



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:23 AM UTC

PDB ID : 1MR1 / pdb_00001mr1
Title : Crystal Structure of a Smad4-Ski Complex
Authors : Wu, J.-W.; Krawitz, A.R.; Chai, J.; Li, W.; Zhang, F.; Luo, K.; Shi, Y.
Deposited on : 2002-09-17
Resolution : 2.85 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
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

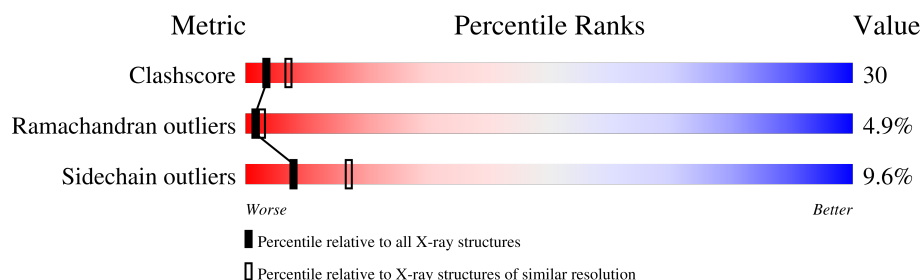
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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))
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	235	46% 31% 6% 17%
1	B	235	39% 36% 6% 18%
2	C	99	43% 44% 9% ••
2	D	99	39% 36% 17% ••

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4684 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 Mothers against decapentaplegic homolog 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	195	Total	C	N	O	S	0	0	0
			1549	978	278	281	12			
1	B	193	Total	C	N	O	S	0	0	0
			1545	979	275	279	12			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	318	MET	-	initiating methionine	UNP Q13485
B	318	MET	-	initiating methionine	UNP Q13485

- Molecule 2 is a protein called Ski oncogene.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	97	Total	C	N	O	S	0	0	0
			789	499	141	140	9			
2	D	96	Total	C	N	O	S	0	0	0
			783	496	140	138	9			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	215	GLY	-	cloning artifact	UNP P12755
C	216	SER	-	cloning artifact	UNP P12755
C	217	HIS	-	cloning artifact	UNP P12755
C	218	MET	-	cloning artifact	UNP P12755
D	215	GLY	-	cloning artifact	UNP P12755
D	216	SER	-	cloning artifact	UNP P12755
D	217	HIS	-	cloning artifact	UNP P12755
D	218	MET	-	cloning artifact	UNP P12755

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	1	Total 1	Zn 1	0	0
3	D	1	Total 1	Zn 1	0	0

- Molecule 4 is water.

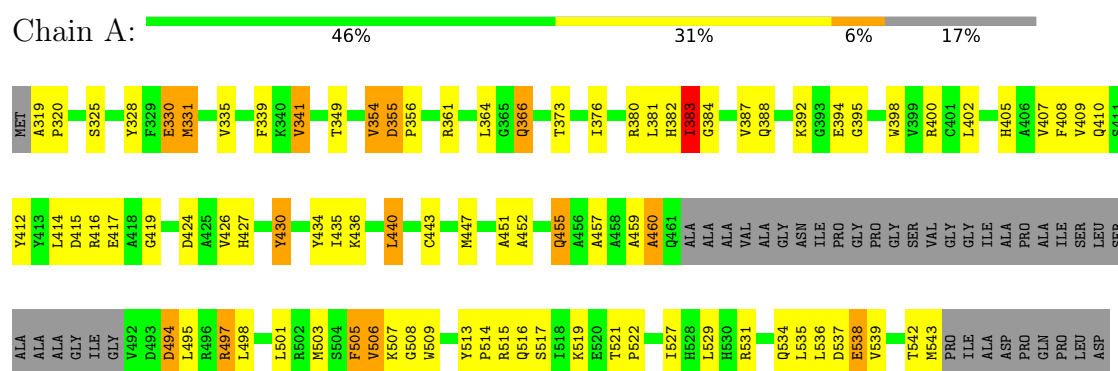
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	7	Total 7	O 7	0	0
4	B	2	Total 2	O 2	0	0
4	C	6	Total 6	O 6	0	0
4	D	1	Total 1	O 1	0	0

3 Residue-property plots

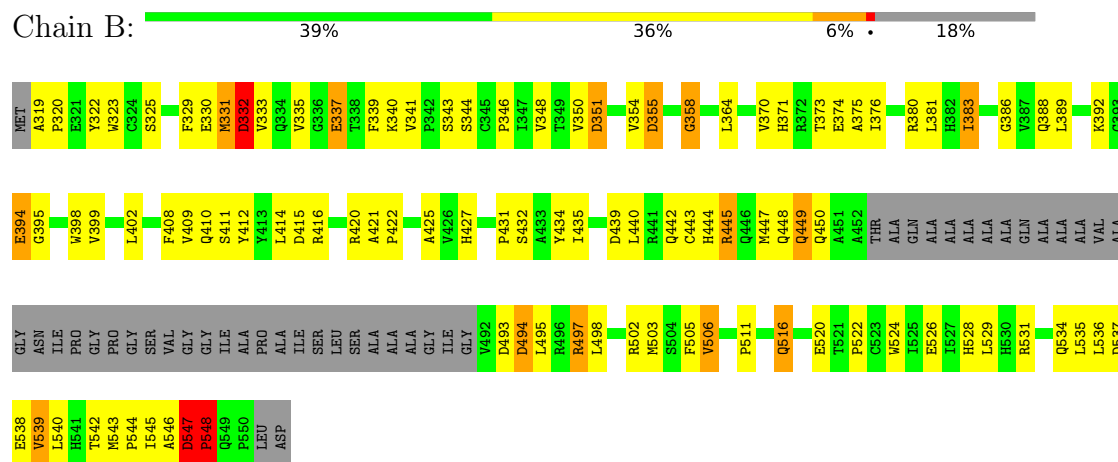
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

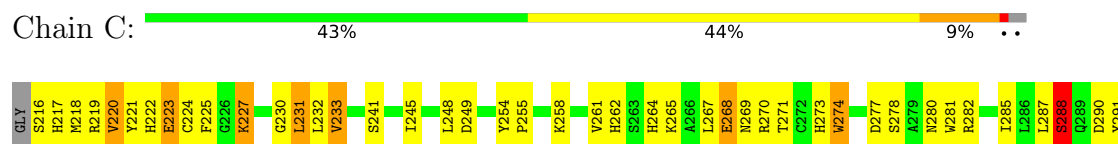
- Molecule 1: Mothers against decapentaplegic homolog 4



- Molecule 1: Mothers against decapentaplegic homolog 4

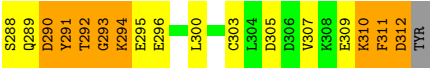
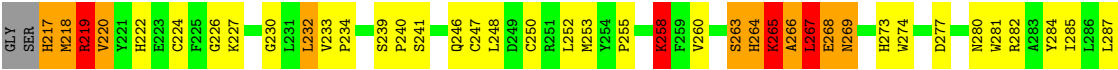


- Molecule 2: Ski oncogene





● Molecule 2: Ski oncogene



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	109.80 Å 109.80 Å 141.10 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.85	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.85)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.231 , 0.280	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4684	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	0.53	0/1586	1.05	12/2149 (0.6%)
1	B	0.44	0/1585	0.98	6/2150 (0.3%)
2	C	0.57	0/811	1.19	8/1093 (0.7%)
2	D	0.62	0/805	1.33	13/1085 (1.2%)
All	All	0.53	0/4787	1.11	39/6477 (0.6%)

There are no bond length outliers.

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	266	ALA	N-CA-C	-10.15	94.97	110.10
1	A	505	PHE	N-CA-C	8.66	122.34	111.69
1	B	539	VAL	N-CA-C	-7.97	105.42	112.12
2	D	263	SER	N-CA-C	-7.90	97.89	110.14
2	D	267	LEU	N-CA-C	-7.86	97.40	109.65
1	B	505	PHE	N-CA-C	7.66	122.39	112.89
2	C	261	VAL	N-CA-C	-7.58	105.62	112.90
2	D	296	GLU	N-CA-C	-7.33	104.95	114.04
2	C	294	LYS	N-CA-C	7.12	125.95	110.80
2	D	255	PRO	N-CA-C	-7.03	102.12	110.70
2	C	241	SER	N-CA-C	6.73	121.36	111.87
2	D	269	ASN	N-CA-C	6.67	121.32	112.25
1	A	455	GLN	N-CA-C	-6.66	103.27	111.33
2	C	295	GLU	N-CA-C	-6.56	103.40	111.40
2	C	288	SER	N-CA-C	6.55	118.76	110.24
1	A	497	ARG	N-CA-C	-6.51	104.03	112.23
1	B	351	ASP	N-CA-C	6.49	116.63	108.45
2	D	226	GLY	N-CA-C	-5.96	99.05	113.18
2	C	225	PHE	CB-CA-C	-5.84	109.82	116.54
2	D	311	PHE	N-CA-C	-5.82	98.41	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	521	THR	CA-C-N	5.78	125.31	119.19
1	A	521	THR	C-N-CA	5.78	125.31	119.19
2	D	232	LEU	N-CA-C	-5.75	99.92	109.46
1	A	430	TYR	N-CA-C	5.58	118.23	110.20
2	D	258	LYS	N-CA-C	-5.53	106.67	113.41
1	A	341	VAL	CA-C-N	5.41	125.17	119.76
1	A	341	VAL	C-N-CA	5.41	125.17	119.76
1	B	394	GLU	N-CA-C	-5.32	106.29	112.89
2	C	233	VAL	CA-C-N	5.27	126.42	119.84
2	C	233	VAL	C-N-CA	5.27	126.42	119.84
2	D	292	THR	N-CA-C	-5.26	103.70	111.81
1	A	457	ALA	N-CA-C	-5.20	98.18	107.28
2	D	219	ARG	N-CA-C	-5.15	100.77	108.96
1	B	421	ALA	CA-C-N	5.12	125.12	119.90
1	B	421	ALA	C-N-CA	5.12	125.12	119.90
1	A	330	GLU	N-CA-C	-5.11	99.08	108.02
1	A	331	MET	CB-CA-C	-5.10	110.71	116.63
1	A	494	ASP	N-CA-C	-5.03	106.66	112.89
2	D	241	SER	N-CA-C	5.00	119.03	113.02

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	1549	0	1509	83	0
1	B	1545	0	1505	94	0
2	C	789	0	757	47	0
2	D	783	0	752	66	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	7	0	0	0	0
4	B	2	0	0	0	0
4	C	6	0	0	1	0
4	D	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4684	0	4523	277	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 30.

All (277) 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:366:GLN:HE21	1:A:366:GLN:N	1.29	1.28
1:A:366:GLN:H	1:A:366:GLN:NE2	1.45	1.14
2:D:218:MET:HB2	2:D:232:LEU:HB3	1.42	1.02
1:B:420:ARG:HH11	1:B:425:ALA:HB2	1.21	1.00
2:D:264:HIS:O	2:D:266:ALA:N	2.01	0.92
2:C:219:ARG:HG3	2:C:219:ARG:HH11	1.36	0.90
2:C:222:HIS:HD2	2:C:224:CYS:H	1.19	0.89
1:A:354:VAL:HG23	1:A:355:ASP:H	1.37	0.88
1:B:331:MET:HE1	1:B:520:GLU:HA	1.57	0.87
2:D:232:LEU:HD21	2:D:307:VAL:HG21	1.58	0.86
2:D:267:LEU:H	2:D:267:LEU:HD23	1.40	0.86
1:A:383:ILE:CG2	1:A:505:PHE:HB3	2.06	0.86
2:D:311:PHE:O	2:D:312:ASP:HB3	1.75	0.84
2:D:222:HIS:HD2	2:D:224:CYS:H	1.26	0.83
1:A:366:GLN:N	1:A:366:GLN:NE2	2.14	0.82
2:D:219:ARG:H	2:D:219:ARG:HD3	1.43	0.82
1:B:427:HIS:CD2	2:C:274:TRP:HZ3	1.99	0.80
1:A:430:TYR:OH	2:D:273:HIS:HD2	1.64	0.80
1:A:356:PRO:HB3	1:A:366:GLN:HG3	1.64	0.80
2:D:246:GLN:HB2	2:D:253:MET:SD	2.23	0.79
2:D:282:ARG:CZ	2:D:312:ASP:OD2	2.30	0.78
1:A:427:HIS:HD2	2:D:274:TRP:HE1	1.30	0.75
2:D:267:LEU:HD23	2:D:267:LEU:N	2.01	0.75
1:B:351:ASP:HA	1:B:383:ILE:HD11	1.68	0.75
2:D:264:HIS:C	2:D:266:ALA:H	1.95	0.73
1:A:319:ALA:HB3	1:A:320:PRO:HD3	1.71	0.71
1:B:420:ARG:NH1	1:B:425:ALA:HB2	2.02	0.71
1:A:366:GLN:HE21	1:A:366:GLN:H	0.73	0.71
1:B:540:LEU:O	1:B:544:PRO:HG3	1.91	0.70
1:A:383:ILE:HG22	1:A:505:PHE:HB3	1.70	0.70
1:A:356:PRO:HA	1:A:366:GLN:OE1	1.92	0.70
2:D:218:MET:HG3	2:D:232:LEU:HD23	1.73	0.69
1:A:427:HIS:CD2	2:D:274:TRP:HE1	2.08	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:370:VAL:HG23	1:B:371:HIS:CD2	2.28	0.69
1:B:374:GLU:HG3	1:B:375:ALA:N	2.07	0.69
2:D:222:HIS:CD2	2:D:224:CYS:H	2.10	0.68
1:A:430:TYR:OH	2:D:273:HIS:CD2	2.47	0.68
1:A:517:SER:OG	1:A:519:LYS:HG2	1.94	0.68
1:B:448:GLN:C	1:B:450:GLN:H	1.99	0.67
1:B:380:ARG:O	1:B:383:ILE:HG23	1.93	0.67
2:C:231:LEU:HD13	2:C:248:LEU:HD21	1.77	0.67
1:B:320:PRO:HG3	1:B:534:GLN:CD	2.21	0.66
1:B:444:HIS:HD2	1:B:535:LEU:HB3	1.61	0.66
1:B:350:VAL:HG13	1:B:364:LEU:HD11	1.79	0.65
2:C:221:TYR:HE2	2:C:223:GLU:OE2	1.79	0.65
2:D:219:ARG:HD3	2:D:219:ARG:N	2.11	0.65
1:A:535:LEU:O	1:A:539:VAL:HG23	1.97	0.65
2:C:230:GLY:HA2	2:C:248:LEU:HG	1.79	0.65
2:C:222:HIS:CD2	2:C:224:CYS:H	2.08	0.64
1:A:426:VAL:HG21	1:A:509:TRP:O	1.96	0.64
1:A:415:ASP:OD2	1:A:427:HIS:HE1	1.81	0.64
1:B:412:TYR:CD1	1:B:422:PRO:HB3	2.32	0.64
1:B:547:ASP:O	1:B:548:PRO:C	2.41	0.64
2:C:219:ARG:HG3	2:C:219:ARG:NH1	2.07	0.64
2:D:230:GLY:HA2	2:D:248:LEU:HG	1.81	0.63
1:B:337:GLU:N	1:B:337:GLU:CD	2.55	0.63
1:A:494:ASP:HA	1:A:497:ARG:HD2	1.79	0.63
2:D:218:MET:HE3	2:D:300:LEU:HD22	1.80	0.63
1:B:320:PRO:HG3	1:B:534:GLN:OE1	1.98	0.63
1:B:354:VAL:O	1:B:355:ASP:HB2	1.97	0.62
2:C:277:ASP:HB3	2:C:280:ASN:ND2	2.14	0.62
2:C:282:ARG:HD3	2:C:308:LYS:O	2.00	0.62
2:C:265:LYS:HD2	2:C:265:LYS:N	2.15	0.62
1:B:351:ASP:C	1:B:383:ILE:HD11	2.24	0.62
2:C:231:LEU:CD1	2:C:248:LEU:HD21	2.30	0.62
2:D:218:MET:HE1	2:D:300:LEU:HB3	1.80	0.61
2:D:263:SER:OG	2:D:266:ALA:HB3	1.99	0.61
2:D:220:VAL:HG13	2:D:285:ILE:HG23	1.82	0.61
1:B:331:MET:CE	1:B:520:GLU:HA	2.29	0.61
1:B:443:CYS:O	1:B:447:MET:HG3	2.00	0.61
2:D:267:LEU:HD12	2:D:269:ASN:OD1	2.00	0.61
1:B:331:MET:O	1:B:333:VAL:N	2.34	0.61
1:A:531:ARG:HH21	1:A:535:LEU:HD21	1.66	0.60
1:B:337:GLU:CD	1:B:337:GLU:H	2.09	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:350:VAL:CG1	1:B:364:LEU:HD11	2.31	0.60
1:A:398:TRP:CE2	1:A:436:LYS:HB2	2.35	0.60
1:A:430:TYR:HE1	2:D:273:HIS:HB3	1.66	0.60
1:B:322:TYR:CD2	1:B:340:LYS:HB3	2.37	0.59
1:A:339:PHE:HE1	1:A:341:VAL:HG22	1.66	0.59
1:B:537:ASP:C	1:B:539:VAL:H	2.09	0.59
2:C:249:ASP:HB2	2:C:264:HIS:CD2	2.37	0.59
1:A:383:ILE:HG21	1:A:505:PHE:HB3	1.83	0.58
2:D:289:GLN:O	2:D:291:TYR:N	2.32	0.58
1:B:427:HIS:CD2	2:C:274:TRP:CZ3	2.88	0.58
2:C:220:VAL:HG13	2:C:285:ILE:HG23	1.85	0.58
1:A:430:TYR:CE1	2:D:273:HIS:HB3	2.38	0.58
1:A:515:ARG:HG3	1:A:515:ARG:HH11	1.69	0.57
1:A:513:TYR:HB3	1:A:514:PRO:HD2	1.87	0.57
1:B:351:ASP:CA	1:B:383:ILE:HD11	2.34	0.57
1:B:412:TYR:CE1	1:B:422:PRO:HB3	2.39	0.57
1:A:409:VAL:HG12	1:A:410:GLN:N	2.19	0.56
1:A:412:TYR:CD2	1:A:498:LEU:HD23	2.40	0.56
1:A:531:ARG:NH2	1:A:535:LEU:HD21	2.20	0.56
1:B:409:VAL:HG22	1:B:503:MET:HB3	1.87	0.56
2:D:295:GLU:O	2:D:295:GLU:HG2	2.06	0.56
1:A:354:VAL:HG23	1:A:355:ASP:N	2.17	0.56
1:B:445:ARG:HD3	1:B:449:GLN:NE2	2.20	0.56
1:B:416:ARG:HD2	1:B:442:GLN:NE2	2.21	0.56
1:A:394:GLU:HG2	1:A:440:LEU:CD1	2.36	0.55
2:C:255:PRO:HD2	2:C:258:LYS:HB2	1.87	0.55
2:C:267:LEU:HD23	2:C:268:GLU:O	2.06	0.55
2:D:260:VAL:HG11	2:D:284:TYR:HD1	1.72	0.55
1:A:495:LEU:HB3	1:A:536:LEU:CD2	2.37	0.55
2:D:260:VAL:HG21	2:D:281:TRP:HB2	1.90	0.54
1:B:329:PHE:HB2	1:B:524:TRP:NE1	2.23	0.54
2:C:219:ARG:NH1	2:C:219:ARG:CG	2.70	0.54
1:B:344:SER:O	1:B:346:PRO:HD3	2.08	0.54
1:B:364:LEU:N	1:B:364:LEU:HD12	2.24	0.53
1:B:412:TYR:CD2	1:B:498:LEU:HD23	2.43	0.53
1:A:536:LEU:C	1:A:536:LEU:HD13	2.34	0.53
1:B:546:ALA:O	1:B:547:ASP:HB2	2.08	0.53
2:D:219:ARG:N	2:D:219:ARG:CD	2.72	0.53
2:D:247:CYS:HB3	2:D:250:CYS:SG	2.48	0.53
2:C:219:ARG:HB2	2:C:291:TYR:CE1	2.43	0.53
1:A:382:HIS:HB3	1:A:405:HIS:CD2	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:290:ASP:HB2	2:D:240:PRO:HG2	1.89	0.53
2:D:220:VAL:CG1	2:D:285:ILE:HG23	2.39	0.53
1:B:531:ARG:HD3	1:B:531:ARG:O	2.08	0.53
1:A:382:HIS:HD2	1:A:405:HIS:NE2	2.07	0.52
1:B:440:LEU:HD11	1:B:535:LEU:HD12	1.91	0.52
2:C:218:MET:HE1	2:C:303:CYS:HB3	1.91	0.52
2:D:305:ASP:O	2:D:309:GLU:HG3	2.09	0.52
1:A:506:VAL:HG22	1:A:507:LYS:HG2	1.91	0.52
1:B:439:ASP:OD2	1:B:442:GLN:HB2	2.10	0.52
2:C:265:LYS:HD2	2:C:265:LYS:H	1.74	0.52
2:D:282:ARG:HH11	2:D:282:ARG:HG3	1.75	0.52
1:A:328:TYR:CD2	1:A:335:VAL:HB	2.46	0.51
1:B:394:GLU:CD	1:B:531:ARG:HE	2.18	0.51
1:A:424:ASP:O	1:A:424:ASP:CG	2.53	0.51
1:A:440:LEU:HD11	1:A:531:ARG:HG3	1.93	0.51
1:B:434:TYR:C	1:B:435:ILE:HD12	2.36	0.51
1:A:539:VAL:O	1:A:543:MET:HB2	2.11	0.51
2:D:222:HIS:HD2	2:D:224:CYS:N	2.02	0.51
1:A:427:HIS:HD2	2:D:274:TRP:NE1	2.06	0.51
1:B:448:GLN:C	1:B:450:GLN:N	2.65	0.51
1:B:542:THR:O	1:B:543:MET:HG2	2.11	0.50
1:A:361:ARG:HH11	1:A:361:ARG:HG2	1.75	0.50
1:A:392:LYS:HD2	1:A:398:TRP:NE1	2.27	0.50
1:A:388:GLN:HB3	1:A:400:ARG:HB3	1.92	0.50
1:A:412:TYR:CE2	1:A:498:LEU:HD23	2.47	0.50
1:A:443:CYS:O	1:A:447:MET:HB2	2.12	0.50
1:A:459:ALA:O	1:A:460:ALA:HB2	2.11	0.50
1:B:511:PRO:HA	1:B:516:GLN:HE21	1.77	0.50
2:D:267:LEU:O	2:D:268:GLU:HB2	2.12	0.50
2:C:219:ARG:CB	2:C:288:SER:HB2	2.41	0.50
1:B:445:ARG:HG2	1:B:449:GLN:HE21	1.76	0.49
1:B:546:ALA:O	1:B:547:ASP:CB	2.60	0.49
1:A:373:THR:OG1	1:A:376:ILE:HG13	2.11	0.49
1:A:515:ARG:HG3	1:A:515:ARG:NH1	2.27	0.49
1:B:392:LYS:HD2	1:B:398:TRP:CD1	2.47	0.49
2:C:291:TYR:O	2:C:292:THR:C	2.56	0.49
2:D:267:LEU:H	2:D:267:LEU:CD2	2.15	0.49
1:B:414:LEU:HB3	2:C:274:TRP:CZ3	2.48	0.49
2:D:240:PRO:HG3	2:D:311:PHE:HB3	1.95	0.49
2:C:282:ARG:NH1	4:C:704:HOH:O	2.45	0.48
1:B:445:ARG:HD3	1:B:449:GLN:HE22	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:493:ASP:O	1:B:494:ASP:C	2.56	0.48
2:D:217:HIS:CD2	2:D:217:HIS:N	2.80	0.48
2:D:260:VAL:HG12	2:D:260:VAL:O	2.14	0.48
2:C:222:HIS:CD2	2:C:222:HIS:C	2.91	0.48
1:A:495:LEU:CB	1:A:536:LEU:HD21	2.44	0.48
2:D:219:ARG:NH1	2:D:288:SER:OG	2.47	0.48
2:D:303:CYS:O	2:D:307:VAL:HG23	2.14	0.48
1:B:330:GLU:HA	1:B:522:PRO:O	2.14	0.47
1:B:447:MET:CE	1:B:536:LEU:HG	2.45	0.47
1:B:440:LEU:O	1:B:443:CYS:HB3	2.15	0.47
1:B:440:LEU:HD13	1:B:440:LEU:C	2.39	0.47
1:B:450:GLN:O	1:B:450:GLN:HG2	2.15	0.47
1:B:408:PHE:O	1:B:503:MET:HA	2.14	0.47
1:B:330:GLU:HG3	1:B:335:VAL:HG21	1.97	0.47
1:B:537:ASP:C	1:B:539:VAL:N	2.71	0.47
1:A:416:ARG:O	1:A:419:GLY:N	2.48	0.47
2:D:310:LYS:HE2	2:D:311:PHE:CZ	2.49	0.47
2:C:254:TYR:OH	2:C:262:HIS:CE1	2.68	0.47
1:B:319:ALA:HB3	1:B:320:PRO:HD3	1.96	0.47
1:B:388:GLN:HG3	1:B:402:LEU:HD11	1.97	0.47
2:C:216:SER:HA	2:C:233:VAL:HG13	1.98	0.46
1:A:387:VAL:CG1	1:A:407:VAL:HG21	2.45	0.46
1:A:495:LEU:HB3	1:A:536:LEU:HD21	1.96	0.46
1:B:348:VAL:CG1	1:B:389:LEU:HB2	2.46	0.46
2:D:265:LYS:HE3	2:D:265:LYS:HB2	1.66	0.46
1:A:407:VAL:HG11	1:A:503:MET:SD	2.56	0.46
1:A:434:TYR:C	1:A:435:ILE:HD12	2.40	0.46
1:A:452:ALA:O	1:A:455:GLN:HB3	2.15	0.46
2:D:277:ASP:HB3	2:D:280:ASN:ND2	2.31	0.46
1:A:383:ILE:HG21	1:A:505:PHE:CB	2.45	0.46
1:A:394:GLU:HG2	1:A:440:LEU:HD13	1.97	0.45
1:A:408:PHE:CG	1:A:508:GLY:HA2	2.51	0.45
1:B:511:PRO:O	1:B:516:GLN:NE2	2.49	0.45
2:C:282:ARG:HG2	2:C:308:LYS:HG2	1.98	0.45
1:A:416:ARG:O	1:A:417:GLU:C	2.59	0.45
1:A:382:HIS:CD2	1:A:405:HIS:NE2	2.85	0.45
2:D:282:ARG:NH2	2:D:312:ASP:OD2	2.50	0.45
2:C:292:THR:O	2:C:292:THR:HG23	2.16	0.45
2:D:260:VAL:O	2:D:260:VAL:CG1	2.64	0.45
1:B:330:GLU:CD	1:B:335:VAL:HG21	2.41	0.45
1:A:398:TRP:CZ2	1:A:436:LYS:HB2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:323:TRP:HE1	1:B:341:VAL:CG1	2.30	0.45
2:C:282:ARG:NH1	2:C:308:LYS:O	2.40	0.45
1:A:414:LEU:HB3	1:A:427:HIS:CD2	2.51	0.44
1:A:339:PHE:CE1	1:A:341:VAL:HG22	2.48	0.44
1:B:323:TRP:NE1	1:B:341:VAL:CG1	2.80	0.44
1:B:339:PHE:HE2	1:B:358:GLY:HA2	1.81	0.44
2:C:219:ARG:HB2	2:C:291:TYR:HE1	1.82	0.44
1:A:494:ASP:O	1:A:497:ARG:HG3	2.16	0.44
1:B:348:VAL:HG13	1:B:389:LEU:HB2	2.00	0.44
2:C:218:MET:CE	2:C:303:CYS:HB3	2.48	0.44
2:D:258:LYS:HB3	2:D:258:LYS:NZ	2.32	0.44
1:A:531:ARG:HA	1:A:531:ARG:HD2	1.80	0.44
1:B:531:ARG:HD3	1:B:531:ARG:C	2.43	0.44
2:D:293:GLY:O	2:D:294:LYS:C	2.60	0.44
1:A:409:VAL:CG1	1:A:410:GLN:N	2.81	0.44
1:B:494:ASP:O	1:B:497:ARG:HB2	2.17	0.44
2:D:217:HIS:CE1	2:D:233:VAL:HG13	2.52	0.44
2:D:217:HIS:HB2	2:D:218:MET:H	1.58	0.44
2:D:292:THR:O	2:D:292:THR:HG22	2.18	0.43
1:B:389:LEU:HD23	1:B:399:VAL:HG22	1.99	0.43
2:D:282:ARG:HG3	2:D:282:ARG:NH1	2.33	0.43
1:A:361:ARG:HG2	1:A:361:ARG:NH1	2.33	0.43
1:B:495:LEU:C	1:B:497:ARG:H	2.26	0.43
2:C:311:PHE:O	2:C:312:ASP:C	2.61	0.43
1:B:330:GLU:CG	1:B:335:VAL:HG21	2.48	0.43
1:B:444:HIS:CD2	1:B:535:LEU:HB3	2.47	0.43
1:A:501:LEU:HB2	1:A:527:ILE:HB	2.00	0.42
1:A:536:LEU:C	1:A:538:GLU:H	2.27	0.42
1:B:354:VAL:O	1:B:354:VAL:HG23	2.19	0.42
1:A:349:THR:HB	1:A:361:ARG:HD2	2.01	0.42
1:A:380:ARG:O	1:A:383:ILE:HG12	2.18	0.42
1:B:444:HIS:CD2	1:B:535:LEU:HD13	2.54	0.42
2:C:269:ASN:CG	2:C:270:ARG:H	2.26	0.42
2:D:292:THR:O	2:D:293:GLY:C	2.61	0.42
1:A:330:GLU:O	1:A:331:MET:HB2	2.19	0.42
1:B:415:ASP:OD2	1:B:427:HIS:HE1	2.01	0.42
2:D:311:PHE:O	2:D:312:ASP:CB	2.55	0.42
1:B:545:ILE:HG22	1:B:546:ALA:N	2.34	0.42
1:B:415:ASP:OD2	1:B:427:HIS:CE1	2.73	0.42
1:A:366:GLN:HE21	1:A:366:GLN:CA	2.15	0.42
1:B:502:ARG:NH2	1:B:526:GLU:OE2	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:246:GLN:HA	2:D:252:LEU:O	2.19	0.42
1:A:447:MET:HE1	1:A:535:LEU:HB2	2.02	0.42
1:B:537:ASP:O	1:B:539:VAL:N	2.53	0.42
2:C:231:LEU:HD13	2:C:248:LEU:CD2	2.47	0.42
1:B:331:MET:O	1:B:332:ASP:OD1	2.38	0.42
1:A:495:LEU:HB3	1:A:536:LEU:HD23	2.01	0.41
1:B:414:LEU:HD22	2:C:274:TRP:CZ3	2.54	0.41
1:B:431:PRO:O	1:B:432:SER:HB2	2.20	0.41
2:C:269:ASN:CG	2:C:270:ARG:N	2.78	0.41
2:D:230:GLY:CA	2:D:248:LEU:HG	2.48	0.41
1:A:320:PRO:HG3	1:A:534:GLN:OE1	2.20	0.41
1:A:503:MET:O	1:A:503:MET:HG3	2.19	0.41
1:B:323:TRP:HE1	1:B:341:VAL:HG12	1.84	0.41
2:C:223:GLU:CB	2:C:227:LYS:HD2	2.50	0.41
2:C:232:LEU:HD21	2:C:307:VAL:HG21	2.02	0.41
2:C:273:HIS:N	2:C:273:HIS:CD2	2.88	0.41
2:D:218:MET:CE	2:D:300:LEU:HB3	2.46	0.41
1:B:331:MET:HG3	1:B:376:ILE:HD11	2.02	0.41
2:D:267:LEU:N	2:D:267:LEU:CD2	2.71	0.41
1:A:451:ALA:HB1	1:A:543:MET:CE	2.51	0.41
1:B:448:GLN:O	1:B:450:GLN:N	2.53	0.41
2:D:222:HIS:CD2	2:D:222:HIS:C	2.98	0.41
1:B:325:SER:OG	1:B:528:HIS:HB2	2.21	0.41
1:B:331:MET:C	1:B:333:VAL:H	2.28	0.41
1:A:400:ARG:HG2	1:A:402:LEU:CD2	2.50	0.41
1:A:538:GLU:O	1:A:542:THR:HG22	2.21	0.41
1:B:414:LEU:HD22	2:C:274:TRP:CH2	2.56	0.41
2:C:278:SER:O	2:C:281:TRP:HD1	2.04	0.41
2:D:265:LYS:O	2:D:266:ALA:C	2.62	0.41
2:C:231:LEU:O	2:C:245:ILE:HA	2.21	0.41
2:D:290:ASP:OD1	2:D:290:ASP:N	2.54	0.41
1:B:444:HIS:O	1:B:447:MET:N	2.54	0.41
2:D:218:MET:CB	2:D:232:LEU:HB3	2.30	0.40
1:B:497:ARG:HG3	1:B:497:ARG:NH1	2.36	0.40
2:C:300:LEU:HD23	2:C:300:LEU:HA	1.84	0.40
1:A:330:GLU:HA	1:A:522:PRO:O	2.22	0.40
1:B:350:VAL:O	1:B:386:GLY:HA3	2.21	0.40
1:B:440:LEU:HD11	1:B:535:LEU:CD1	2.51	0.40
2:C:310:LYS:HE2	2:C:311:PHE:CZ	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	191/235 (81%)	164 (86%)	21 (11%)	6 (3%)	3	7
1	B	189/235 (80%)	159 (84%)	19 (10%)	11 (6%)	1	2
2	C	95/99 (96%)	80 (84%)	12 (13%)	3 (3%)	3	7
2	D	94/99 (95%)	74 (79%)	12 (13%)	8 (8%)	0	1
All	All	569/668 (85%)	477 (84%)	64 (11%)	28 (5%)	1	3

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	384	GLY
1	B	332	ASP
1	B	355	ASP
1	B	547	ASP
2	C	294	LYS
2	D	265	LYS
2	D	268	GLU
2	D	290	ASP
1	A	460	ALA
2	C	292	THR
2	D	293	GLY
2	D	294	LYS
1	B	449	GLN
1	B	538	GLU
2	D	310	LYS
1	A	355	ASP
1	B	358	GLY
1	B	506	VAL
1	B	548	PRO
2	D	291	TYR
1	A	354	VAL
1	B	494	ASP

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Mol	Chain	Res	Type
2	C	217	HIS
1	B	331	MET
1	A	383	ILE
1	A	395	GLY
1	B	395	GLY
2	D	239	SER

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	164/187 (88%)	153 (93%)	11 (7%)	15	31
1	B	167/187 (89%)	152 (91%)	15 (9%)	9	19
2	C	86/87 (99%)	76 (88%)	10 (12%)	5	10
2	D	85/87 (98%)	73 (86%)	12 (14%)	3	6
All	All	502/548 (92%)	454 (90%)	48 (10%)	8	17

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	325	SER
1	A	364	LEU
1	A	366	GLN
1	A	381	LEU
1	A	383	ILE
1	A	440	LEU
1	A	506	VAL
1	A	516	GLN
1	A	529	LEU
1	A	537	ASP
1	A	538	GLU
1	B	332	ASP
1	B	337	GLU
1	B	343	SER
1	B	373	THR

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Mol	Chain	Res	Type
1	B	381	LEU
1	B	383	ILE
1	B	410	GLN
1	B	411	SER
1	B	445	ARG
1	B	497	ARG
1	B	506	VAL
1	B	516	GLN
1	B	529	LEU
1	B	547	ASP
1	B	548	PRO
2	C	220	VAL
2	C	223	GLU
2	C	227	LYS
2	C	231	LEU
2	C	268	GLU
2	C	271	THR
2	C	274	TRP
2	C	287	LEU
2	C	288	SER
2	C	304	LEU
2	D	217	HIS
2	D	218	MET
2	D	219	ARG
2	D	220	VAL
2	D	227	LYS
2	D	234	PRO
2	D	258	LYS
2	D	264	HIS
2	D	265	LYS
2	D	267	LEU
2	D	287	LEU
2	D	312	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	366	GLN
1	A	382	HIS
1	A	427	HIS
1	A	442	GLN
1	A	446	GLN

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Mol	Chain	Res	Type
1	B	334	GLN
1	B	382	HIS
1	B	388	GLN
1	B	405	HIS
1	B	427	HIS
1	B	442	GLN
1	B	444	HIS
1	B	449	GLN
1	B	516	GLN
1	B	528	HIS
1	B	541	HIS
2	C	222	HIS
2	C	269	ASN
2	C	280	ASN
2	D	217	HIS
2	D	222	HIS
2	D	264	HIS
2	D	273	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.