3
1	A	459	CYS	2.3
1	A	479	LEU	2.3
1	A	468	GLU	2.2
2	B	719	ASP	2.2
1	A	721	LEU	2.2
2	B	574	LEU	2.1
2	B	849	GLU	2.1
2	B	679	LEU	2.1
1	A	653	THR	2.1
2	B	802	LYS	2.1
1	A	698	ASN	2.1
2	B	937	ASN	2.1
2	B	565	LEU	2.1
2	B	847	THR	2.1
1	A	674	GLU	2.1
1	A	470	GLY	2.0
1	A	505	THR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

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
3	PO4	B	1001	5/5	0.92	0.11	84,93,93,98	0
3	PO4	A	801	5/5	0.93	0.09	85,95,105,122	0

6.5 Other polymers [i](#)

There are no such residues in this entry.