



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:00 PM UTC

PDB ID : 1NOB / pdb_00001nob
Title : KNOB DOMAIN FROM ADENOVIRUS SEROTYPE 12
Authors : Bewley, M.C.; Springer, K.; Zhang, Y.B.; Freimuth, P.; Flanagan, J.M.
Deposited on : 1999-05-05
Resolution : 2.60 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

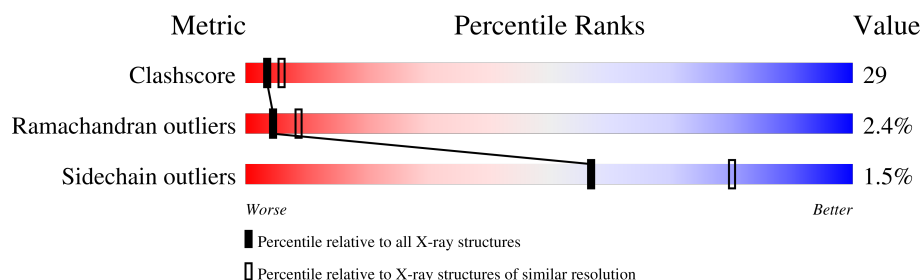
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)

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	185	55% 42% .
1	B	185	52% 44% .
1	C	185	49% 49% .
1	D	185	42% 52% 6%
1	E	185	49% 47% .
1	F	185	48% 49% .

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 8406 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 PROTEIN (FIBER KNOB PROTEIN).

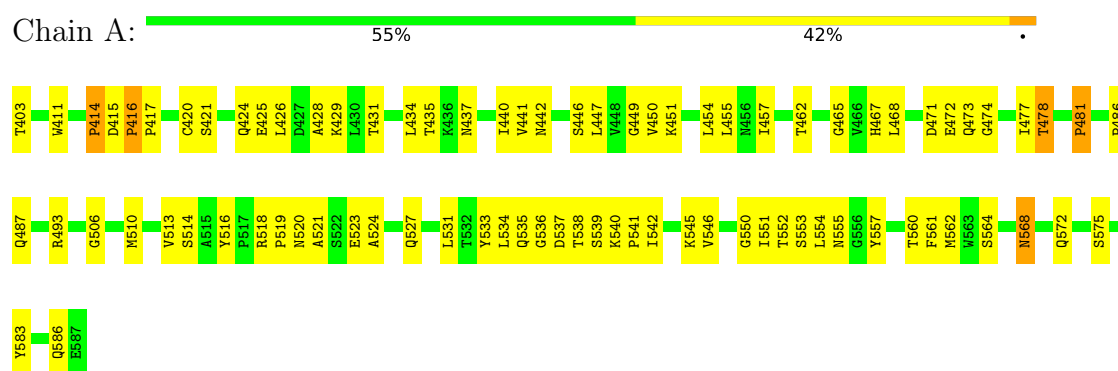
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	185	Total	C	N	O	S	0	0	0
			1401	888	228	278	7			
1	B	185	Total	C	N	O	S	0	0	0
			1401	888	228	278	7			
1	C	185	Total	C	N	O	S	0	0	0
			1401	888	228	278	7			
1	D	185	Total	C	N	O	S	0	0	0
			1401	888	228	278	7			
1	E	185	Total	C	N	O	S	0	0	0
			1401	888	228	278	7			
1	F	185	Total	C	N	O	S	0	0	0
			1401	888	228	278	7			

3 Residue-property plots

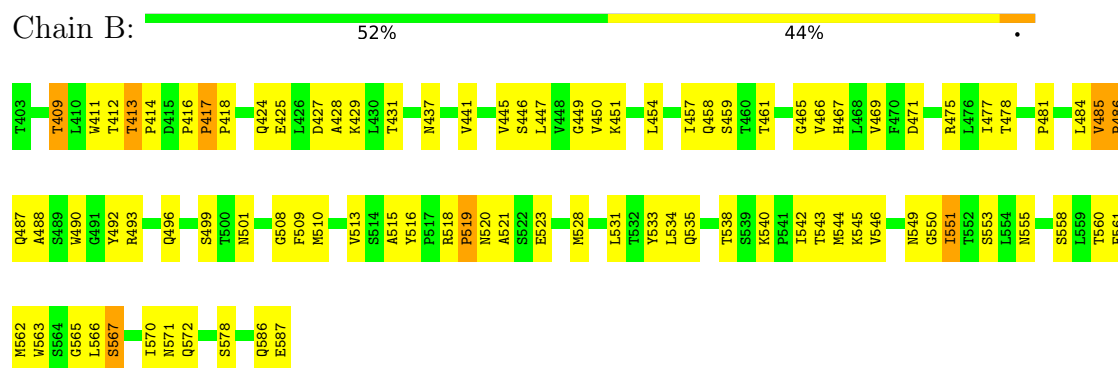
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

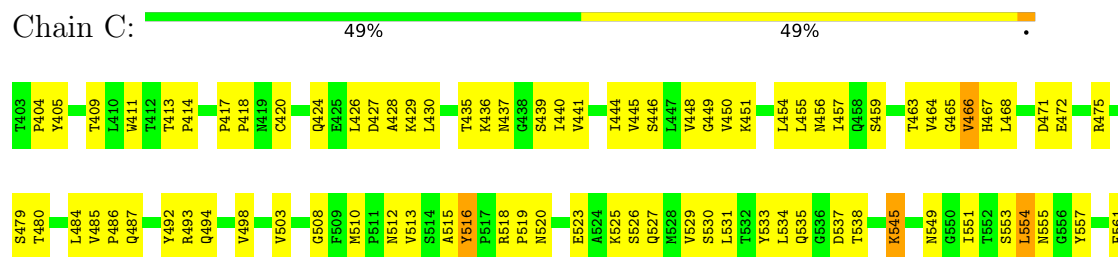
• Molecule 1: PROTEIN (FIBER KNOB PROTEIN)

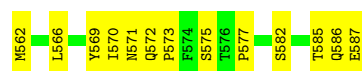


• Molecule 1: PROTEIN (FIBER KNOB PROTEIN)



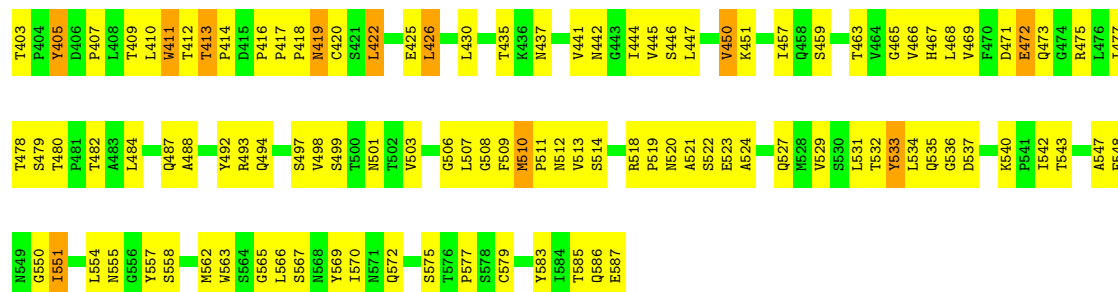
• Molecule 1: PROTEIN (FIBER KNOB PROTEIN)





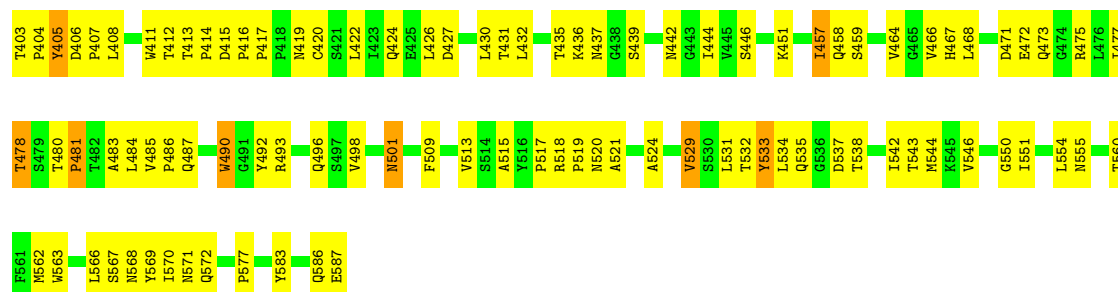
• Molecule 1: PROTEIN (FIBER KNOB PROTEIN)

Chain D: 42% 52% 6%



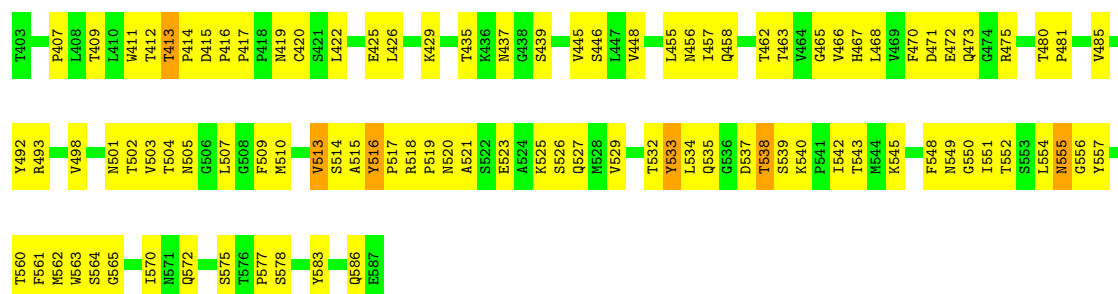
• Molecule 1: PROTEIN (FIBER KNOB PROTEIN)

Chain E: 49% 47% .



• Molecule 1: PROTEIN (FIBER KNOB PROTEIN)

Chain F: 48% 49% .



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	61.91Å 104.82Å 77.19Å 90.00° 96.90° 90.00°	Depositor
Resolution (Å)	20.00 – 2.60	Depositor
% Data completeness (in resolution range)	93.0 (20.00-2.60)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 5.0	Depositor
R, R_{free}	0.240 , 0.290	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8406	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.51	0/1434	1.11	7/1964 (0.4%)
1	B	0.51	0/1434	1.13	10/1964 (0.5%)
1	C	0.51	0/1434	1.09	3/1964 (0.2%)
1	D	0.45	0/1434	1.10	8/1964 (0.4%)
1	E	0.47	0/1434	1.11	6/1964 (0.3%)
1	F	0.50	0/1434	1.07	6/1964 (0.3%)
All	All	0.49	0/8604	1.10	40/11784 (0.3%)

There are no bond length outliers.

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	415	ASP	CA-C-N	9.64	126.60	119.66
1	A	415	ASP	C-N-CA	9.64	126.60	119.66
1	F	565	GLY	N-CA-C	-9.09	101.86	115.32
1	B	417	PRO	N-CA-C	-8.70	100.09	110.70
1	B	425	GLU	N-CA-C	7.17	121.06	110.30
1	B	409	THR	N-CA-C	6.85	119.58	108.34
1	D	533	TYR	N-CA-C	6.71	119.87	109.07
1	B	578	SER	N-CA-C	-6.50	100.04	109.59
1	A	533	TYR	N-CA-C	6.48	119.71	108.76
1	D	565	GLY	N-CA-C	-6.24	106.29	115.72
1	D	411	TRP	N-CA-C	6.03	116.05	108.45
1	E	496	GLN	N-CA-C	-5.94	105.94	112.72
1	A	516	TYR	CA-C-N	5.88	125.84	119.78
1	A	516	TYR	C-N-CA	5.88	125.84	119.78
1	F	514	SER	N-CA-C	-5.70	104.45	111.40
1	F	533	TYR	N-CA-C	5.68	118.16	108.90
1	E	415	ASP	CA-C-N	5.67	123.74	119.66
1	E	415	ASP	C-N-CA	5.67	123.74	119.66
1	B	417	PRO	CA-C-N	-5.64	114.14	119.90
1	B	417	PRO	C-N-CA	-5.64	114.14	119.90
1	D	403	THR	CA-C-N	5.47	124.66	118.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	403	THR	C-N-CA	5.47	124.66	118.97
1	B	558	SER	N-CA-C	5.44	116.79	108.42
1	F	578	SER	N-CA-C	-5.41	100.28	108.67
1	D	522	SER	N-CA-C	-5.34	106.61	113.02
1	E	533	TYR	N-CA-C	5.33	117.77	108.76
1	C	516	TYR	CA-C-N	5.32	125.26	119.78
1	C	516	TYR	C-N-CA	5.32	125.26	119.78
1	A	416	PRO	N-CA-C	5.27	116.22	110.58
1	D	558	SER	N-CA-C	5.27	115.49	108.38
1	E	480	THR	N-CA-C	-5.24	103.18	109.83
1	B	485	VAL	CA-C-N	5.20	126.34	119.84
1	B	485	VAL	C-N-CA	5.20	126.34	119.84
1	A	414	PRO	N-CA-C	5.15	120.83	113.47
1	E	436	LYS	N-CA-C	5.13	116.63	108.67
1	B	528	MET	N-CA-C	-5.11	99.96	108.34
1	D	510	MET	N-CA-C	5.10	117.33	110.29
1	C	428	ALA	N-CA-C	5.10	116.81	108.76
1	F	516	TYR	CA-C-N	5.03	125.02	119.89
1	F	516	TYR	C-N-CA	5.03	125.02	119.89

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	1401	0	1389	75	0
1	B	1401	0	1389	76	0
1	C	1401	0	1389	92	0
1	D	1401	0	1389	109	0
1	E	1401	0	1389	88	0
1	F	1401	0	1389	94	0
All	All	8406	0	8334	493	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 29.

All (493) 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:435:THR:HG21	1:B:437:ASN:O	1.58	1.01
1:E:416:PRO:HB2	1:E:419:ASN:HD21	1.32	0.94
1:D:419:ASN:HD21	1:D:430:LEU:H	1.18	0.90
1:E:435:THR:HG21	1:F:437:ASN:O	1.73	0.88
1:D:422:LEU:HD21	1:D:466:VAL:HG12	1.55	0.87
1:F:520:ASN:HD22	1:F:523:GLU:HG3	1.42	0.85
1:D:435:THR:HG21	1:E:437:ASN:O	1.76	0.85
1:B:508:GLY:HA2	1:B:587:GLU:OXT	1.78	0.84
1:E:472:GLU:HB3	1:E:555:ASN:HB3	1.60	0.84
1:B:428:ALA:HB1	1:B:447:LEU:HD11	1.61	0.82
1:C:529:VAL:HG22	1:C:545:LYS:HG3	1.62	0.82
1:D:513:VAL:HG22	1:D:586:GLN:OE1	1.80	0.81
1:B:535:GLN:HE22	1:B:540:LYS:NZ	1.79	0.81
1:C:456:ASN:ND2	1:E:486:PRO:HB2	1.96	0.81
1:B:535:GLN:HE22	1:B:540:LYS:HZ2	1.28	0.80
1:A:465:GLY:HA3	1:A:562:MET:SD	2.21	0.80
1:C:472:GLU:HB3	1:C:555:ASN:HB3	1.62	0.80
1:F:520:ASN:HB3	1:F:523:GLU:HG3	1.64	0.79
1:D:450:VAL:HG23	1:D:451:LYS:H	1.47	0.78
1:C:424:GLN:NE2	1:C:451:LYS:HG2	1.99	0.78
1:B:424:GLN:NE2	1:B:451:LYS:HB3	1.98	0.78
1:E:416:PRO:HB2	1:E:419:ASN:ND2	1.98	0.77
1:E:521:ALA:HB2	1:E:550:GLY:HA2	1.64	0.77
1:A:527:GLN:HE21	1:A:545:LYS:HD3	1.47	0.77
1:F:520:ASN:ND2	1:F:523:GLU:HG3	2.01	0.76
1:A:411:TRP:CH2	1:A:414:PRO:HD3	2.21	0.76
1:E:403:THR:N	1:E:404:PRO:HD3	2.01	0.75
1:D:535:GLN:HE22	1:D:540:LYS:HZ2	1.34	0.75
1:C:424:GLN:HE21	1:C:451:LYS:HE3	1.52	0.73
1:D:467:HIS:O	1:D:468:LEU:HD23	1.88	0.73
1:E:411:TRP:CH2	1:E:414:PRO:HD3	2.22	0.73
1:D:529:VAL:HG11	1:F:538:THR:HG22	1.71	0.73
1:C:492:TYR:OH	1:C:503:VAL:HA	1.89	0.72
1:C:424:GLN:HG3	1:C:451:LYS:HD3	1.71	0.72
1:A:527:GLN:NE2	1:A:545:LYS:HD3	2.03	0.72
1:C:427:ASP:HB3	1:C:451:LYS:HB3	1.71	0.72
1:D:419:ASN:ND2	1:D:430:LEU:H	1.86	0.72
1:C:534:LEU:HG	1:C:535:GLN:HG3	1.73	0.71
1:E:427:ASP:HA	1:E:451:LYS:HB2	1.73	0.71
1:C:512:ASN:HB3	1:C:515:ALA:HB3	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:429:LYS:HB2	1:C:448:VAL:CG1	2.22	0.70
1:C:404:PRO:O	1:C:494:GLN:HG3	1.92	0.69
1:C:508:GLY:HA2	1:C:587:GLU:OXT	1.92	0.69
1:A:467:HIS:O	1:A:468:LEU:HD23	1.94	0.68
1:A:540:LYS:NZ	1:A:572:GLN:HE22	1.91	0.68
1:B:411:TRP:CH2	1:B:414:PRO:HD3	2.29	0.68
1:B:424:GLN:HE21	1:B:451:LYS:HB3	1.58	0.68
1:E:459:SER:HA	1:E:570:ILE:HD12	1.76	0.68
1:D:524:ALA:O	1:F:577:PRO:HA	1.94	0.67
1:B:520:ASN:HD22	1:B:523:GLU:HG3	1.59	0.67
1:C:449:GLY:HA3	1:C:454:LEU:HB3	1.77	0.67
1:D:507:LEU:HD22	1:D:557:TYR:HE2	1.59	0.67
1:C:429:LYS:HB2	1:C:448:VAL:HG13	1.77	0.67
1:C:513:VAL:HG13	1:C:557:TYR:HE1	1.59	0.67
1:F:543:THR:HG22	1:F:564:SER:O	1.95	0.67
1:C:467:HIS:O	1:C:468:LEU:HD23	1.94	0.67
1:E:411:TRP:O	1:E:490:TRP:HA	1.95	0.67
1:E:467:HIS:O	1:E:468:LEU:HD23	1.95	0.67
1:B:518:ARG:N	1:B:519:PRO:HD2	2.09	0.67
1:D:535:GLN:HE22	1:D:540:LYS:NZ	1.93	0.67
1:F:516:TYR:HB2	1:F:549:ASN:HD22	1.60	0.66
1:E:532:THR:HG23	1:E:542:ILE:HG13	1.76	0.66
1:E:481:PRO:HG3	1:E:551:ILE:HD11	1.77	0.66
1:E:481:PRO:HG3	1:E:551:ILE:CD1	2.26	0.66
1:B:437:ASN:HB2	1:C:437:ASN:ND2	2.10	0.66
1:C:427:ASP:CB	1:C:451:LYS:HB3	2.24	0.66
1:D:410:LEU:HG	1:D:509:PHE:CE2	2.29	0.66
1:D:551:ILE:HG23	1:D:551:ILE:O	1.96	0.66
1:F:513:VAL:HG22	1:F:586:GLN:OE1	1.95	0.66
1:D:450:VAL:HG23	1:D:451:LYS:N	2.11	0.66
1:A:478:THR:HG21	1:A:486:PRO:HA	1.78	0.66
1:C:465:GLY:HA2	1:C:561:PHE:O	1.97	0.65
1:D:422:LEU:CD2	1:D:466:VAL:HG12	2.26	0.65
1:F:520:ASN:CB	1:F:523:GLU:HG3	2.27	0.65
1:F:411:TRP:CZ2	1:F:493:ARG:HG3	2.32	0.65
1:C:457:ILE:HG13	1:C:572:GLN:O	1.97	0.65
1:D:471:ASP:OD2	1:D:475:ARG:HB2	1.97	0.64
1:D:532:THR:O	1:D:542:ILE:HG12	1.98	0.64
1:D:535:GLN:NE2	1:D:540:LYS:HZ2	1.96	0.64
1:B:520:ASN:HB3	1:B:523:GLU:HG2	1.80	0.64
1:B:533:TYR:CD2	1:B:538:THR:HA	2.33	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:534:LEU:HD12	1:D:575:SER:O	1.97	0.64
1:E:424:GLN:HE21	1:E:451:LYS:HE2	1.63	0.63
1:C:463:THR:HG22	1:C:464:VAL:N	2.14	0.63
1:D:520:ASN:HB3	1:D:523:GLU:HG3	1.81	0.63
1:E:467:HIS:HD2	1:E:551:ILE:HG21	1.63	0.63
1:F:420:CYS:O	1:F:426:LEU:HA	1.98	0.63
1:B:520:ASN:HB3	1:B:523:GLU:CG	2.28	0.62
1:D:531:LEU:HD12	1:D:542:ILE:O	1.99	0.62
1:D:472:GLU:HB3	1:D:555:ASN:HB3	1.82	0.62
1:F:540:LYS:HE2	1:F:572:GLN:OE1	1.99	0.62
1:D:507:LEU:HD22	1:D:557:TYR:CE2	2.35	0.62
1:D:437:ASN:HB2	1:E:437:ASN:OD1	1.99	0.62
1:C:411:TRP:CH2	1:C:414:PRO:HD3	2.35	0.62
1:D:445:VAL:HG22	1:D:446:SER:N	2.13	0.61
1:B:424:GLN:HE21	1:B:451:LYS:HD3	1.63	0.61
1:C:471:ASP:OD2	1:C:475:ARG:HB2	1.99	0.61
1:E:411:TRP:CZ3	1:E:414:PRO:HD3	2.36	0.61
1:F:519:PRO:HG2	1:F:520:ASN:OD1	2.01	0.61
1:B:457:ILE:HG23	1:B:461:THR:HB	1.83	0.61
1:C:527:GLN:OE1	1:C:545:LYS:HD3	2.00	0.61
1:E:534:LEU:HG	1:E:535:GLN:HG3	1.83	0.61
1:C:424:GLN:HE21	1:C:451:LYS:CE	2.14	0.60
1:B:543:THR:O	1:B:563:TRP:HA	2.00	0.60
1:C:409:THR:O	1:C:492:TYR:HA	2.01	0.60
1:B:542:ILE:HG22	1:B:565:GLY:O	2.02	0.60
1:C:427:ASP:O	1:C:454:LEU:HD12	2.01	0.60
1:E:521:ALA:HB2	1:E:550:GLY:CA	2.30	0.60
1:A:437:ASN:O	1:C:435:THR:HG21	2.01	0.60
1:B:519:PRO:HG2	1:B:520:ASN:OD1	2.02	0.60
1:C:485:VAL:HB	1:C:486:PRO:HD2	1.84	0.59
1:A:514:SER:HB3	1:C:414:PRO:HB2	1.84	0.59
1:E:457:ILE:HG13	1:E:572:GLN:O	2.02	0.59
1:D:507:LEU:CD2	1:D:557:TYR:HE2	2.14	0.59
1:D:437:ASN:O	1:F:435:THR:HG21	2.01	0.59
1:D:501:ASN:N	1:D:501:ASN:HD22	2.00	0.59
1:A:486:PRO:HG2	1:A:487:GLN:OE1	2.02	0.59
1:F:471:ASP:OD2	1:F:475:ARG:HB2	2.03	0.59
1:E:473:GLN:CD	1:E:475:ARG:HH12	2.11	0.58
1:F:467:HIS:O	1:F:468:LEU:HD23	2.03	0.58
1:B:509:PHE:C	1:B:510:MET:HE2	2.27	0.58
1:A:540:LYS:HZ1	1:A:572:GLN:HE22	1.49	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:472:GLU:HB3	1:F:555:ASN:HB3	1.85	0.58
1:F:465:GLY:HA3	1:F:562:MET:SD	2.44	0.58
1:D:465:GLY:HA3	1:D:562:MET:SD	2.43	0.58
1:E:467:HIS:CD2	1:E:551:ILE:HG21	2.38	0.58
1:F:480:THR:HG23	1:F:481:PRO:HA	1.86	0.58
1:D:510:MET:HE2	1:D:510:MET:HA	1.85	0.58
1:E:554:LEU:C	1:E:555:ASN:HD22	2.12	0.58
1:E:413:THR:HG22	1:E:498:VAL:HG23	1.86	0.57
1:E:458:GLN:HA	1:E:458:GLN:OE1	2.03	0.57
1:F:492:TYR:HE1	1:F:505:ASN:HD21	1.50	0.57
1:B:521:ALA:CB	1:B:550:GLY:HA2	2.35	0.57
1:D:411:TRP:CZ2	1:D:414:PRO:HD3	2.38	0.57
1:E:546:VAL:HA	1:E:560:THR:O	2.03	0.57
1:B:518:ARG:N	1:B:519:PRO:CD	2.67	0.57
1:C:525:LYS:C	1:C:527:GLN:H	2.12	0.57
1:E:501:ASN:N	1:E:501:ASN:HD22	2.01	0.57
1:A:551:ILE:HG23	1:A:551:ILE:O	2.03	0.57
1:B:411:TRP:CZ2	1:B:493:ARG:HG3	2.39	0.57
1:B:521:ALA:HB2	1:B:550:GLY:HA2	1.87	0.57
1:E:533:TYR:CD2	1:E:538:THR:HA	2.39	0.57
1:C:420:CYS:O	1:C:426:LEU:HA	2.03	0.57
1:D:459:SER:HA	1:D:570:ILE:HD11	1.87	0.57
1:F:518:ARG:N	1:F:519:PRO:HD2	2.19	0.57
1:F:419:ASN:O	1:F:485:VAL:HG22	2.05	0.57
1:A:424:GLN:NE2	1:A:451:LYS:HE2	2.19	0.56
1:B:492:TYR:HB2	1:B:499:SER:OG	2.05	0.56
1:C:518:ARG:N	1:C:519:PRO:HD2	2.20	0.56
1:F:413:THR:HG22	1:F:498:VAL:HG23	1.86	0.56
1:C:533:TYR:HB3	1:C:537:ASP:O	2.05	0.56
1:D:566:LEU:O	1:D:569:TYR:HB2	2.05	0.56
1:F:456:ASN:O	1:F:457:ILE:C	2.49	0.56
1:C:424:GLN:HE21	1:C:451:LYS:CD	2.18	0.56
1:E:412:THR:O	1:E:413:THR:OG1	2.20	0.56
1:E:569:TYR:HA	1:E:572:GLN:NE2	2.20	0.56
1:B:519:PRO:HG2	1:B:520:ASN:N	2.21	0.56
1:B:417:PRO:O	1:B:418:PRO:C	2.49	0.55
1:C:424:GLN:HE21	1:C:451:LYS:HG2	1.70	0.55
1:C:553:SER:O	1:C:555:ASN:N	2.37	0.55
1:B:510:MET:HE2	1:B:510:MET:HA	1.88	0.55
1:E:533:TYR:HB3	1:E:537:ASP:O	2.07	0.55
1:B:535:GLN:NE2	1:B:540:LYS:NZ	2.53	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:554:LEU:C	1:F:556:GLY:H	2.15	0.55
1:D:469:VAL:HG12	1:D:477:ILE:HD12	1.89	0.54
1:A:481:PRO:HG3	1:A:551:ILE:CD1	2.36	0.54
1:E:518:ARG:N	1:E:519:PRO:HD2	2.22	0.54
1:F:501:ASN:N	1:F:501:ASN:HD22	2.06	0.54
1:A:531:LEU:HD22	1:C:531:LEU:HD23	1.89	0.54
1:D:567:SER:C	1:D:569:TYR:H	2.16	0.54
1:D:471:ASP:C	1:D:473:GLN:H	2.15	0.54
1:B:513:VAL:HG22	1:B:586:GLN:OE1	2.07	0.54
1:A:518:ARG:HD3	1:A:552:THR:OG1	2.08	0.54
1:D:520:ASN:HB3	1:D:523:GLU:CG	2.37	0.54
1:A:524:ALA:HB2	1:C:535:GLN:HA	1.90	0.54
1:A:534:LEU:O	1:A:535:GLN:HB2	2.08	0.54
1:C:516:TYR:HB2	1:C:549:ASN:HD22	1.72	0.53
1:D:419:ASN:HD22	1:D:419:ASN:C	2.15	0.53
1:A:411:TRP:CZ3	1:A:414:PRO:HD3	2.43	0.53
1:B:519:PRO:HG2	1:B:520:ASN:H	1.72	0.53
1:E:513:VAL:HG22	1:E:586:GLN:OE1	2.08	0.53
1:F:492:TYR:OH	1:F:503:VAL:HA	2.09	0.53
1:D:457:ILE:HG13	1:D:572:GLN:O	2.09	0.53
1:D:533:TYR:HB3	1:D:537:ASP:O	2.09	0.53
1:E:411:TRP:CZ2	1:E:493:ARG:HG3	2.43	0.53
1:D:512:ASN:HA	1:D:586:GLN:HA	1.90	0.53
1:F:520:ASN:HB3	1:F:523:GLU:CG	2.36	0.53
1:F:532:THR:O	1:F:542:ILE:HG12	2.09	0.53
1:E:493:ARG:NH1	1:F:439:SER:OG	2.42	0.53
1:C:519:PRO:HG2	1:C:520:ASN:OD1	2.10	0.52
1:D:521:ALA:HB2	1:D:550:GLY:HA2	1.91	0.52
1:D:479:SER:H	1:D:482:THR:HB	1.74	0.52
1:C:466:VAL:HG22	1:C:561:PHE:HD2	1.74	0.52
1:B:412:THR:O	1:B:413:THR:OG1	2.16	0.52
1:F:555:ASN:HD22	1:F:555:ASN:N	2.08	0.52
1:D:412:THR:O	1:D:413:THR:OG1	2.28	0.51
1:B:471:ASP:OD2	1:B:475:ARG:HB2	2.10	0.51
1:D:442:ASN:ND2	1:E:442:ASN:HD21	2.07	0.51
1:D:518:ARG:N	1:D:519:PRO:HD2	2.25	0.51
1:E:587:GLU:O	1:E:587:GLU:HG2	2.11	0.51
1:F:534:LEU:O	1:F:535:GLN:HB2	2.09	0.51
1:A:471:ASP:O	1:A:473:GLN:N	2.43	0.51
1:D:409:THR:HG21	1:E:439:SER:HB3	1.91	0.51
1:E:411:TRP:HA	1:E:432:LEU:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:554:LEU:O	1:F:556:GLY:N	2.43	0.51
1:E:543:THR:O	1:E:563:TRP:HA	2.10	0.51
1:A:442:ASN:HD22	1:B:437:ASN:ND2	2.08	0.51
1:E:471:ASP:HB3	1:E:477:ILE:HD11	1.92	0.51
1:E:577:PRO:HB2	1:F:527:GLN:O	2.11	0.51
1:E:551:ILE:HG23	1:E:551:ILE:O	2.10	0.51
1:D:497:SER:OG	1:D:498:VAL:N	2.44	0.51
1:D:506:GLY:O	1:D:510:MET:HG2	2.11	0.51
1:D:537:ASP:OD2	1:D:540:LYS:HE3	2.11	0.51
1:E:413:THR:CG2	1:E:498:VAL:HG23	2.42	0.50
1:F:415:ASP:OD1	1:F:415:ASP:O	2.29	0.50
1:B:424:GLN:HG3	1:B:427:ASP:HB3	1.93	0.50
1:F:516:TYR:HB2	1:F:549:ASN:ND2	2.26	0.50
1:C:441:VAL:HG23	1:C:585:THR:CG2	2.41	0.50
1:C:554:LEU:N	1:C:554:LEU:HD22	2.26	0.50
1:A:414:PRO:CB	1:B:515:ALA:HB2	2.41	0.50
1:B:465:GLY:HA2	1:B:561:PHE:O	2.11	0.50
1:B:553:SER:C	1:B:555:ASN:H	2.18	0.50
1:D:548:PHE:CZ	1:D:583:TYR:HB3	2.47	0.50
1:E:475:ARG:HG3	1:E:475:ARG:HH11	1.77	0.50
1:F:422:LEU:HD21	1:F:466:VAL:HG12	1.93	0.50
1:B:409:THR:HG21	1:C:439:SER:HB2	1.94	0.50
1:C:436:LYS:HD2	1:C:508:GLY:O	2.11	0.50
1:D:445:VAL:HG22	1:D:446:SER:H	1.76	0.50
1:C:424:GLN:NE2	1:C:451:LYS:HE3	2.26	0.50
1:D:494:GLN:HE21	1:D:499:SER:HA	1.76	0.50
1:E:430:LEU:HD23	1:E:484:LEU:HD21	1.94	0.50
1:A:510:MET:HE2	1:A:510:MET:HA	1.93	0.49
1:D:459:SER:HA	1:D:570:ILE:CD1	2.41	0.49
1:E:519:PRO:HG2	1:E:520:ASN:OD1	2.11	0.49
1:D:419:ASN:HD21	1:D:430:LEU:N	1.99	0.49
1:D:478:THR:HA	1:D:482:THR:HG21	1.94	0.49
1:E:517:PRO:HB2	1:E:520:ASN:OD1	2.12	0.49
1:A:421:SER:HB3	1:A:425:GLU:HA	1.93	0.49
1:B:551:ILE:HG12	1:B:551:ILE:O	2.11	0.49
1:C:551:ILE:O	1:C:551:ILE:HG13	2.12	0.49
1:D:412:THR:O	1:D:413:THR:HG23	2.12	0.49
1:E:403:THR:N	1:E:404:PRO:CD	2.74	0.49
1:E:570:ILE:HG22	1:E:571:ASN:ND2	2.28	0.49
1:A:420:CYS:O	1:A:426:LEU:HA	2.13	0.49
1:A:531:LEU:HD12	1:A:542:ILE:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:435:THR:HG22	1:E:437:ASN:ND2	2.28	0.49
1:C:455:LEU:O	1:C:573:PRO:HA	2.13	0.49
1:A:521:ALA:HB2	1:A:550:GLY:HA2	1.94	0.48
1:C:440:ILE:HG22	1:C:441:VAL:N	2.28	0.48
1:C:569:TYR:HA	1:C:572:GLN:NE2	2.28	0.48
1:F:407:PRO:HA	1:F:492:TYR:CD1	2.48	0.48
1:F:472:GLU:HA	1:F:555:ASN:O	2.14	0.48
1:B:445:VAL:HG22	1:B:446:SER:N	2.28	0.48
1:F:462:THR:O	1:F:462:THR:HG22	2.12	0.48
1:D:501:ASN:N	1:D:501:ASN:ND2	2.60	0.48
1:E:432:LEU:HD12	1:E:444:ILE:O	2.14	0.48
1:A:450:VAL:O	1:A:455:LEU:HD11	2.14	0.48
1:D:484:LEU:HD22	1:D:488:ALA:HB1	1.95	0.48
1:A:520:ASN:HB3	1:A:523:GLU:CG	2.43	0.48
1:A:568:ASN:HD22	1:A:568:ASN:N	2.10	0.48
1:B:510:MET:HE2	1:B:510:MET:CA	2.43	0.48
1:B:544:MET:HA	1:B:562:MET:O	2.14	0.48
1:D:425:GLU:O	1:D:426:LEU:C	2.56	0.48
1:A:553:SER:O	1:A:554:LEU:HB2	2.12	0.48
1:C:513:VAL:HG13	1:C:557:TYR:CE1	2.45	0.48
1:A:437:ASN:HB2	1:B:437:ASN:OD1	2.13	0.48
1:F:548:PHE:CZ	1:F:583:TYR:HB3	2.48	0.48
1:F:465:GLY:HA2	1:F:561:PHE:O	2.14	0.48
1:A:524:ALA:O	1:C:577:PRO:HA	2.13	0.47
1:B:431:THR:HB	1:B:446:SER:OG	2.14	0.47
1:D:411:TRP:CD1	1:D:413:THR:H	2.32	0.47
1:A:471:ASP:O	1:A:474:GLY:N	2.38	0.47
1:E:473:GLN:CB	1:E:475:ARG:HH12	2.27	0.47
1:B:467:HIS:HB2	1:B:481:PRO:O	2.14	0.47
1:B:534:LEU:HG	1:B:535:GLN:HG3	1.96	0.47
1:D:513:VAL:HG13	1:D:557:TYR:HE1	1.80	0.47
1:F:518:ARG:N	1:F:519:PRO:CD	2.77	0.47
1:C:510:MET:O	1:C:586:GLN:N	2.46	0.47
1:E:427:ASP:CA	1:E:451:LYS:HB2	2.42	0.47
1:B:513:VAL:HA	1:B:516:TYR:O	2.14	0.47
1:C:424:GLN:HE21	1:C:451:LYS:CG	2.26	0.47
1:D:479:SER:H	1:D:482:THR:CB	2.28	0.47
1:D:493:ARG:NH1	1:E:439:SER:OG	2.47	0.47
1:B:412:THR:HG22	1:B:490:TRP:HE3	1.80	0.47
1:E:487:GLN:OE1	1:E:487:GLN:N	2.33	0.47
1:A:424:GLN:HE21	1:A:451:LYS:HE2	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:531:LEU:HD22	1:C:531:LEU:CD2	2.45	0.47
1:F:412:THR:O	1:F:413:THR:OG1	2.20	0.47
1:A:519:PRO:HG2	1:A:520:ASN:OD1	2.14	0.47
1:A:520:ASN:HB3	1:A:523:GLU:HG3	1.97	0.47
1:D:527:GLN:HE21	1:D:547:ALA:HB2	1.79	0.47
1:F:534:LEU:HB2	1:F:542:ILE:HG21	1.96	0.47
1:B:478:THR:HG21	1:B:486:PRO:HA	1.97	0.47
1:D:577:PRO:HA	1:E:524:ALA:O	2.14	0.47
1:F:445:VAL:HG22	1:F:446:SER:N	2.30	0.47
1:A:429:LYS:O	1:A:447:LEU:HD12	2.15	0.47
1:D:445:VAL:CG2	1:D:446:SER:N	2.77	0.47
1:D:479:SER:O	1:D:480:THR:C	2.58	0.47
1:F:457:ILE:HG13	1:F:572:GLN:O	2.14	0.47
1:F:472:GLU:HB3	1:F:555:ASN:CB	2.45	0.47
1:D:405:TYR:CD1	1:D:405:TYR:C	2.93	0.46
1:E:435:THR:HG22	1:F:437:ASN:ND2	2.29	0.46
1:D:407:PRO:HA	1:D:492:TYR:CD2	2.50	0.46
1:D:521:ALA:CB	1:D:550:GLY:HA2	2.45	0.46
1:B:510:MET:HE2	1:B:510:MET:N	2.30	0.46
1:C:520:ASN:HB3	1:C:523:GLU:CG	2.46	0.46
1:E:420:CYS:HA	1:E:483:ALA:O	2.15	0.46
1:E:478:THR:HG21	1:E:486:PRO:HA	1.97	0.46
1:F:502:THR:O	1:F:504:THR:HG23	2.15	0.46
1:A:462:THR:O	1:A:564:SER:HA	2.16	0.46
1:A:434:LEU:HD22	1:A:441:VAL:HG11	1.98	0.46
1:D:444:ILE:HA	1:D:579:CYS:O	2.15	0.46
1:F:413:THR:O	1:F:416:PRO:HD3	2.16	0.46
1:F:458:GLN:C	1:F:570:ILE:HD12	2.39	0.46
1:C:463:THR:CG2	1:C:464:VAL:N	2.78	0.46
1:B:566:LEU:O	1:B:567:SER:C	2.59	0.46
1:B:570:ILE:HG22	1:B:571:ASN:N	2.31	0.46
1:C:533:TYR:CD2	1:C:538:THR:HA	2.51	0.46
1:F:515:ALA:HB1	1:F:525:LYS:NZ	2.31	0.46
1:A:478:THR:CG2	1:A:486:PRO:HA	2.45	0.46
1:E:501:ASN:N	1:E:501:ASN:ND2	2.59	0.46
1:F:533:TYR:N	1:F:533:TYR:CD1	2.83	0.45
1:A:535:GLN:HE22	1:A:540:LYS:NZ	2.14	0.45
1:C:427:ASP:C	1:C:450:VAL:HG22	2.42	0.45
1:F:551:ILE:HG13	1:F:551:ILE:O	2.15	0.45
1:A:518:ARG:N	1:A:519:PRO:HD2	2.31	0.45
1:C:471:ASP:C	1:C:471:ASP:OD1	2.58	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:487:GLN:H	1:D:487:GLN:CD	2.16	0.45
1:E:475:ARG:HG3	1:E:475:ARG:NH1	2.32	0.45
1:E:513:VAL:C	1:E:515:ALA:N	2.68	0.45
1:E:532:THR:CG2	1:E:542:ILE:HG13	2.46	0.45
1:F:448:VAL:HG13	1:F:448:VAL:O	2.17	0.45
1:D:534:LEU:HG	1:D:535:GLN:HG3	1.97	0.45
1:B:427:ASP:O	1:B:454:LEU:HD12	2.16	0.45
1:D:441:VAL:HG23	1:D:585:THR:CG2	2.47	0.45
1:F:472:GLU:CB	1:F:555:ASN:HB3	2.46	0.45
1:F:554:LEU:C	1:F:556:GLY:N	2.72	0.45
1:C:440:ILE:CG2	1:C:441:VAL:N	2.80	0.45
1:F:521:ALA:HB2	1:F:550:GLY:HA2	1.98	0.45
1:C:525:LYS:C	1:C:527:GLN:N	2.75	0.45
1:D:533:TYR:HD1	1:E:529:VAL:HB	1.82	0.45
1:F:467:HIS:CD2	1:F:560:THR:OG1	2.69	0.45
1:B:531:LEU:HD12	1:B:542:ILE:O	2.16	0.45
1:E:426:LEU:O	1:E:451:LYS:HD3	2.17	0.45
1:C:405:TYR:HB2	1:C:493:ARG:O	2.17	0.45
1:C:535:GLN:HG2	1:C:575:SER:OG	2.16	0.45
1:E:544:MET:HA	1:E:562:MET:O	2.17	0.45
1:D:410:LEU:HG	1:D:509:PHE:CD2	2.52	0.45
1:D:435:THR:CG2	1:E:437:ASN:ND2	2.80	0.45
1:D:508:GLY:HA2	1:D:587:GLU:OXT	2.17	0.45
1:A:546:VAL:HG22	1:A:561:PHE:CD2	2.52	0.44
1:A:583:TYR:HA	1:C:444:ILE:HD13	1.97	0.44
1:F:455:LEU:C	1:F:456:ASN:OD1	2.60	0.44
1:F:492:TYR:CZ	1:F:503:VAL:HA	2.52	0.44
1:A:536:GLY:O	1:B:545:LYS:NZ	2.49	0.44
1:D:411:TRP:NE1	1:D:413:THR:HA	2.32	0.44
1:E:533:TYR:O	1:E:577:PRO:HD3	2.16	0.44
1:A:513:VAL:HG13	1:A:557:TYR:HE2	1.82	0.44
1:C:529:VAL:HG12	1:C:530:SER:N	2.32	0.44
1:C:569:TYR:HD1	1:C:572:GLN:HE22	1.65	0.44
1:C:405:TYR:CD1	1:C:405:TYR:C	2.95	0.44
1:F:554:LEU:N	1:F:554:LEU:HD22	2.31	0.44
1:B:412:THR:O	1:B:416:PRO:HG3	2.17	0.44
1:B:534:LEU:CD1	1:B:535:GLN:HG3	2.48	0.44
1:C:445:VAL:HG22	1:C:446:SER:N	2.32	0.44
1:E:473:GLN:CB	1:E:475:ARG:NH1	2.81	0.44
1:F:425:GLU:O	1:F:426:LEU:C	2.60	0.44
1:A:586:GLN:O	1:C:493:ARG:NH2	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:430:LEU:HD23	1:C:484:LEU:HD21	1.99	0.44
1:F:473:GLN:HB2	1:F:475:ARG:NH1	2.33	0.44
1:A:553:SER:C	1:A:555:ASN:H	2.25	0.44
1:C:465:GLY:CA	1:C:561:PHE:O	2.66	0.44
1:B:546:VAL:HA	1:B:560:THR:O	2.18	0.43
1:F:534:LEU:HD12	1:F:575:SER:O	2.17	0.43
1:B:409:THR:HG21	1:C:439:SER:CB	2.48	0.43
1:B:458:GLN:C	1:B:570:ILE:HD12	2.43	0.43
1:A:467:HIS:CD2	1:A:560:THR:HG23	2.53	0.43
1:D:524:ALA:C	1:F:577:PRO:HA	2.43	0.43
1:A:440:ILE:HD13	1:C:444:ILE:HG13	2.00	0.43
1:A:513:VAL:HG13	1:A:557:TYR:CE2	2.53	0.43
1:D:437:ASN:HB2	1:E:437:ASN:CG	2.43	0.43
1:F:409:THR:O	1:F:492:TYR:HA	2.18	0.43
1:F:413:THR:CG2	1:F:498:VAL:HG23	2.48	0.43
1:F:509:PHE:O	1:F:510:MET:HE2	2.19	0.43
1:F:543:THR:O	1:F:563:TRP:HA	2.17	0.43
1:D:442:ASN:HD22	1:E:437:ASN:ND2	2.17	0.43
1:D:492:TYR:OH	1:D:503:VAL:HA	2.19	0.43
1:C:535:GLN:HG2	1:C:575:SER:HG	1.84	0.43
1:A:411:TRP:CD1	1:A:411:TRP:C	2.97	0.43
1:A:540:LYS:NZ	1:A:572:GLN:NE2	2.64	0.43
1:D:417:PRO:O	1:D:418:PRO:C	2.61	0.43
1:D:422:LEU:HD11	1:D:447:LEU:HD21	1.99	0.43
1:E:413:THR:O	1:E:416:PRO:HD3	2.19	0.43
1:F:533:TYR:CD2	1:F:538:THR:HA	2.54	0.43
1:D:405:TYR:HB3	1:D:499:SER:HB2	1.99	0.43
1:F:480:THR:CG2	1:F:481:PRO:HA	2.48	0.43
1:F:534:LEU:HG	1:F:535:GLN:HG3	2.01	0.43
1:A:520:ASN:HD22	1:A:523:GLU:HG3	1.83	0.42
1:C:427:ASP:HA	1:C:451:LYS:CB	2.48	0.42
1:F:519:PRO:HG2	1:F:520:ASN:N	2.34	0.42
1:A:537:ASP:C	1:A:539:SER:H	2.27	0.42
1:D:419:ASN:ND2	1:D:419:ASN:C	2.77	0.42
1:D:471:ASP:O	1:D:473:GLN:N	2.53	0.42
1:F:462:THR:C	1:F:463:THR:HG1	2.27	0.42
1:A:534:LEU:HD12	1:A:575:SER:O	2.19	0.42
1:B:450:VAL:HG23	1:B:451:LYS:HG3	2.01	0.42
1:B:520:ASN:HB3	1:B:523:GLU:HG3	2.01	0.42
1:D:416:PRO:HA	1:D:417:PRO:HD3	1.84	0.42
1:D:492:TYR:O	1:D:498:VAL:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:501:ASN:N	1:F:501:ASN:ND2	2.65	0.42
1:F:520:ASN:CG	1:F:523:GLU:HG3	2.44	0.42
1:F:529:VAL:HG22	1:F:545:LYS:HG3	2.02	0.42
1:A:431:THR:HB	1:A:446:SER:HB3	2.00	0.42
1:D:510:MET:HA	1:D:511:PRO:HD3	1.80	0.42
1:F:416:PRO:HA	1:F:417:PRO:HD3	1.81	0.42
1:F:518:ARG:NE	1:F:554:LEU:O	2.52	0.42
1:B:459:SER:HA	1:B:570:ILE:HD11	2.02	0.42
1:E:531:LEU:HD12	1:E:542:ILE:O	2.20	0.42
1:A:420:CYS:HB2	1:A:428:ALA:O	2.19	0.42
1:B:416:PRO:O	1:B:429:LYS:HD3	2.20	0.42
1:C:485:VAL:HG23	1:C:487:GLN:HG3	2.01	0.42
1:C:570:ILE:HG22	1:C:571:ASN:ND2	2.34	0.42
1:E:405:TYR:CE1	1:E:407:PRO:HB3	2.55	0.42
1:C:411:TRP:CZ2	1:C:493:ARG:HG3	2.55	0.42
1:D:513:VAL:HG13	1:D:557:TYR:CE1	2.54	0.42
1:F:467:HIS:HD2	1:F:560:THR:OG1	2.02	0.42
1:E:431:THR:HB	1:E:446:SER:HB3	2.01	0.42
1:F:555:ASN:N	1:F:555:ASN:ND2	2.67	0.42
1:A:428:ALA:HB2	1:A:454:LEU:CD1	2.50	0.42
1:C:459:SER:HA	1:C:570:ILE:CD1	2.50	0.42
1:E:416:PRO:HA	1:E:417:PRO:HD3	1.83	0.42
1:F:411:TRP:CD1	1:F:411:TRP:C	2.97	0.42
1:A:414:PRO:HB2	1:B:515:ALA:HB2	2.01	0.41
1:A:457:ILE:HG13	1:A:572:GLN:O	2.19	0.41
1:E:407:PRO:HA	1:E:492:TYR:CD1	2.55	0.41
1:D:411:TRP:CH2	1:D:414:PRO:HD3	2.54	0.41
1:D:412:THR:C	1:D:413:THR:HG23	2.44	0.41
1:F:516:TYR:HD1	1:F:526:SER:HA	1.85	0.41
1:B:457:ILE:HG13	1:B:572:GLN:O	2.21	0.41
1:B:469:VAL:HG12	1:B:477:ILE:HD12	2.03	0.41
1:C:510:MET:HE2	1:C:510:MET:HA	2.02	0.41
1:A:403:THR:O	1:A:403:THR:HG23	2.19	0.41
1:A:411:TRP:CZ2	1:A:493:ARG:HG3	2.55	0.41
1:B:551:ILE:O	1:B:551:ILE:HG23	2.20	0.41
1:D:419:ASN:ND2	1:D:420:CYS:SG	2.93	0.41
1:E:464:VAL:HG23	1:E:566:LEU:CD1	2.49	0.41
1:F:552:THR:HG22	1:F:557:TYR:C	2.45	0.41
1:B:449:GLY:HA3	1:B:454:LEU:HB3	2.03	0.41
1:D:535:GLN:NE2	1:D:540:LYS:NZ	2.62	0.41
1:D:543:THR:HG22	1:F:533:TYR:OH	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:473:GLN:HB3	1:E:475:ARG:HH12	1.85	0.41
1:B:553:SER:O	1:B:555:ASN:N	2.50	0.41
1:C:427:ASP:HA	1:C:451:LYS:HB2	2.02	0.41
1:C:513:VAL:CG1	1:C:557:TYR:CE1	3.03	0.41
1:E:406:ASP:C	1:E:408:LEU:H	2.28	0.41
1:E:422:LEU:HD11	1:E:466:VAL:HG12	2.02	0.41
1:E:485:VAL:HB	1:E:487:GLN:OE1	2.20	0.41
1:D:514:SER:HB2	1:F:414:PRO:HB2	2.02	0.41
1:C:479:SER:O	1:C:480:THR:C	2.62	0.41
1:A:416:PRO:HA	1:A:417:PRO:HD3	1.84	0.41
1:B:484:LEU:HA	1:B:484:LEU:HD23	1.87	0.41
1:D:450:VAL:CG2	1:D:451:LYS:H	2.19	0.41
1:D:554:LEU:HD22	1:D:554:LEU:N	2.36	0.41
1:E:509:PHE:O	1:E:583:TYR:OH	2.28	0.41
1:F:517:PRO:C	1:F:519:PRO:HD2	2.46	0.41
1:C:441:VAL:O	1:C:582:SER:HA	2.21	0.41
1:F:429:LYS:HB2	1:F:448:VAL:HG13	2.03	0.41
1:A:471:ASP:HB3	1:A:477:ILE:HD11	2.03	0.40
1:A:539:SER:O	1:A:541:PRO:HD2	2.21	0.40
1:C:464:VAL:HG23	1:C:566:LEU:CD1	2.51	0.40
1:D:465:GLY:C	1:D:466:VAL:HG13	2.46	0.40
1:D:471:ASP:C	1:D:473:GLN:N	2.77	0.40
1:F:470:PHE:CD1	1:F:470:PHE:N	2.89	0.40
1:F:537:ASP:C	1:F:539:SER:H	2.29	0.40
1:A:568:ASN:HD22	1:A:568:ASN:H	1.68	0.40
1:A:568:ASN:H	1:A:568:ASN:ND2	2.19	0.40
1:B:414:PRO:HG3	1:B:496:GLN:OE1	2.20	0.40
1:B:485:VAL:HG22	1:B:488:ALA:HB2	2.03	0.40
1:B:499:SER:HB2	1:B:501:ASN:OD1	2.21	0.40
1:B:516:TYR:HB2	1:B:549:ASN:HD22	1.87	0.40
1:D:463:THR:HA	1:D:563:TRP:O	2.21	0.40
1:D:551:ILE:O	1:D:551:ILE:CG2	2.67	0.40
1:E:478:THR:CG2	1:E:486:PRO:HA	2.51	0.40
1:D:534:LEU:C	1:D:536:GLY:H	2.30	0.40
1:A:437:ASN:OD1	1:C:437:ASN:HB2	2.22	0.40
1:A:481:PRO:HG3	1:A:551:ILE:HD13	2.03	0.40
1:A:506:GLY:O	1:A:510:MET:HG2	2.21	0.40
1:C:417:PRO:O	1:C:418:PRO:C	2.65	0.40
1:C:465:GLY:HA3	1:C:562:MET:SD	2.61	0.40
1:D:478:THR:O	1:D:479:SER:HB3	2.21	0.40
1:F:551:ILE:O	1:F:551:ILE:HG23	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:449:GLY:HA3	1:A:454:LEU:HB3	2.04	0.40
1:C:569:TYR:HA	1:C:572:GLN:HE21	1.86	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	183/185 (99%)	160 (87%)	21 (12%)	2 (1%)	11	25
1	B	183/185 (99%)	162 (88%)	15 (8%)	6 (3%)	3	5
1	C	183/185 (99%)	164 (90%)	16 (9%)	3 (2%)	7	16
1	D	183/185 (99%)	153 (84%)	24 (13%)	6 (3%)	3	5
1	E	183/185 (99%)	154 (84%)	24 (13%)	5 (3%)	4	7
1	F	183/185 (99%)	156 (85%)	23 (13%)	4 (2%)	5	10
All	All	1098/1110 (99%)	949 (86%)	123 (11%)	26 (2%)	4	9

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	472	GLU
1	B	551	ILE
1	E	405	TYR
1	A	538	THR
1	D	472	GLU
1	E	490	TRP
1	B	487	GLN
1	B	567	SER
1	C	554	LEU
1	D	426	LEU

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Mol	Chain	Res	Type
1	D	551	ILE
1	F	538	THR
1	F	555	ASN
1	C	526	SER
1	D	422	LEU
1	D	450	VAL
1	F	507	LEU
1	D	413	THR
1	E	478	THR
1	E	567	SER
1	B	519	PRO
1	F	413	THR
1	B	486	PRO
1	C	413	THR
1	E	457	ILE
1	B	413	THR

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	164/164 (100%)	161 (98%)	3 (2%)	51	76
1	B	164/164 (100%)	162 (99%)	2 (1%)	63	83
1	C	164/164 (100%)	161 (98%)	3 (2%)	51	76
1	D	164/164 (100%)	162 (99%)	2 (1%)	63	83
1	E	164/164 (100%)	160 (98%)	4 (2%)	43	70
1	F	164/164 (100%)	163 (99%)	1 (1%)	78	91
All	All	984/984 (100%)	969 (98%)	15 (2%)	57	80

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	478	THR
1	A	481	PRO

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Mol	Chain	Res	Type
1	A	568	ASN
1	B	441	VAL
1	B	466	VAL
1	C	466	VAL
1	C	498	VAL
1	C	545	LYS
1	D	405	TYR
1	D	419	ASN
1	E	481	PRO
1	E	501	ASN
1	E	529	VAL
1	E	568	ASN
1	F	513	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (48) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	424	GLN
1	A	442	ASN
1	A	467	HIS
1	A	501	ASN
1	A	527	GLN
1	A	535	GLN
1	A	555	ASN
1	A	568	ASN
1	A	572	GLN
1	B	424	GLN
1	B	467	HIS
1	B	535	GLN
1	B	549	ASN
1	C	424	GLN
1	C	437	ASN
1	C	456	ASN
1	C	467	HIS
1	C	473	GLN
1	C	535	GLN
1	C	549	ASN
1	C	555	ASN
1	C	571	ASN
1	D	419	ASN
1	D	437	ASN
1	D	442	ASN

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Mol	Chain	Res	Type
1	D	467	HIS
1	D	494	GLN
1	D	501	ASN
1	D	527	GLN
1	D	535	GLN
1	D	568	ASN
1	D	571	ASN
1	E	419	ASN
1	E	424	GLN
1	E	437	ASN
1	E	442	ASN
1	E	467	HIS
1	E	501	ASN
1	E	527	GLN
1	E	535	GLN
1	E	555	ASN
1	E	571	ASN
1	F	437	ASN
1	F	467	HIS
1	F	501	ASN
1	F	505	ASN
1	F	549	ASN
1	F	555	ASN

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 ⓘ

There are no ligands in this entry.

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

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.