



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 01:12 AM EDT

PDB ID : 1QU7 / pdb_00001qu7
Title : FOUR HELICAL-BUNDLE STRUCTURE OF THE CYTOPLASMIC DOMAIN OF A SERINE CHEMOTAXIS RECEPTOR
Authors : Kim, K.K.; Yokota, H.; Kim, S.-H.
Deposited on : 1999-07-07
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)	:	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

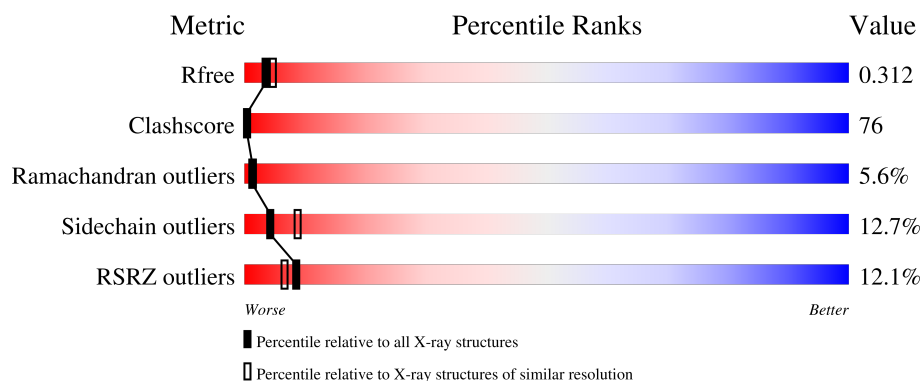
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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))
R_{free}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (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 $\leq 5\%$. 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	227	
1	B	227	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3430 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 METHYL-ACCEPTING CHEMOTAXIS PROTEIN I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	227	Total	C	N	O	S	0	0	0
			1643	989	302	347	5			
1	B	221	Total	C	N	O	S	0	0	0
			1600	966	292	337	5			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	304	GLN	GLU	engineered mutation	UNP P02942
A	493	GLN	GLU	engineered mutation	UNP P02942
B	304	GLN	GLU	engineered mutation	UNP P02942
B	493	GLN	GLU	engineered mutation	UNP P02942

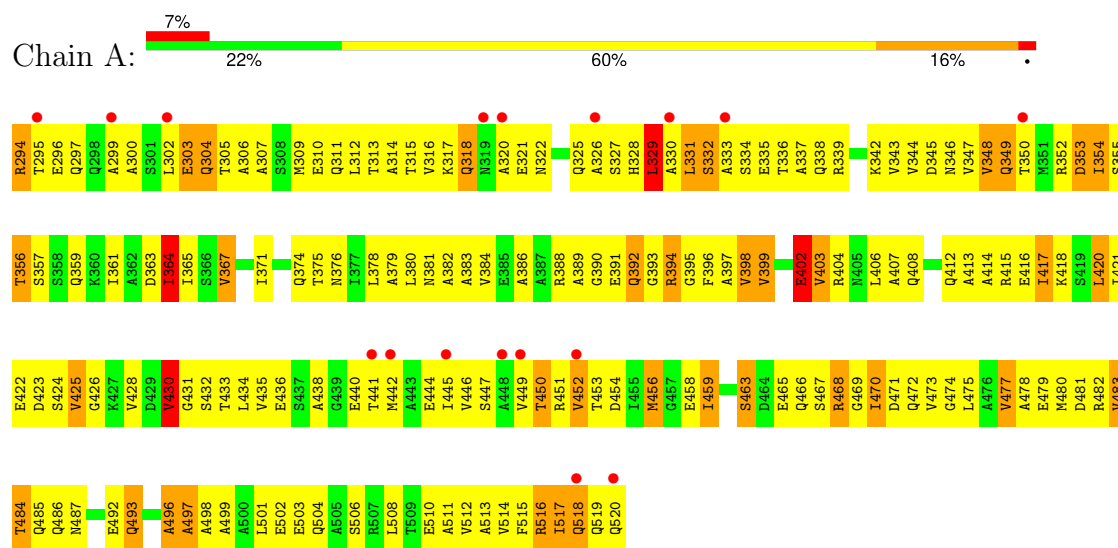
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	87	Total	O	0	0
			87	87		
2	B	100	Total	O	0	0
			100	100		

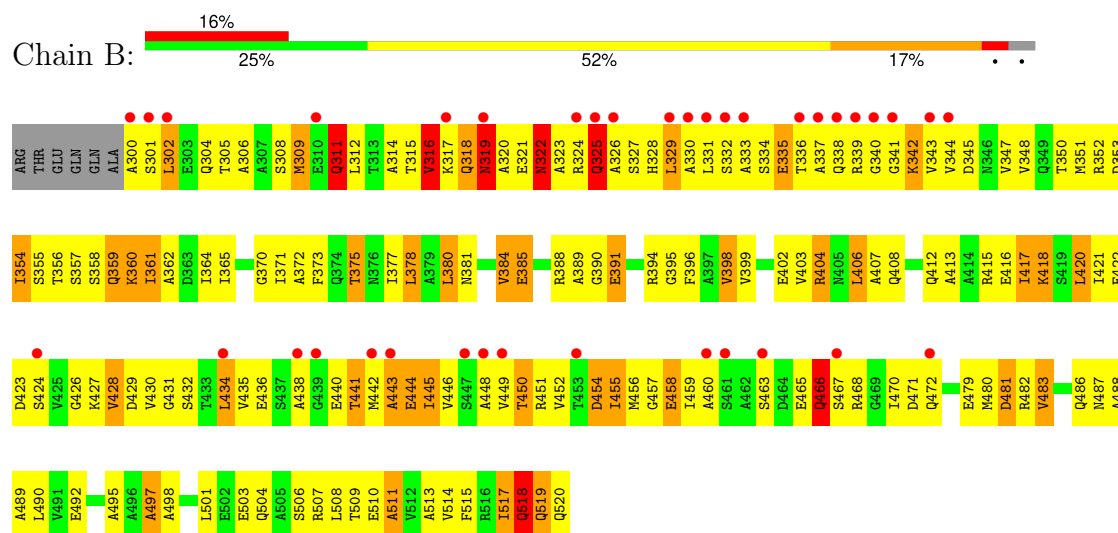
3 Residue-property plots

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 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: METHYL-ACCEPTING CHEMOTAXIS PROTEIN I



• Molecule 1: METHYL-ACCEPTING CHEMOTAXIS PROTEIN I



4 Data and refinement statistics

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α , β , γ	132.44Å 132.44Å 134.59Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	100.00 – 2.60 100.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	(Not available) (100.00-2.60) 59.5 (100.00-2.60)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.84 (at 2.58Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.243 , 0.276 0.265 , 0.312	Depositor DCC
R_{free} test set	1452 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	35.6	Xtriage
Anisotropy	0.951	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 87.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.032 for -h,-k,l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3430	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.13% 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

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	0.80	0/1646	1.31	21/2226 (0.9%)
1	B	0.79	1/1603 (0.1%)	1.29	23/2168 (1.1%)
All	All	0.79	1/3249 (0.0%)	1.30	44/4394 (1.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	384	VAL	CA-CB	5.04	1.61	1.54

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	518	GLN	N-CA-C	-12.39	98.41	113.15
1	A	484	THR	N-CA-C	-10.79	100.06	113.01
1	A	516	ARG	N-CA-C	-9.30	102.06	113.50
1	B	445	ILE	N-CA-C	-8.52	103.53	111.45
1	A	364	ILE	N-CA-C	-8.48	101.75	111.00
1	A	329	LEU	N-CA-C	-8.00	102.97	112.89
1	B	337	ALA	N-CA-C	-7.59	102.95	112.90
1	B	466	GLN	N-CA-C	-7.46	102.31	111.33
1	B	359	GLN	N-CA-C	-7.37	104.91	114.04
1	A	514	VAL	N-CA-C	7.30	117.28	110.42
1	B	329	LEU	N-CA-C	-7.25	104.17	112.87
1	B	517	ILE	N-CA-C	-7.20	104.83	111.67
1	A	450	THR	N-CA-C	-7.16	104.58	113.38
1	A	332	SER	N-CA-C	-7.11	103.61	111.36
1	B	384	VAL	N-CA-C	-6.91	102.17	111.44
1	B	497	ALA	N-CA-C	-6.86	103.49	110.97
1	A	508	LEU	N-CA-C	-6.85	103.90	111.36
1	B	322	ASN	N-CA-C	-6.83	103.85	111.71
1	A	322	ASN	N-CA-C	-6.81	103.88	111.71
1	B	450	THR	N-CA-C	-6.76	103.71	112.23
1	B	325	GLN	N-CA-C	-6.73	103.88	111.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	311	GLN	N-CA-C	-6.46	104.24	111.28
1	B	428	VAL	N-CA-C	-6.40	104.63	112.76
1	A	452	VAL	N-CA-C	-6.36	104.68	112.76
1	B	441	THR	N-CA-C	-6.16	105.73	113.18
1	A	348	VAL	N-CA-C	-6.11	104.35	111.00
1	A	430	VAL	N-CA-C	-6.04	104.44	110.30
1	A	328	HIS	N-CA-C	-5.97	106.33	113.97
1	A	331	LEU	N-CA-C	-5.85	106.18	113.38
1	B	443	ALA	N-CA-C	-5.79	106.56	113.97
1	B	444	GLU	N-CA-C	-5.77	106.24	113.28
1	B	511	ALA	N-CA-C	-5.73	104.94	111.07
1	A	463	SER	N-CA-C	-5.67	105.86	112.89
1	B	360	LYS	N-CA-C	-5.59	105.29	111.71
1	A	303	GLU	N-CA-C	-5.51	104.91	111.03
1	B	354	ILE	N-CA-C	-5.43	104.66	110.36
1	B	417	ILE	N-CA-C	-5.43	104.66	110.36
1	A	402	GLU	N-CA-C	-5.43	105.44	111.36
1	B	391	GLU	N-CA-C	5.42	117.26	111.36
1	B	302	LEU	N-CA-C	-5.41	105.94	112.54
1	A	344	VAL	N-CA-C	-5.35	106.04	113.00
1	A	367	VAL	CB-CA-C	-5.28	105.22	111.81
1	B	308	SER	N-CA-C	-5.14	105.67	111.28
1	A	459	ILE	N-CA-C	-5.01	104.91	110.62

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	1643	0	1632	296	0
1	B	1600	0	1600	265	0
2	A	87	0	0	27	0
2	B	100	0	0	29	0
All	All	3430	0	3232	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 76.

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:406:LEU:HD23	1:B:375:THR:HG22	1.20	1.18
1:A:438:ALA:HB2	1:B:343:VAL:HG11	1.26	1.16
1:B:312:LEU:HB3	1:B:470:ILE:HD11	1.25	1.08
1:B:432:SER:O	1:B:436:GLU:HG2	1.61	1.00
1:A:312:LEU:HB3	1:A:470:ILE:HD11	1.44	0.99
1:B:467:SER:O	1:B:470:ILE:HG22	1.68	0.93
1:A:294:ARG:HH11	1:A:294:ARG:HB3	1.36	0.89
1:A:516:ARG:O	1:A:518:GLN:N	2.05	0.89
1:A:517:ILE:C	1:A:519:GLN:H	1.78	0.89
1:B:420:LEU:HD23	1:B:420:LEU:C	1.97	0.89
1:A:338:GLN:HE21	1:A:338:GLN:HA	1.39	0.87
1:B:345:ASP:O	1:B:348:VAL:HG12	1.73	0.87
1:A:309:MET:HE1	1:A:473:VAL:HG12	1.56	0.85
1:B:412:GLN:HB2	2:B:652:HOH:O	1.75	0.85
1:A:425:VAL:O	1:A:428:VAL:HG12	1.77	0.85
1:B:354:ILE:HD11	1:B:428:VAL:HG22	1.59	0.84
1:B:483:VAL:O	1:B:486:GLN:HB2	1.77	0.84
1:A:347:VAL:HG22	1:B:434:LEU:HB3	1.60	0.82
1:A:459:ILE:HG12	1:B:319:ASN:ND2	1.95	0.82
1:A:336:THR:HG22	1:B:445:ILE:HG12	1.60	0.81
1:A:300:ALA:HA	1:A:303:GLU:HG2	1.62	0.81
1:B:312:LEU:HB3	1:B:470:ILE:CD1	2.10	0.80
1:B:450:THR:HA	2:B:640:HOH:O	1.81	0.79
1:A:438:ALA:CB	1:B:343:VAL:HG11	2.10	0.79
1:A:516:ARG:C	1:A:518:GLN:H	1.91	0.79
1:A:361:ILE:HD11	1:B:420:LEU:HD21	1.63	0.78
1:B:463:SER:HA	1:B:466:GLN:HB2	1.63	0.78
1:A:332:SER:HB3	1:B:448:ALA:HB2	1.65	0.78
1:A:472:GLN:HB2	2:B:756:HOH:O	1.82	0.78
1:A:481:ASP:HA	1:A:484:THR:HG22	1.66	0.77
1:A:329:LEU:HD21	1:B:451:ARG:HD3	1.66	0.77
1:A:422:GLU:O	1:A:425:VAL:HG22	1.86	0.76
1:A:497:ALA:O	1:A:501:LEU:HD13	1.86	0.76
1:B:378:LEU:HD23	1:B:378:LEU:C	2.10	0.76
1:A:325:GLN:HE21	1:B:455:ILE:HD11	1.51	0.75
1:B:302:LEU:HB2	1:B:480:MET:HE1	1.70	0.74
1:A:325:GLN:HE21	1:B:455:ILE:CD1	1.99	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:454:ASP:O	1:B:458:GLU:HG2	1.87	0.74
1:B:316:VAL:CG2	1:B:466:GLN:HG2	2.18	0.74
1:A:503:GLU:HG3	2:A:628:HOH:O	1.88	0.73
1:B:441:THR:O	1:B:445:ILE:HG12	1.89	0.73
1:B:316:VAL:HG21	1:B:466:GLN:HG2	1.68	0.73
1:A:446:VAL:O	1:A:450:THR:HB	1.89	0.73
1:B:302:LEU:CD2	1:B:481:ASP:HB2	2.18	0.73
1:B:302:LEU:HB2	1:B:480:MET:CE	2.18	0.72
1:A:329:LEU:O	1:B:448:ALA:HB1	1.89	0.72
1:A:330:ALA:HB1	1:A:452:VAL:CG1	2.19	0.72
1:B:318:GLN:HG3	1:B:319:ASN:H	1.54	0.72
1:A:300:ALA:HA	1:A:303:GLU:CG	2.19	0.72
1:B:415:ARG:O	1:B:418:LYS:HB3	1.89	0.72
1:B:336:THR:HA	1:B:339:ARG:HD3	1.70	0.72
1:A:327:SER:O	1:A:331:LEU:HD23	1.89	0.72
1:B:311:GLN:OE1	1:B:312:LEU:HD12	1.89	0.71
1:B:432:SER:HB2	2:B:613:HOH:O	1.89	0.71
1:B:354:ILE:HG13	1:B:355:SER:N	2.05	0.71
1:B:312:LEU:CB	1:B:470:ILE:HD11	2.13	0.71
1:A:459:ILE:HG12	1:B:319:ASN:HD21	1.53	0.70
1:A:378:LEU:HA	1:A:381:ASN:HD22	1.56	0.70
1:B:381:ASN:O	1:B:384:VAL:HG22	1.92	0.70
1:A:459:ILE:HA	1:B:319:ASN:HD21	1.57	0.70
1:B:371:ILE:O	1:B:375:THR:HG23	1.90	0.70
1:A:406:LEU:HD23	1:B:375:THR:CG2	2.12	0.70
1:A:338:GLN:HA	1:A:338:GLN:NE2	2.06	0.69
1:A:304:GLN:HG3	1:A:305:THR:N	2.07	0.69
1:B:452:VAL:O	1:B:456:MET:HG2	1.92	0.69
1:B:301:SER:O	1:B:305:THR:HG23	1.92	0.69
1:A:395:GLY:O	1:A:398:VAL:HG13	1.91	0.69
1:B:309:MET:HE1	1:B:470:ILE:O	1.93	0.69
1:B:454:ASP:C	1:B:458:GLU:HG2	2.18	0.69
1:A:329:LEU:HD11	1:B:451:ARG:HB2	1.75	0.69
1:A:417:ILE:C	1:A:417:ILE:HD13	2.18	0.69
1:B:450:THR:HG23	2:B:651:HOH:O	1.92	0.68
1:A:517:ILE:C	1:A:519:GLN:N	2.49	0.68
1:B:361:ILE:HG22	1:B:362:ALA:N	2.09	0.68
1:A:361:ILE:HG23	1:B:417:ILE:HD12	1.76	0.68
1:A:361:ILE:CG1	1:B:420:LEU:HD21	2.24	0.67
1:A:333:ALA:HB2	1:B:448:ALA:HB3	1.77	0.67
1:A:361:ILE:CD1	1:B:420:LEU:HD21	2.25	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:481:ASP:HA	1:A:484:THR:CG2	2.24	0.67
1:B:378:LEU:C	1:B:378:LEU:CD2	2.68	0.67
1:A:480:MET:HE1	1:B:479:GLU:HB2	1.77	0.67
1:A:420:LEU:HD11	1:B:360:LYS:HD2	1.77	0.67
1:A:336:THR:HG21	1:B:444:GLU:C	2.20	0.66
1:A:343:VAL:HG12	1:B:438:ALA:HB2	1.76	0.66
1:A:365:ILE:HG13	1:A:417:ILE:HD11	1.77	0.66
1:A:451:ARG:HB2	1:B:329:LEU:HD21	1.78	0.66
1:A:309:MET:HE2	1:A:474:GLY:HA2	1.78	0.66
1:B:355:SER:HB2	1:B:428:VAL:HG11	1.78	0.66
1:A:452:VAL:O	1:A:456:MET:HB2	1.96	0.66
1:B:373:PHE:HA	2:B:645:HOH:O	1.95	0.66
1:B:443:ALA:O	1:B:446:VAL:HG12	1.95	0.65
1:B:420:LEU:HD23	1:B:421:ILE:N	2.10	0.65
1:A:375:THR:OG1	1:B:406:LEU:HD23	1.95	0.65
1:A:418:LYS:O	1:A:421:ILE:HG22	1.97	0.65
1:B:311:GLN:O	1:B:314:ALA:HB3	1.96	0.65
1:A:493:GLN:O	1:A:496:ALA:HB3	1.97	0.65
1:B:436:GLU:HA	2:B:616:HOH:O	1.95	0.65
1:A:315:THR:CB	1:B:466:GLN:HE22	2.09	0.65
1:B:517:ILE:C	1:B:519:GLN:H	2.04	0.65
1:B:416:GLU:HB3	2:B:620:HOH:O	1.96	0.64
1:A:312:LEU:HB3	1:A:470:ILE:CD1	2.25	0.64
1:A:442:MET:HA	1:A:442:MET:HE2	1.79	0.64
1:B:443:ALA:HB3	2:B:610:HOH:O	1.98	0.64
1:A:361:ILE:HD11	1:B:420:LEU:CD2	2.27	0.64
1:B:514:VAL:O	1:B:518:GLN:HB3	1.97	0.64
1:A:313:THR:O	1:A:316:VAL:HG12	1.97	0.64
1:A:451:ARG:HH11	1:A:451:ARG:HG2	1.63	0.64
1:A:406:LEU:CD2	1:B:375:THR:HG22	2.13	0.64
1:A:339:ARG:HA	1:A:342:LYS:HE2	1.79	0.64
1:A:350:THR:O	1:A:354:ILE:HD13	1.97	0.64
1:B:443:ALA:HB1	2:B:625:HOH:O	1.96	0.64
1:A:361:ILE:O	1:A:364:ILE:N	2.27	0.63
1:B:318:GLN:C	1:B:320:ALA:H	2.05	0.63
1:B:450:THR:HG21	2:B:636:HOH:O	1.97	0.63
1:A:479:GLU:O	1:A:483:VAL:HG22	1.98	0.63
1:B:511:ALA:O	1:B:514:VAL:HG22	1.99	0.63
1:A:420:LEU:HD22	1:B:361:ILE:HD11	1.79	0.63
1:A:380:LEU:C	1:A:380:LEU:HD23	2.24	0.63
1:A:447:SER:O	1:A:450:THR:HG22	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:468:ARG:O	1:B:472:GLN:HG3	1.98	0.62
1:A:332:SER:HB3	1:B:448:ALA:CB	2.29	0.62
1:A:336:THR:C	1:B:445:ILE:HD11	2.23	0.62
1:A:417:ILE:HG22	1:B:364:ILE:HG21	1.80	0.62
1:A:451:ARG:HG2	1:A:451:ARG:NH1	2.14	0.62
1:A:483:VAL:C	1:A:485:GLN:N	2.52	0.62
1:B:520:GLN:HA	2:B:637:HOH:O	1.99	0.62
1:A:396:PHE:HA	1:B:396:PHE:CZ	2.34	0.62
1:A:304:GLN:HG3	1:A:305:THR:CG2	2.30	0.62
1:B:316:VAL:HG21	1:B:466:GLN:CG	2.29	0.62
1:A:503:GLU:O	1:A:506:SER:N	2.32	0.61
1:B:347:VAL:O	1:B:351:MET:HG2	2.00	0.61
1:A:300:ALA:CA	1:A:303:GLU:HG2	2.28	0.61
1:A:330:ALA:HB1	1:A:452:VAL:HG11	1.81	0.61
1:A:364:ILE:CG2	1:B:417:ILE:HD11	2.31	0.60
1:A:295:THR:HG23	2:A:765:HOH:O	2.01	0.60
1:B:305:THR:HG22	2:B:756:HOH:O	2.01	0.60
1:B:302:LEU:HD22	1:B:481:ASP:HB2	1.83	0.60
1:B:302:LEU:HD23	1:B:481:ASP:HB2	1.82	0.60
1:A:326:ALA:O	1:A:330:ALA:HB2	2.02	0.60
1:A:378:LEU:HD21	1:B:402:GLU:CG	2.32	0.60
1:A:483:VAL:C	1:A:485:GLN:H	2.10	0.60
1:A:456:MET:HE2	1:A:456:MET:N	2.17	0.60
1:A:503:GLU:O	1:A:504:GLN:C	2.43	0.60
1:B:320:ALA:HB1	2:B:760:HOH:O	2.02	0.60
1:B:465:GLU:OE1	1:B:465:GLU:HA	2.02	0.59
1:A:393:GLY:O	1:A:394:ARG:C	2.45	0.59
1:A:317:LYS:HG3	1:A:318:GLN:N	2.16	0.59
1:B:311:GLN:OE1	1:B:311:GLN:C	2.45	0.59
1:B:309:MET:O	1:B:312:LEU:HB2	2.03	0.59
1:A:325:GLN:HG3	1:A:326:ALA:N	2.17	0.59
1:A:428:VAL:O	1:A:432:SER:HB2	2.03	0.59
1:A:359:GLN:C	1:A:361:ILE:N	2.61	0.58
1:A:393:GLY:O	1:A:396:PHE:N	2.36	0.58
1:B:451:ARG:O	1:B:454:ASP:N	2.35	0.58
1:A:329:LEU:HD11	1:B:448:ALA:O	2.03	0.58
1:A:354:ILE:HG22	1:A:355:SER:N	2.18	0.58
1:A:454:ASP:O	1:A:458:GLU:HG2	2.03	0.58
1:A:315:THR:HB	1:B:466:GLN:HE22	1.69	0.58
1:B:427:LYS:C	1:B:429:ASP:H	2.10	0.58
1:A:300:ALA:C	1:A:303:GLU:HG2	2.28	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:695:HOH:O	1:B:339:ARG:HB3	2.02	0.58
1:A:316:VAL:O	1:A:320:ALA:HB2	2.04	0.58
1:B:510:GLU:O	1:B:513:ALA:HB3	2.03	0.57
1:A:352:ARG:C	1:A:354:ILE:H	2.11	0.57
1:A:392:GLN:N	1:A:392:GLN:OE1	2.36	0.57
1:B:318:GLN:C	1:B:320:ALA:N	2.61	0.57
1:B:420:LEU:C	1:B:420:LEU:CD2	2.72	0.57
1:A:449:VAL:HG12	1:A:449:VAL:O	2.03	0.57
1:B:318:GLN:CG	1:B:319:ASN:H	2.17	0.57
1:B:354:ILE:CG1	1:B:355:SER:N	2.67	0.57
1:B:427:LYS:C	1:B:429:ASP:N	2.58	0.57
1:A:394:ARG:O	1:A:397:ALA:HB3	2.05	0.57
1:A:420:LEU:HD22	1:B:361:ILE:CD1	2.35	0.57
1:B:378:LEU:HD23	1:B:378:LEU:O	2.04	0.57
1:A:481:ASP:CA	1:A:484:THR:HG22	2.34	0.56
1:A:378:LEU:O	1:A:379:ALA:C	2.48	0.56
1:A:314:ALA:HB3	2:A:654:HOH:O	2.05	0.56
1:A:402:GLU:O	1:A:406:LEU:HD13	2.05	0.56
1:A:304:GLN:CG	1:A:305:THR:N	2.69	0.56
1:B:350:THR:O	1:B:353:ASP:HB2	2.04	0.56
1:A:306:ALA:O	1:A:310:GLU:HG3	2.06	0.56
1:B:479:GLU:O	1:B:480:MET:C	2.49	0.56
1:A:415:ARG:O	1:A:418:LYS:N	2.34	0.56
1:B:451:ARG:O	1:B:454:ASP:HB2	2.06	0.56
1:B:483:VAL:HA	1:B:486:GLN:HG3	1.88	0.56
1:A:364:ILE:O	1:A:367:VAL:HB	2.06	0.55
1:B:328:HIS:C	1:B:330:ALA:N	2.63	0.55
1:B:412:GLN:O	1:B:416:GLU:HG3	2.05	0.55
1:A:433:THR:O	1:A:436:GLU:HB3	2.07	0.55
1:B:334:SER:O	1:B:338:GLN:HG3	2.07	0.55
1:A:492:GLU:HB3	2:A:678:HOH:O	2.06	0.55
1:B:468:ARG:O	1:B:471:ASP:HB3	2.05	0.55
2:A:695:HOH:O	1:B:339:ARG:CB	2.53	0.55
1:B:357:SER:HB3	2:B:778:HOH:O	2.06	0.55
1:A:315:THR:OG1	1:B:466:GLN:NE2	2.39	0.55
1:A:395:GLY:O	1:A:396:PHE:C	2.50	0.55
1:A:510:GLU:O	1:A:511:ALA:C	2.50	0.55
1:A:512:VAL:O	1:A:513:ALA:C	2.50	0.55
1:A:361:ILE:HG21	1:A:421:ILE:CD1	2.36	0.55
1:A:515:PHE:O	2:A:741:HOH:O	2.18	0.55
1:A:304:GLN:HB2	2:A:702:HOH:O	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:378:LEU:HD12	2:A:680:HOH:O	2.06	0.54
1:B:402:GLU:OE1	1:B:402:GLU:HA	2.06	0.54
1:B:511:ALA:HA	2:B:712:HOH:O	2.07	0.54
1:A:325:GLN:O	1:A:329:LEU:N	2.35	0.54
1:A:393:GLY:O	1:A:395:GLY:N	2.40	0.54
1:A:440:GLU:C	1:A:442:MET:H	2.14	0.54
1:A:467:SER:OG	1:A:468:ARG:N	2.37	0.54
1:B:318:GLN:O	1:B:320:ALA:N	2.41	0.54
1:A:336:THR:HB	1:B:445:ILE:HD13	1.88	0.54
1:B:342:LYS:HZ2	1:B:342:LYS:HB3	1.73	0.54
1:B:360:LYS:C	1:B:360:LYS:HD3	2.32	0.54
1:A:309:MET:HE1	1:A:473:VAL:CG1	2.33	0.53
1:B:334:SER:HB2	1:B:449:VAL:HG12	1.90	0.53
1:A:422:GLU:HG3	1:A:423:ASP:N	2.23	0.53
1:B:332:SER:C	1:B:334:SER:H	2.15	0.53
1:A:415:ARG:O	1:A:416:GLU:C	2.52	0.53
1:A:332:SER:CB	1:B:448:ALA:HB2	2.36	0.53
1:A:399:VAL:O	1:A:403:VAL:HG23	2.08	0.53
1:B:365:ILE:HG13	1:B:417:ILE:HG21	1.91	0.53
1:B:455:ILE:O	1:B:459:ILE:HG23	2.09	0.53
1:A:359:GLN:C	1:A:361:ILE:H	2.16	0.53
1:A:376:ASN:ND2	1:A:404:ARG:HE	2.07	0.53
1:A:434:LEU:HD12	2:B:749:HOH:O	2.08	0.53
1:A:466:GLN:O	1:A:470:ILE:HB	2.09	0.53
1:A:516:ARG:O	1:A:519:GLN:N	2.42	0.53
1:A:304:GLN:HG3	1:A:305:THR:HG22	1.91	0.52
1:A:420:LEU:HD13	1:B:361:ILE:HG13	1.91	0.52
1:A:434:LEU:HD21	2:A:627:HOH:O	2.09	0.52
1:A:474:GLY:O	1:A:477:VAL:HG23	2.09	0.52
1:B:304:GLN:CD	1:B:304:GLN:C	2.77	0.52
1:A:352:ARG:C	1:A:354:ILE:N	2.66	0.52
2:A:663:HOH:O	1:B:329:LEU:HD23	2.09	0.52
1:B:328:HIS:C	1:B:330:ALA:H	2.16	0.52
1:B:454:ASP:HA	2:B:604:HOH:O	2.09	0.52
1:A:315:THR:HG23	2:A:654:HOH:O	2.08	0.52
1:A:345:ASP:HA	2:A:728:HOH:O	2.09	0.52
1:A:367:VAL:O	1:A:371:ILE:HD13	2.10	0.52
1:A:361:ILE:O	1:A:364:ILE:HB	2.09	0.52
1:A:403:VAL:O	1:A:404:ARG:C	2.51	0.52
1:B:330:ALA:HB2	1:B:452:VAL:HG12	1.92	0.52
1:B:340:GLY:O	1:B:344:VAL:HB	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:440:GLU:HA	2:B:610:HOH:O	2.10	0.52
1:A:422:GLU:HG3	1:A:423:ASP:H	1.74	0.52
1:A:425:VAL:C	1:A:428:VAL:HG12	2.35	0.52
1:A:313:THR:C	1:A:316:VAL:HG12	2.34	0.52
1:A:330:ALA:CB	1:A:452:VAL:CG1	2.88	0.52
1:B:343:VAL:O	1:B:347:VAL:HG23	2.10	0.52
1:A:402:GLU:HB3	1:B:378:LEU:HD11	1.92	0.51
1:B:321:GLU:OE1	1:B:321:GLU:HA	2.09	0.51
1:A:418:LYS:O	1:A:422:GLU:HG2	2.10	0.51
1:B:395:GLY:O	1:B:398:VAL:HG22	2.10	0.51
1:A:379:ALA:O	1:A:382:ALA:HB3	2.11	0.51
1:A:496:ALA:O	1:A:499:ALA:N	2.43	0.51
1:A:518:GLN:CB	2:A:658:HOH:O	2.58	0.51
1:B:506:SER:O	1:B:510:GLU:HG2	2.10	0.51
1:A:485:GLN:OE1	1:A:485:GLN:HA	2.10	0.51
1:B:432:SER:C	1:B:435:VAL:HG12	2.36	0.51
1:A:480:MET:O	1:A:484:THR:HG22	2.11	0.51
1:B:318:GLN:CG	1:B:319:ASN:N	2.73	0.51
1:B:323:ALA:CB	1:B:459:ILE:HD11	2.41	0.51
1:A:376:ASN:HD21	1:A:404:ARG:HE	1.59	0.51
1:A:331:LEU:HA	1:A:334:SER:HB3	1.94	0.50
1:A:517:ILE:HA	2:A:665:HOH:O	2.11	0.50
1:B:321:GLU:OE1	1:B:324:ARG:HB2	2.11	0.50
1:B:391:GLU:OE1	1:B:391:GLU:HA	2.11	0.50
1:A:404:ARG:O	1:A:408:GLN:HG3	2.12	0.50
1:A:420:LEU:CD1	1:B:361:ILE:HG13	2.40	0.50
1:A:498:ALA:O	1:A:502:GLU:HG3	2.11	0.50
1:A:357:SER:C	1:A:359:GLN:H	2.20	0.50
1:B:327:SER:HB2	1:B:456:MET:HB2	1.94	0.50
1:A:374:GLN:HG3	2:A:743:HOH:O	2.12	0.50
1:A:402:GLU:HG3	2:A:641:HOH:O	2.10	0.50
1:A:434:LEU:N	1:A:434:LEU:HD23	2.27	0.50
1:A:469:GLY:O	1:A:472:GLN:HG2	2.12	0.50
1:A:496:ALA:O	1:A:497:ALA:C	2.55	0.50
1:A:456:MET:SD	1:B:456:MET:SD	3.09	0.49
1:A:517:ILE:C	1:A:520:GLN:H	2.19	0.49
1:A:316:VAL:HG23	1:A:466:GLN:HB2	1.94	0.49
1:A:452:VAL:HG22	1:A:456:MET:HE3	1.93	0.49
1:A:475:LEU:O	1:A:478:ALA:HB3	2.12	0.49
1:A:294:ARG:HH11	1:A:294:ARG:CB	2.15	0.49
1:A:501:LEU:HD21	1:B:501:LEU:HD21	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:754:HOH:O	1:B:333:ALA:HA	2.11	0.49
1:B:306:ALA:O	1:B:309:MET:HB2	2.12	0.49
1:B:328:HIS:HA	2:B:607:HOH:O	2.12	0.49
1:B:514:VAL:HG23	1:B:515:PHE:N	2.26	0.49
1:A:361:ILE:CG2	1:A:421:ILE:CD1	2.90	0.49
1:B:332:SER:C	1:B:334:SER:N	2.69	0.49
1:B:340:GLY:HA3	1:B:442:MET:HG2	1.94	0.49
1:A:384:VAL:O	1:A:388:ARG:HG3	2.12	0.49
1:A:451:ARG:C	1:A:453:THR:N	2.66	0.49
1:B:375:THR:OG1	1:B:407:ALA:HB2	2.13	0.49
1:A:438:ALA:HB2	1:B:343:VAL:CG1	2.18	0.48
1:A:463:SER:HA	1:A:466:GLN:HG3	1.94	0.48
1:A:474:GLY:HA2	1:A:477:VAL:CG2	2.43	0.48
1:A:465:GLU:CD	1:A:468:ARG:HE	2.19	0.48
1:B:316:VAL:HG23	1:B:466:GLN:HG2	1.94	0.48
1:B:353:ASP:HB3	2:B:758:HOH:O	2.12	0.48
1:A:376:ASN:HD21	1:A:404:ARG:NE	2.12	0.48
1:A:485:GLN:C	1:A:487:ASN:N	2.71	0.48
1:A:303:GLU:O	1:A:307:ALA:HB3	2.14	0.48
1:A:347:VAL:CG2	1:B:434:LEU:HB3	2.38	0.48
1:A:389:ALA:O	1:A:390:GLY:C	2.57	0.48
1:A:481:ASP:O	1:A:485:GLN:HB2	2.14	0.48
1:A:503:GLU:HA	2:A:768:HOH:O	2.12	0.48
1:B:426:GLY:O	1:B:429:ASP:HB3	2.13	0.48
1:B:353:ASP:O	1:B:354:ILE:C	2.54	0.48
1:B:513:ALA:HA	2:B:706:HOH:O	2.14	0.48
1:A:304:GLN:OE1	1:B:472:GLN:HB3	2.13	0.48
1:A:496:ALA:O	1:A:498:ALA:N	2.47	0.48
1:B:318:GLN:OE1	1:B:319:ASN:N	2.46	0.48
1:B:350:THR:OG1	1:B:351:MET:N	2.47	0.48
1:B:454:ASP:O	1:B:457:GLY:N	2.46	0.48
1:B:479:GLU:O	1:B:482:ARG:N	2.46	0.48
1:A:353:ASP:HA	1:A:356:THR:HG23	1.94	0.47
1:A:361:ILE:CG1	1:B:420:LEU:CD2	2.92	0.47
1:A:417:ILE:HD13	1:A:417:ILE:O	2.14	0.47
1:B:388:ARG:C	1:B:390:GLY:H	2.22	0.47
1:A:430:VAL:O	1:A:434:LEU:HG	2.14	0.47
1:A:481:ASP:O	1:A:484:THR:HG22	2.14	0.47
1:B:331:LEU:O	1:B:335:GLU:OE1	2.32	0.47
1:A:299:ALA:O	1:A:303:GLU:OE2	2.32	0.47
1:A:451:ARG:C	1:A:453:THR:H	2.21	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:353:ASP:C	1:A:353:ASP:OD2	2.56	0.47
1:A:424:SER:O	1:A:426:GLY:N	2.47	0.47
1:B:314:ALA:O	1:B:315:THR:C	2.58	0.47
1:B:456:MET:N	1:B:456:MET:HE2	2.29	0.47
1:B:488:ALA:O	1:B:492:GLU:HG2	2.13	0.47
1:A:374:GLN:HG2	1:B:406:LEU:HD21	1.96	0.47
1:A:487:ASN:HB2	1:B:487:ASN:OD1	2.14	0.47
1:B:508:LEU:O	1:B:509:THR:C	2.58	0.47
1:A:459:ILE:O	1:A:463:SER:HB3	2.14	0.47
1:B:334:SER:HB2	1:B:449:VAL:CG1	2.44	0.47
1:B:357:SER:C	1:B:359:GLN:H	2.23	0.47
1:B:446:VAL:HG13	2:B:609:HOH:O	2.14	0.47
1:A:431:GLY:O	1:A:435:VAL:HG12	2.14	0.47
1:A:458:GLU:OE1	1:A:458:GLU:HA	2.15	0.47
1:B:324:ARG:NH1	1:B:327:SER:HB3	2.29	0.47
1:B:504:GLN:O	1:B:507:ARG:HB3	2.15	0.47
1:B:300:ALA:HB3	2:B:770:HOH:O	2.14	0.47
1:B:311:GLN:OE1	1:B:312:LEU:N	2.48	0.47
1:A:352:ARG:O	1:A:354:ILE:N	2.47	0.47
1:A:456:MET:HE2	1:A:456:MET:H	1.79	0.47
1:A:442:MET:C	1:A:444:GLU:N	2.73	0.47
1:B:360:LYS:HD3	1:B:360:LYS:O	2.15	0.47
1:B:399:VAL:O	1:B:403:VAL:HG23	2.15	0.47
1:A:342:LYS:HG3	2:A:642:HOH:O	2.15	0.46
1:A:302:LEU:HB2	2:A:623:HOH:O	2.14	0.46
1:A:415:ARG:O	1:A:418:LYS:HB3	2.16	0.46
1:B:356:THR:OG1	1:B:357:SER:N	2.49	0.46
1:A:303:GLU:O	1:A:304:GLN:C	2.58	0.46
1:A:332:SER:O	1:A:336:THR:OG1	2.25	0.46
1:A:469:GLY:O	1:A:471:ASP:N	2.48	0.46
1:B:302:LEU:HB2	1:B:480:MET:HE2	1.92	0.46
1:B:342:LYS:HA	1:B:345:ASP:HB3	1.97	0.46
1:B:348:VAL:O	1:B:352:ARG:HG2	2.15	0.46
1:B:385:GLU:OE2	1:B:385:GLU:HA	2.15	0.46
1:B:422:GLU:O	1:B:423:ASP:C	2.57	0.46
1:A:420:LEU:HB2	2:A:783:HOH:O	2.15	0.46
1:B:415:ARG:HD2	2:B:742:HOH:O	2.16	0.46
1:B:358:SER:C	2:B:639:HOH:O	2.59	0.46
1:A:468:ARG:HH11	1:A:468:ARG:HG2	1.81	0.46
1:A:356:THR:OG1	1:A:357:SER:N	2.48	0.46
1:A:364:ILE:HG22	1:B:417:ILE:HD11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:420:LEU:C	1:A:420:LEU:HD23	2.41	0.46
1:A:465:GLU:HA	1:A:468:ARG:HD3	1.98	0.46
1:A:482:ARG:O	1:A:485:GLN:HB3	2.16	0.46
1:B:455:ILE:HG22	1:B:456:MET:HE2	1.98	0.46
1:A:343:VAL:HG12	1:B:438:ALA:CB	2.44	0.45
1:A:459:ILE:HD11	1:B:323:ALA:HB2	1.97	0.45
1:A:466:GLN:NE2	1:B:315:THR:OG1	2.49	0.45
1:A:430:VAL:HG12	1:A:431:GLY:N	2.31	0.45
1:A:420:LEU:HD13	1:B:361:ILE:CG1	2.46	0.45
1:B:495:ALA:HA	2:B:699:HOH:O	2.15	0.45
1:A:304:GLN:HG3	1:A:305:THR:H	1.81	0.45
1:A:338:GLN:HE21	1:A:338:GLN:CA	2.11	0.45
1:B:370:GLY:O	1:B:373:PHE:HB3	2.16	0.45
1:B:432:SER:HA	2:B:608:HOH:O	2.16	0.45
1:A:316:VAL:CG2	1:A:466:GLN:HB2	2.47	0.45
1:B:517:ILE:O	1:B:519:GLN:N	2.50	0.45
1:A:367:VAL:HG12	1:A:371:ILE:HD13	1.97	0.45
1:A:304:GLN:HG3	1:A:305:THR:HG23	1.97	0.45
1:A:326:ALA:HB2	1:B:455:ILE:HG21	1.98	0.45
1:A:440:GLU:C	1:A:442:MET:N	2.74	0.45
1:A:446:VAL:O	1:A:446:VAL:HG12	2.15	0.45
1:A:485:GLN:O	1:A:487:ASN:N	2.50	0.45
1:A:394:ARG:O	1:A:398:VAL:HG12	2.17	0.45
1:A:412:GLN:O	1:A:413:ALA:C	2.60	0.45
1:B:327:SER:HB2	1:B:456:MET:CB	2.47	0.45
1:B:508:LEU:O	1:B:511:ALA:N	2.49	0.45
1:B:412:GLN:HG3	1:B:413:ALA:N	2.32	0.44
1:B:514:VAL:CG2	1:B:515:PHE:N	2.80	0.44
1:A:396:PHE:HD1	1:A:396:PHE:H	1.63	0.44
1:A:297:GLN:HA	1:A:300:ALA:HB3	1.99	0.44
1:A:442:MET:O	1:A:445:ILE:N	2.51	0.44
1:A:469:GLY:C	1:A:471:ASP:N	2.73	0.44
1:A:378:LEU:HD21	1:B:402:GLU:HG2	1.99	0.44
1:A:510:GLU:HA	1:A:510:GLU:OE2	2.18	0.44
1:B:506:SER:O	1:B:507:ARG:C	2.61	0.44
1:A:516:ARG:C	1:A:518:GLN:N	2.54	0.44
1:B:341:GLY:O	1:B:342:LYS:HD2	2.17	0.44
1:B:354:ILE:CG1	1:B:355:SER:H	2.30	0.44
1:B:404:ARG:HD3	1:B:408:GLN:NE2	2.33	0.44
1:B:510:GLU:HG3	1:B:511:ALA:N	2.32	0.44
1:B:315:THR:O	1:B:318:GLN:HG3	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:339:ARG:O	1:B:340:GLY:C	2.61	0.43
1:B:489:ALA:O	1:B:492:GLU:HB2	2.17	0.43
1:A:512:VAL:O	1:A:516:ARG:HB3	2.18	0.43
1:B:483:VAL:HA	1:B:486:GLN:CG	2.48	0.43
1:A:329:LEU:O	1:A:332:SER:HB3	2.18	0.43
1:A:330:ALA:CB	1:A:452:VAL:HG11	2.46	0.43
1:A:356:THR:O	1:A:357:SER:C	2.61	0.43
1:B:465:GLU:O	1:B:466:GLN:C	2.62	0.43
1:A:459:ILE:O	1:A:463:SER:CB	2.67	0.43
1:A:449:VAL:O	1:A:449:VAL:CG1	2.65	0.43
1:B:306:ALA:C	1:B:309:MET:HB2	2.43	0.43
1:B:454:ASP:O	1:B:455:ILE:C	2.62	0.43
1:A:361:ILE:HG21	1:A:421:ILE:HD12	2.01	0.43
1:A:363:ASP:OD2	1:A:363:ASP:N	2.50	0.43
1:A:404:ARG:O	1:A:407:ALA:HB3	2.19	0.43
1:A:481:ASP:C	1:A:484:THR:HG22	2.44	0.43
1:B:371:ILE:O	1:B:372:ALA:C	2.62	0.43
1:A:463:SER:O	1:A:466:GLN:HB2	2.19	0.43
1:B:427:LYS:HA	2:B:611:HOH:O	2.19	0.43
1:A:363:ASP:HB3	2:A:672:HOH:O	2.18	0.42
1:A:406:LEU:CD1	1:A:406:LEU:N	2.82	0.42
1:A:417:ILE:O	1:A:417:ILE:HG12	2.18	0.42
1:B:316:VAL:O	1:B:320:ALA:HB2	2.19	0.42
1:B:344:VAL:O	1:B:345:ASP:C	2.60	0.42
1:B:426:GLY:O	1:B:429:ASP:CB	2.67	0.42
1:B:497:ALA:O	1:B:498:ALA:C	2.62	0.42
1:A:339:ARG:HB3	2:A:757:HOH:O	2.18	0.42
1:A:417:ILE:O	1:A:417:ILE:CG1	2.66	0.42
1:B:316:VAL:HG21	1:B:466:GLN:HB3	2.02	0.42
1:B:394:ARG:O	1:B:398:VAL:HG13	2.19	0.42
1:B:406:LEU:HD12	1:B:406:LEU:HA	1.55	0.42
1:B:428:VAL:HG12	1:B:428:VAL:O	2.19	0.42
1:A:303:GLU:O	1:A:307:ALA:CB	2.68	0.42
1:A:424:SER:C	1:A:426:GLY:N	2.77	0.42
1:B:377:ILE:HD13	1:B:377:ILE:HA	1.94	0.42
1:A:496:ALA:C	1:A:498:ALA:N	2.76	0.42
1:A:310:GLU:O	1:A:311:GLN:C	2.62	0.42
1:A:442:MET:HE2	1:A:442:MET:CA	2.49	0.42
1:A:356:THR:O	1:A:359:GLN:HB3	2.20	0.42
1:A:361:ILE:HG12	1:B:420:LEU:CD2	2.49	0.42
1:A:364:ILE:HG21	1:B:417:ILE:CD1	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:493:GLN:HG3	2:A:698:HOH:O	2.20	0.42
1:A:305:THR:O	1:A:306:ALA:C	2.62	0.42
1:B:339:ARG:C	1:B:341:GLY:N	2.77	0.42
1:B:467:SER:O	1:B:468:ARG:C	2.63	0.42
1:B:315:THR:OG1	1:B:316:VAL:N	2.53	0.41
1:B:315:THR:O	1:B:317:LYS:N	2.53	0.41
1:B:449:VAL:HG12	1:B:449:VAL:O	2.20	0.41
1:A:307:ALA:HB3	2:A:614:HOH:O	2.19	0.41
1:A:383:ALA:O	1:A:386:ALA:HB3	2.20	0.41
1:A:458:GLU:OE1	1:A:458:GLU:CA	2.68	0.41
1:A:348:VAL:HG13	1:A:352:ARG:NH2	2.36	0.41
1:B:321:GLU:OE1	1:B:460:ALA:HB1	2.20	0.41
1:B:354:ILE:CD1	1:B:428:VAL:HG22	2.40	0.41
1:B:432:SER:O	1:B:435:VAL:HG12	2.20	0.41
1:A:354:ILE:CD1	1:B:427:LYS:HE3	2.50	0.41
1:A:425:VAL:HA	1:A:428:VAL:HG12	2.02	0.41
1:B:318:GLN:O	1:B:322:ASN:HB3	2.21	0.41
1:B:465:GLU:C	1:B:467:SER:N	2.76	0.41
1:A:331:LEU:HA	1:A:334:SER:CB	2.51	0.41
1:A:422:GLU:O	1:A:423:ASP:C	2.63	0.41
1:B:514:VAL:O	1:B:518:GLN:CB	2.66	0.41
1:A:336:THR:HG22	1:B:441:THR:O	2.21	0.41
1:A:337:ALA:N	1:B:445:ILE:HD11	2.36	0.41
1:A:352:ARG:NH2	2:A:724:HOH:O	2.53	0.41
1:A:399:VAL:HG22	1:B:396:PHE:HZ	1.85	0.41
1:A:483:VAL:HB	1:B:483:VAL:CG1	2.50	0.41
1:B:306:ALA:HA	1:B:309:MET:HB2	2.03	0.41
1:A:414:ALA:O	1:A:415:ARG:C	2.63	0.41
1:A:474:GLY:HA2	1:A:477:VAL:HG22	2.02	0.41
1:B:325:GLN:OE1	1:B:326:ALA:N	2.54	0.41
1:B:429:ASP:C	1:B:431:GLY:N	2.79	0.41
1:B:430:VAL:O	1:B:430:VAL:HG12	2.20	0.41
1:A:335:GLU:O	1:A:339:ARG:HG3	2.21	0.41
1:A:380:LEU:O	1:A:381:ASN:C	2.63	0.41
1:B:380:LEU:HA	1:B:380:LEU:HD13	1.86	0.41
1:B:404:ARG:O	1:B:408:GLN:HG2	2.20	0.41
1:A:300:ALA:HA	1:A:303:GLU:HG3	2.02	0.40
1:A:346:ASN:HB2	1:B:434:LEU:CD1	2.51	0.40
1:A:349:GLN:HG3	1:A:350:THR:N	2.36	0.40
1:B:324:ARG:HG3	1:B:324:ARG:HH11	1.86	0.40
1:A:311:GLN:H	1:A:311:GLN:HG3	1.64	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:441:THR:O	1:A:442:MET:HE2	2.21	0.40
1:A:406:LEU:O	1:A:407:ALA:C	2.64	0.40
1:B:377:ILE:O	1:B:378:LEU:C	2.63	0.40
1:A:481:ASP:O	1:A:484:THR:CG2	2.69	0.40
1:B:324:ARG:NH1	1:B:324:ARG:HG3	2.37	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	225/227 (99%)	164 (73%)	46 (20%)	15 (7%)	1	1
1	B	219/227 (96%)	169 (77%)	40 (18%)	10 (5%)	2	2
All	All	444/454 (98%)	333 (75%)	86 (19%)	25 (6%)	1	1

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	394	ARG
1	A	517	ILE
1	A	391	GLU
1	A	496	ALA
1	B	389	ALA
1	B	424	SER
1	B	454	ASP
1	B	455	ILE
1	B	518	GLN
1	A	296	GLU
1	A	304	GLN
1	A	349	GLN
1	A	497	ALA

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Mol	Chain	Res	Type
1	B	319	ASN
1	A	318	GLN
1	A	353	ASP
1	A	425	VAL
1	A	468	ARG
1	A	486	GLN
1	B	309	MET
1	B	316	VAL
1	B	418	LYS
1	B	519	GLN
1	A	403	VAL
1	A	470	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	167/171 (98%)	150 (90%)	17 (10%)	7	15
1	B	164/171 (96%)	139 (85%)	25 (15%)	3	5
All	All	331/342 (97%)	289 (87%)	42 (13%)	4	9

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	294	ARG
1	A	321	GLU
1	A	329	LEU
1	A	354	ILE
1	A	356	THR
1	A	364	ILE
1	A	392	GLN
1	A	398	VAL
1	A	399	VAL
1	A	402	GLU
1	A	417	ILE

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Mol	Chain	Res	Type
1	A	420	LEU
1	A	430	VAL
1	A	456	MET
1	A	477	VAL
1	A	483	VAL
1	A	493	GLN
1	B	311	GLN
1	B	316	VAL
1	B	318	GLN
1	B	319	ASN
1	B	322	ASN
1	B	325	GLN
1	B	335	GLU
1	B	342	LYS
1	B	361	ILE
1	B	375	THR
1	B	378	LEU
1	B	380	LEU
1	B	385	GLU
1	B	398	VAL
1	B	404	ARG
1	B	406	LEU
1	B	420	LEU
1	B	434	LEU
1	B	458	GLU
1	B	466	GLN
1	B	481	ASP
1	B	483	VAL
1	B	490	LEU
1	B	503	GLU
1	B	518	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	311	GLN
1	A	318	GLN
1	A	325	GLN
1	A	328	HIS
1	A	338	GLN
1	A	346	ASN
1	A	374	GLN

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Mol	Chain	Res	Type
1	A	376	ASN
1	A	381	ASN
1	A	466	GLN
1	A	486	GLN
1	B	304	GLN
1	B	319	ASN
1	B	338	GLN
1	B	408	GLN
1	B	466	GLN
1	B	518	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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 ⓘ

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	227/227 (100%)	0.31	17 (7%)	20 16	13, 71, 116, 139	0
1	B	221/227 (97%)	0.54	37 (16%)	4 3	8, 70, 110, 128	0
All	All	448/454 (98%)	0.42	54 (12%)	8 6	8, 71, 114, 139	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	449	VAL	6.3
1	B	442	MET	5.1
1	B	438	ALA	5.0
1	A	319	ASN	5.0
1	B	300	ALA	4.9
1	B	302	LEU	4.7
1	B	340	GLY	4.3
1	A	302	LEU	4.1
1	B	447	SER	4.0
1	B	330	ALA	3.8
1	B	333	ALA	3.8
1	A	320	ALA	3.6
1	A	445	ILE	3.4
1	B	439	GLY	3.4
1	B	443	ALA	3.4
1	B	343	VAL	3.4
1	B	461	SER	3.1
1	A	330	ALA	3.1
1	A	452	VAL	3.0
1	A	448	ALA	2.9
1	A	299	ALA	2.9
1	B	326	ALA	2.9
1	B	424	SER	2.8
1	B	344	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	337	ALA	2.7
1	B	324	ARG	2.6
1	A	333	ALA	2.6
1	B	310	GLU	2.6
1	B	467	SER	2.6
1	A	449	VAL	2.6
1	B	453	THR	2.5
1	B	338	GLN	2.4
1	A	326	ALA	2.4
1	B	448	ALA	2.4
1	B	332	SER	2.3
1	B	325	GLN	2.3
1	B	341	GLY	2.3
1	A	295	THR	2.3
1	B	336	THR	2.3
1	B	463	SER	2.3
1	A	518	GLN	2.3
1	A	520	GLN	2.2
1	B	460	ALA	2.2
1	B	339	ARG	2.2
1	B	301	SER	2.2
1	B	331	LEU	2.2
1	A	441	THR	2.1
1	B	319	ASN	2.1
1	B	472	GLN	2.1
1	A	350	THR	2.1
1	A	442	MET	2.1
1	B	329	LEU	2.1
1	B	317	LYS	2.1
1	B	434	LEU	2.1

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.