



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:17 PM UTC

PDB ID : 3PFL / pdb_00003pfl
Title : CRYSTAL STRUCTURE OF PFL FROM E.COLI IN COMPLEX WITH
SUBSTRATE ANALOGUE OXAMATE
Authors : Becker, A.; Fritz-Wolf, K.; Kabsch, W.; Knappe, J.; Schultz, S.; Wagner,
A.F.V.
Deposited on : 1999-05-14
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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

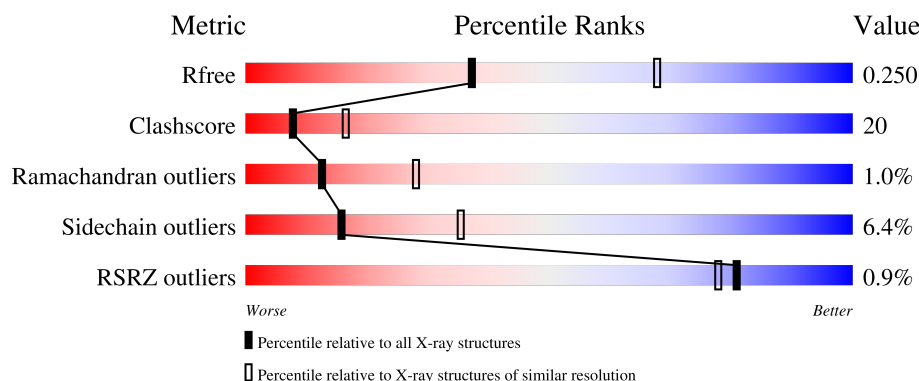
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	759	67% 28% 5%
1	B	759	63% 32% 5%

2 Entry composition [i](#)

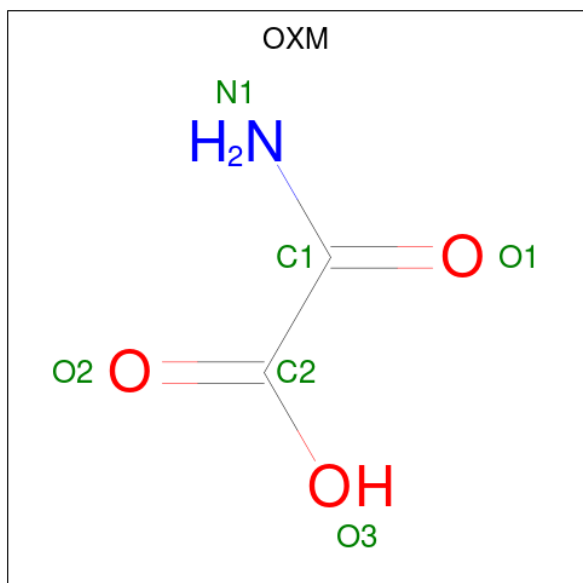
There are 3 unique types of molecules in this entry. The entry contains 12515 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 (FORMATE ACETYLTRANSFERASE 1).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	759	Total	C	N	O	S	0	0	0
			5988	3784	1023	1145	36			
1	B	759	Total	C	N	O	S	0	0	0
			5988	3784	1023	1145	36			

- Molecule 2 is OXAMIC ACID (CCD ID: OXM) (formula: $C_2H_3NO_3$).



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

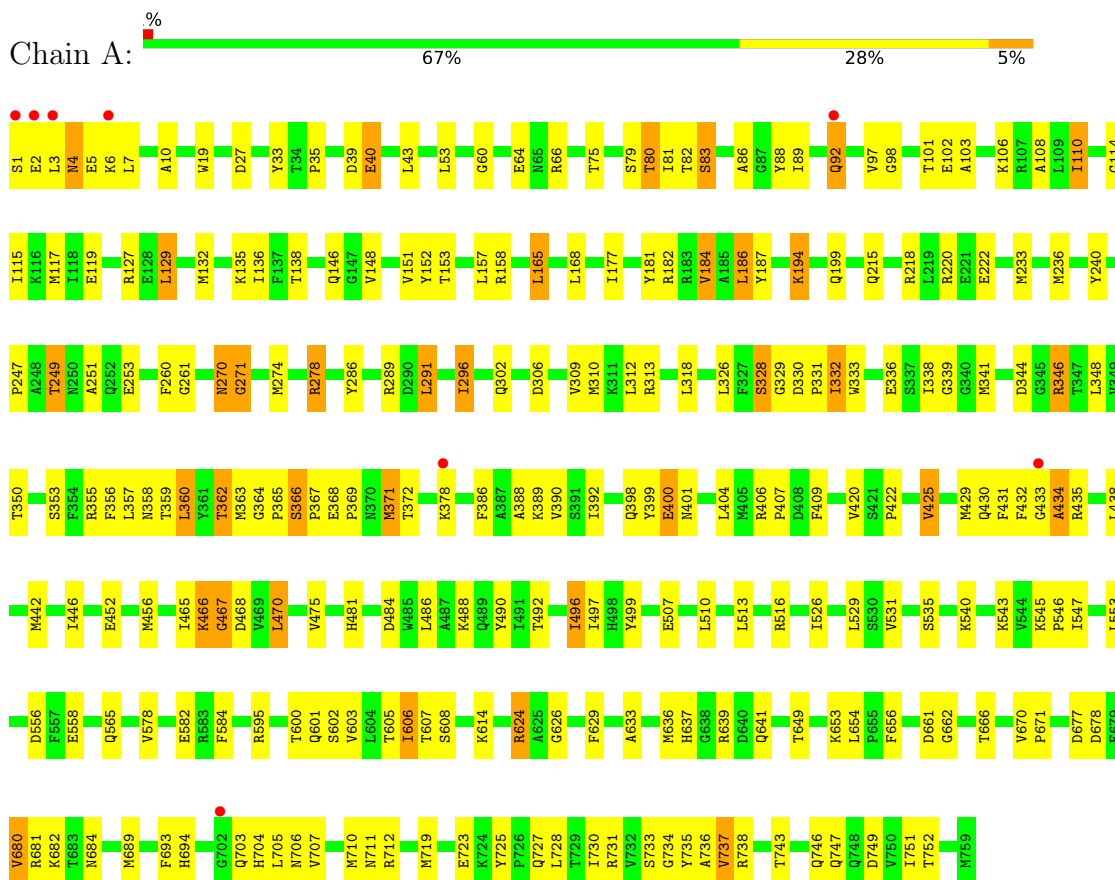
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	294	Total 294	O 294	0	0
3	B	233	Total 233	O 233	0	0

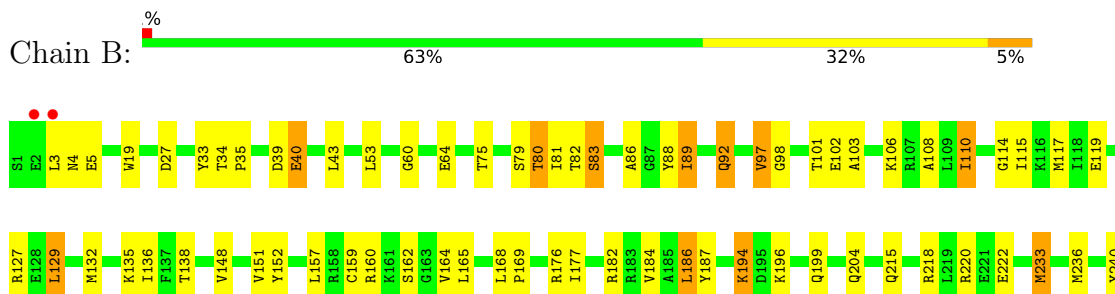
3 Residue-property plots

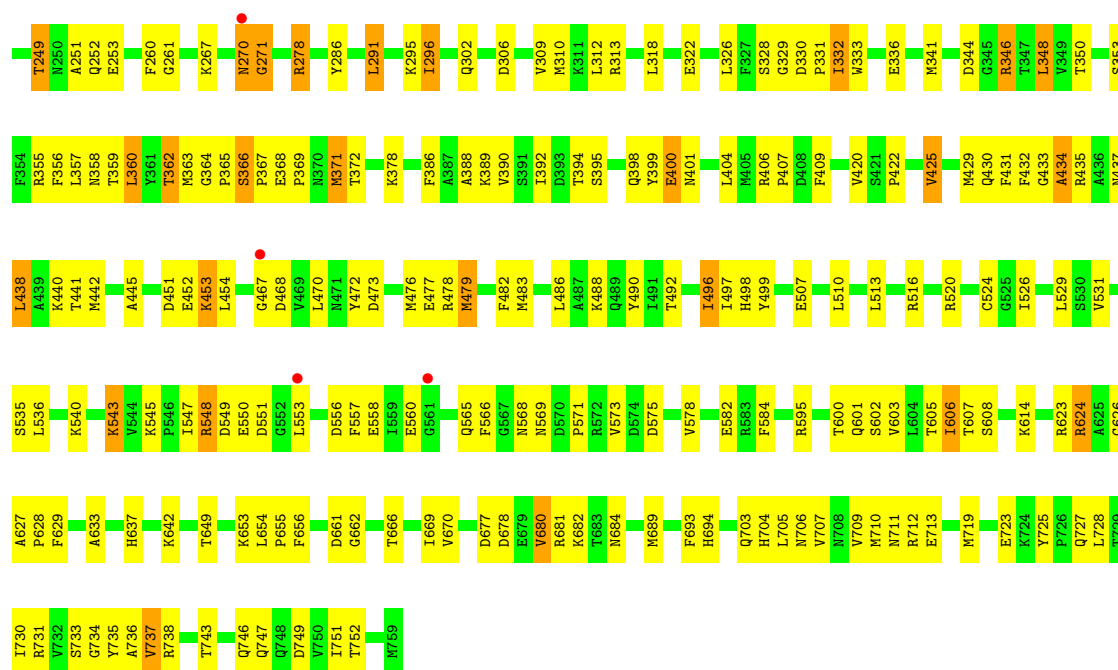
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: PROTEIN (FORMATE ACETYLTRANSFERASE 1)



• Molecule 1: PROTEIN (FORMATE ACETYLTRANSFERASE 1)





4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	159.21Å 159.21Å 160.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.60 50.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	96.1 (50.00-2.60) 96.1 (50.00-2.60)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.50 (at 2.61Å)	Xtriage
Refinement program	CNS CNS 0.5	Depositor
R, R_{free}	0.212 , 0.251 0.212 , 0.250	Depositor DCC
R_{free} test set	2927 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	48.1	Xtriage
Anisotropy	0.254	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 36.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.017 for -h,l,k 0.005 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12515	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.09% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.49	0/6109	0.92	17/8253 (0.2%)
1	B	0.50	1/6109 (0.0%)	0.93	15/8253 (0.2%)
All	All	0.50	1/12218 (0.0%)	0.93	32/16506 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	233	MET	SD-CE	-5.17	1.66	1.79

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	89	ILE	N-CA-C	-10.58	102.71	111.81
1	B	89	ILE	N-CA-C	-10.10	103.12	111.81
1	A	468	ASP	N-CA-C	-6.68	105.16	113.38
1	A	2	GLU	N-CA-C	-6.16	106.44	112.97
1	A	366	SER	CA-C-N	6.12	125.68	119.19
1	A	366	SER	C-N-CA	6.12	125.68	119.19
1	B	654	LEU	CA-C-N	5.99	127.32	119.84
1	B	654	LEU	C-N-CA	5.99	127.32	119.84
1	A	425	VAL	N-CA-C	5.90	117.03	109.30
1	B	499	TYR	N-CA-C	-5.88	104.78	111.14
1	A	629	PHE	N-CA-C	-5.62	102.59	110.35
1	B	629	PHE	N-CA-C	-5.61	102.61	110.35
1	A	654	LEU	CA-C-N	5.57	126.80	119.84
1	A	654	LEU	C-N-CA	5.57	126.80	119.84
1	B	425	VAL	N-CA-C	5.55	116.58	109.30
1	B	110	ILE	CA-C-N	5.48	125.31	119.28
1	B	110	ILE	C-N-CA	5.48	125.31	119.28
1	B	366	SER	CA-C-N	5.44	124.95	119.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	366	SER	C-N-CA	5.44	124.95	119.19
1	A	707	VAL	N-CA-C	5.39	115.86	107.28
1	A	466	LYS	N-CA-C	5.35	119.88	112.45
1	A	432	PHE	N-CA-C	5.26	117.86	110.23
1	A	83	SER	N-CA-C	5.24	116.99	111.28
1	A	110	ILE	CA-C-N	5.23	125.03	119.28
1	A	110	ILE	C-N-CA	5.23	125.03	119.28
1	B	97	VAL	N-CA-C	5.20	117.10	108.99
1	B	267	LYS	N-CA-C	-5.19	107.12	113.50
1	B	707	VAL	N-CA-C	5.14	115.45	107.28
1	B	548	ARG	N-CA-C	5.12	117.41	110.35
1	A	499	TYR	N-CA-C	-5.11	105.62	111.14
1	B	83	SER	N-CA-C	5.02	116.76	111.28
1	A	328	SER	N-CA-C	5.00	117.13	110.53

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	5988	0	5914	225	0
1	B	5988	0	5914	252	0
2	A	6	0	2	0	0
2	B	6	0	2	0	0
3	A	294	0	0	13	0
3	B	233	0	0	14	0
All	All	12515	0	11832	474	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 20.

All (474) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:332:ILE:HB	3:B:951:HOH:O	1.45	1.12
1:A:602:SER:HB3	1:A:661:ASP:HB3	1.40	1.03
1:B:602:SER:HB3	1:B:661:ASP:HB3	1.43	0.97
1:B:362:THR:HG23	1:B:363:MET:HG3	1.47	0.97
1:A:614:LYS:HA	1:A:626:GLY:HA2	1.47	0.96
1:B:614:LYS:HA	1:B:626:GLY:HA2	1.48	0.93
1:A:362:THR:HG23	1:A:363:MET:HG3	1.50	0.92
1:A:712:ARG:NH1	1:A:751:ILE:HG22	1.88	0.89
1:B:712:ARG:NH1	1:B:751:ILE:HG22	1.88	0.88
1:A:712:ARG:HH11	1:A:751:ILE:HG22	1.41	0.86
1:A:710:MET:HE1	1:A:730:ILE:HG22	1.59	0.85
1:B:712:ARG:HH11	1:B:751:ILE:HG22	1.40	0.85
1:A:101:THR:HG21	1:A:106:LYS:HB3	1.58	0.85
1:B:101:THR:HG21	1:B:106:LYS:HB3	1.58	0.84
1:A:670:VAL:HG13	1:A:711:ASN:HD21	1.41	0.84
1:A:359:THR:HA	1:A:362:THR:HG22	1.60	0.83
1:B:710:MET:HE1	1:B:730:ILE:HG22	1.58	0.83
1:A:182:ARG:NH2	1:A:425:VAL:HG21	1.94	0.83
1:B:359:THR:HA	1:B:362:THR:HG22	1.61	0.82
1:A:406:ARG:HB3	1:A:407:PRO:HD3	1.62	0.82
1:B:182:ARG:NH2	1:B:425:VAL:HG21	1.95	0.81
1:B:40:GLU:HG2	1:B:386:PHE:CD1	2.15	0.81
1:B:606:ILE:HG22	1:B:607:THR:H	1.44	0.81
1:B:438:LEU:HD21	1:B:483:MET:HE2	1.63	0.80
1:A:40:GLU:HG2	1:A:386:PHE:CD1	2.17	0.80
1:B:406:ARG:HB3	1:B:407:PRO:HD3	1.63	0.80
1:B:34:THR:HG23	3:B:799:HOH:O	1.81	0.80
1:A:606:ILE:HG22	1:A:607:THR:H	1.47	0.79
1:B:101:THR:HG23	1:B:103:ALA:H	1.47	0.78
1:A:670:VAL:HG13	1:A:711:ASN:ND2	1.99	0.77
1:B:92:GLN:H	1:B:92:GLN:NE2	1.82	0.77
1:A:101:THR:HG23	1:A:103:ALA:H	1.49	0.77
1:B:399:TYR:CD1	1:B:689:MET:HE1	2.19	0.77
1:B:543:LYS:HB2	1:B:560:GLU:HB3	1.66	0.77
1:A:92:GLN:NE2	1:A:92:GLN:H	1.82	0.76
1:A:4:ASN:HD22	1:A:6:LYS:H	1.29	0.76
1:B:600:THR:HG22	1:B:661:ASP:HB2	1.66	0.76
1:A:4:ASN:H	1:A:7:LEU:HD12	1.51	0.75
1:A:80:THR:HG22	1:A:82:THR:H	1.51	0.74
1:B:80:THR:HG22	1:B:82:THR:H	1.51	0.74
1:A:600:THR:HG22	1:A:661:ASP:HB2	1.68	0.74
1:A:399:TYR:CD1	1:A:689:MET:HE1	2.21	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:545:LYS:HB3	1:B:558:GLU:HB2	1.69	0.73
1:B:252:GLN:HG2	3:B:901:HOH:O	1.87	0.73
1:A:4:ASN:HB3	1:A:7:LEU:HG	1.72	0.72
1:A:4:ASN:ND2	1:A:6:LYS:H	1.88	0.71
1:B:132:MET:HE2	1:B:136:ILE:HG13	1.72	0.71
1:B:670:VAL:HG13	1:B:711:ASN:HD21	1.55	0.71
1:A:356:PHE:O	1:A:371:MET:HE1	1.91	0.70
1:A:310:MET:HE2	3:A:830:HOH:O	1.89	0.70
1:A:725:TYR:HB3	1:A:728:LEU:HB2	1.73	0.70
1:B:356:PHE:O	1:B:371:MET:HE1	1.92	0.70
1:A:278:ARG:HD2	3:A:925:HOH:O	1.92	0.70
1:B:332:ILE:HG23	1:B:368:GLU:CD	2.17	0.70
1:B:725:TYR:HB3	1:B:728:LEU:HB2	1.74	0.70
1:A:332:ILE:HG23	1:A:368:GLU:CD	2.17	0.70
1:B:182:ARG:HH22	1:B:425:VAL:HG21	1.57	0.69
1:B:310:MET:HE2	3:B:791:HOH:O	1.91	0.69
1:A:719:MET:SD	1:A:751:ILE:HD11	2.32	0.69
1:B:442:MET:HE1	1:B:535:SER:HB3	1.74	0.69
1:A:689:MET:CE	1:A:705:LEU:HD23	2.22	0.69
1:A:389:LYS:HG2	1:A:682:LYS:HD3	1.75	0.68
1:A:182:ARG:HH22	1:A:425:VAL:HG21	1.59	0.68
1:A:132:MET:HE2	1:A:136:ILE:HG13	1.73	0.68
1:B:101:THR:HG22	3:B:807:HOH:O	1.92	0.68
1:A:743:THR:O	1:A:747:GLN:HG3	1.95	0.67
1:A:442:MET:HE1	1:A:535:SER:HB3	1.75	0.67
1:A:364:GLY:HA3	1:A:727:GLN:HE22	1.60	0.67
1:B:719:MET:SD	1:B:751:ILE:HD11	2.34	0.67
1:B:389:LYS:HG2	1:B:682:LYS:HD3	1.77	0.67
1:A:677:ASP:OD1	1:A:680:VAL:HG23	1.95	0.66
1:B:547:ILE:HB	1:B:556:ASP:HB3	1.76	0.66
1:A:545:LYS:HG2	1:A:558:GLU:HB2	1.76	0.66
1:B:689:MET:CE	1:B:705:LEU:HD23	2.26	0.66
1:B:372:THR:HG23	1:B:398:GLN:HG3	1.78	0.66
1:A:80:THR:HB	1:A:83:SER:HB3	1.78	0.65
1:A:372:THR:HG23	1:A:398:GLN:HG3	1.77	0.65
1:A:624:ARG:HH11	1:A:624:ARG:HG3	1.61	0.65
1:B:80:THR:HB	1:B:83:SER:HB3	1.78	0.65
1:A:233:MET:CE	1:A:261:GLY:HA2	2.26	0.65
1:B:176:ARG:HH11	1:B:430:GLN:HE21	1.43	0.65
1:B:680:VAL:HG12	1:B:684:ASN:ND2	2.11	0.65
1:B:680:VAL:HG12	1:B:684:ASN:HD21	1.62	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:743:THR:O	1:B:747:GLN:HG3	1.96	0.65
1:B:40:GLU:HG2	1:B:386:PHE:CE1	2.32	0.65
1:B:566:PHE:N	1:B:573:VAL:HG21	2.12	0.64
1:B:220:ARG:NH2	3:B:873:HOH:O	2.25	0.64
1:B:364:GLY:HA3	1:B:727:GLN:HE22	1.62	0.64
1:A:151:VAL:O	1:B:220:ARG:NH1	2.30	0.64
1:B:233:MET:CE	1:B:261:GLY:HA2	2.28	0.64
1:A:359:THR:HA	1:A:362:THR:CG2	2.28	0.64
1:A:680:VAL:HG12	1:A:684:ASN:ND2	2.12	0.64
1:B:476:MET:HE1	1:B:536:LEU:HD13	1.79	0.63
1:B:624:ARG:HG3	1:B:624:ARG:HH11	1.63	0.63
1:B:306:ASP:OD1	1:B:362:THR:HG21	1.99	0.63
1:B:438:LEU:HD21	1:B:483:MET:CE	2.28	0.63
1:A:666:THR:HA	1:A:706:ASN:HB2	1.81	0.62
1:A:680:VAL:HG12	1:A:684:ASN:HD21	1.64	0.62
1:A:115:ILE:HG21	1:A:138:THR:CG2	2.30	0.62
1:A:220:ARG:NH2	3:A:885:HOH:O	2.31	0.62
1:B:115:ILE:HG21	1:B:138:THR:CG2	2.30	0.62
1:B:565:GLN:C	1:B:573:VAL:HG11	2.25	0.62
1:A:40:GLU:HG2	1:A:386:PHE:CE1	2.34	0.61
1:A:578:VAL:O	1:A:582:GLU:HG3	2.01	0.61
1:B:578:VAL:O	1:B:582:GLU:HG3	2.01	0.61
1:B:332:ILE:HD12	3:B:831:HOH:O	2.01	0.61
1:A:306:ASP:OD1	1:A:362:THR:HG21	2.01	0.60
1:B:496:ILE:HG13	1:B:497:ILE:N	2.17	0.60
1:B:649:THR:HG22	1:B:653:LYS:HE3	1.83	0.60
1:B:359:THR:HA	1:B:362:THR:CG2	2.29	0.60
1:A:249:THR:HB	1:A:253:GLU:OE1	2.02	0.60
1:B:148:VAL:HG13	1:B:496:ILE:HD11	1.84	0.60
1:B:677:ASP:OD1	1:B:680:VAL:HG23	2.01	0.60
1:B:249:THR:HB	1:B:253:GLU:OE1	2.02	0.60
1:A:148:VAL:HG13	1:A:496:ILE:HD11	1.82	0.59
1:B:53:LEU:HB3	1:B:310:MET:HE1	1.84	0.59
1:B:600:THR:CG2	1:B:661:ASP:HB2	2.32	0.59
1:B:656:PHE:CD1	1:B:703:GLN:HG3	2.38	0.59
1:A:706:ASN:HD21	1:A:734:GLY:N	2.01	0.59
1:A:165:LEU:HD22	1:A:168:LEU:HD11	1.84	0.58
1:A:689:MET:HE2	1:A:705:LEU:HD23	1.83	0.58
1:B:39:ASP:HB2	1:B:40:GLU:OE2	2.03	0.58
1:B:168:LEU:HD12	1:B:434:ALA:HB3	1.83	0.58
1:B:442:MET:HE1	1:B:535:SER:CB	2.32	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:706:ASN:HD21	1:B:734:GLY:N	2.02	0.58
1:B:291:LEU:HD13	1:B:296:ILE:HG22	1.85	0.58
1:A:291:LEU:HD13	1:A:296:ILE:HG22	1.84	0.58
1:A:649:THR:O	1:A:653:LYS:HG3	2.03	0.58
1:B:409:PHE:HE2	1:B:422:PRO:HB2	1.69	0.58
1:B:278:ARG:HD2	3:B:793:HOH:O	2.02	0.58
1:B:492:THR:O	1:B:496:ILE:HG23	2.04	0.58
1:B:218:ARG:O	1:B:222:GLU:HG3	2.03	0.58
1:A:218:ARG:O	1:A:222:GLU:HG3	2.04	0.58
1:A:656:PHE:CD1	1:A:703:GLN:HG3	2.38	0.58
1:A:39:ASP:HB2	1:A:40:GLU:OE2	2.04	0.57
1:B:689:MET:HE3	1:B:705:LEU:HD23	1.85	0.57
1:A:53:LEU:HB3	1:A:310:MET:HE1	1.86	0.57
1:A:678:ASP:O	1:A:682:LYS:HG3	2.04	0.57
1:B:176:ARG:HH11	1:B:430:GLN:NE2	2.03	0.57
1:B:565:GLN:O	1:B:573:VAL:HG11	2.04	0.57
1:A:689:MET:HE3	1:A:705:LEU:HD23	1.85	0.57
1:B:470:LEU:HD11	1:B:557:PHE:HE2	1.68	0.57
1:A:433:GLY:O	1:A:434:ALA:O	2.23	0.57
1:A:442:MET:HE1	1:A:535:SER:CB	2.35	0.57
1:A:719:MET:SD	1:A:751:ILE:CD1	2.92	0.57
1:B:606:ILE:HG22	1:B:607:THR:N	2.18	0.57
1:B:40:GLU:CD	1:B:40:GLU:H	2.12	0.57
1:A:220:ARG:NH1	1:B:151:VAL:O	2.37	0.57
1:B:176:ARG:HG3	1:B:432:PHE:HB2	1.87	0.57
1:B:215:GLN:CD	1:B:215:GLN:H	2.13	0.57
1:A:409:PHE:HE2	1:A:422:PRO:HB2	1.68	0.56
1:A:328:SER:HB3	1:A:746:GLN:NE2	2.20	0.56
1:A:649:THR:HG22	1:A:653:LYS:HE3	1.87	0.56
1:A:80:THR:HG23	3:A:874:HOH:O	2.06	0.56
1:A:289:ARG:HD2	3:A:1031:HOH:O	2.06	0.56
1:B:176:ARG:CG	1:B:432:PHE:HB2	2.35	0.56
1:B:719:MET:SD	1:B:751:ILE:CD1	2.94	0.56
1:A:158:ARG:HG2	1:A:456:MET:HE1	1.87	0.56
1:B:670:VAL:HG13	1:B:711:ASN:ND2	2.20	0.56
1:A:215:GLN:CD	1:A:215:GLN:H	2.13	0.56
1:B:678:ASP:O	1:B:682:LYS:HG3	2.05	0.56
1:B:476:MET:O	1:B:477:GLU:C	2.48	0.56
1:A:496:ILE:HG13	1:A:497:ILE:N	2.17	0.55
1:A:40:GLU:H	1:A:40:GLU:CD	2.14	0.55
1:A:80:THR:CG2	3:A:874:HOH:O	2.54	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:177:ILE:HG12	1:A:429:MET:HE3	1.89	0.55
1:A:600:THR:CG2	1:A:661:ASP:HB2	2.36	0.55
1:A:670:VAL:HG13	1:A:671:PRO:HD2	1.87	0.55
1:B:186:LEU:HD13	1:B:187:TYR:CE2	2.41	0.55
1:B:332:ILE:CG2	1:B:368:GLU:HG3	2.37	0.55
1:A:547:ILE:HD12	1:A:556:ASP:HB3	1.87	0.55
1:B:322:GLU:CD	3:B:900:HOH:O	2.48	0.55
1:A:492:THR:O	1:A:496:ILE:HG23	2.06	0.55
1:B:470:LEU:HD11	1:B:557:PHE:CE2	2.42	0.55
1:A:344:ASP:OD1	1:A:346:ARG:HG2	2.07	0.54
1:B:420:VAL:HG23	1:B:662:GLY:HA3	1.88	0.54
1:A:186:LEU:HD13	1:A:187:TYR:CE2	2.42	0.54
1:A:353:SER:O	1:A:357:LEU:HD13	2.07	0.54
1:B:313:ARG:HG2	1:B:368:GLU:O	2.06	0.54
1:B:649:THR:O	1:B:653:LYS:HG3	2.07	0.54
1:A:677:ASP:CG	1:A:680:VAL:HG23	2.33	0.54
1:B:490:TYR:CE2	1:B:524:CYS:HB3	2.42	0.54
1:B:549:ASP:OD1	1:B:553:LEU:HB3	2.07	0.54
1:A:420:VAL:HG23	1:A:662:GLY:HA3	1.89	0.54
1:B:114:GLY:HA3	1:B:117:MET:HE1	1.90	0.54
1:B:313:ARG:CZ	1:B:366:SER:HB2	2.38	0.54
1:B:353:SER:O	1:B:357:LEU:HD13	2.08	0.54
1:B:372:THR:CG2	1:B:400:GLU:HG3	2.38	0.54
1:A:114:GLY:HA3	1:A:117:MET:HE1	1.89	0.54
1:A:313:ARG:HG2	1:A:368:GLU:O	2.07	0.54
1:A:486:LEU:HD12	1:A:584:PHE:CZ	2.43	0.54
1:B:92:GLN:H	1:B:92:GLN:HE21	1.54	0.54
1:B:605:THR:O	1:B:608:SER:HB2	2.08	0.54
1:B:747:GLN:O	1:B:751:ILE:HG13	2.08	0.53
1:A:313:ARG:CZ	1:A:366:SER:HB2	2.38	0.53
1:A:602:SER:HB3	1:A:661:ASP:CB	2.27	0.53
1:A:601:GLN:HG2	1:A:602:SER:N	2.24	0.53
1:B:486:LEU:HD12	1:B:584:PHE:CZ	2.43	0.53
1:B:556:ASP:OD1	1:B:557:PHE:N	2.42	0.53
1:A:452:GLU:HA	1:A:553:LEU:HD21	1.90	0.53
1:A:368:GLU:HA	1:A:369:PRO:C	2.33	0.53
1:A:115:ILE:HG21	1:A:138:THR:HG23	1.91	0.53
1:B:472:TYR:HD1	1:B:473:ASP:OD1	1.92	0.53
1:A:146:GLN:HG2	3:A:1019:HOH:O	2.08	0.53
1:B:520:ARG:NH1	3:B:790:HOH:O	2.40	0.53
1:B:194:LYS:NZ	1:B:194:LYS:HB3	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:601:GLN:HG2	1:B:602:SER:N	2.23	0.52
1:B:689:MET:HE2	1:B:705:LEU:HD23	1.90	0.52
1:A:606:ILE:HG22	1:A:607:THR:N	2.19	0.52
1:B:437:ASN:ND2	1:B:440:LYS:HB2	2.25	0.52
1:B:677:ASP:CG	1:B:680:VAL:HG23	2.34	0.52
1:A:4:ASN:ND2	1:A:5:GLU:N	2.58	0.52
1:A:372:THR:CG2	1:A:400:GLU:HG3	2.39	0.52
1:B:666:THR:HA	1:B:706:ASN:HB2	1.92	0.52
1:A:80:THR:CG2	1:A:81:ILE:N	2.72	0.52
1:A:747:GLN:O	1:A:751:ILE:HG13	2.09	0.52
1:B:291:LEU:CD1	1:B:296:ILE:HG22	2.40	0.52
1:B:115:ILE:HG21	1:B:138:THR:HG23	1.91	0.52
1:A:466:LYS:O	1:A:467:GLY:O	2.27	0.51
1:B:252:GLN:NE2	3:B:841:HOH:O	2.43	0.51
1:A:4:ASN:ND2	1:A:5:GLU:H	2.08	0.51
1:A:332:ILE:CG2	1:A:368:GLU:HG3	2.40	0.51
1:B:233:MET:HE3	1:B:261:GLY:HA2	1.92	0.51
1:B:401:ASN:ND2	1:B:404:LEU:HB2	2.24	0.51
1:A:360:LEU:HD12	1:A:365:PRO:HA	1.92	0.51
1:A:624:ARG:HH11	1:A:624:ARG:CG	2.23	0.51
1:B:752:THR:O	1:B:752:THR:HG22	2.09	0.51
1:A:115:ILE:HG22	3:A:1006:HOH:O	2.08	0.51
1:A:194:LYS:NZ	1:A:194:LYS:HB3	2.26	0.51
1:A:80:THR:HG22	1:A:82:THR:N	2.23	0.51
1:B:80:THR:CG2	1:B:81:ILE:N	2.73	0.51
1:B:344:ASP:OD1	1:B:346:ARG:HG2	2.10	0.51
1:B:127:ARG:HG3	1:B:127:ARG:HH11	1.76	0.51
1:A:752:THR:HG22	1:A:752:THR:O	2.10	0.51
1:B:119:GLU:HG2	1:B:129:LEU:HD12	1.93	0.51
1:B:433:GLY:O	1:B:434:ALA:O	2.28	0.51
1:A:233:MET:HE3	1:A:261:GLY:HA2	1.92	0.50
1:A:302:GLN:HG2	3:A:899:HOH:O	2.10	0.50
1:B:624:ARG:HH11	1:B:624:ARG:CG	2.25	0.50
1:A:526:ILE:HD11	1:A:584:PHE:CD2	2.46	0.50
1:A:386:PHE:O	1:A:390:VAL:HG23	2.12	0.50
1:A:341:MET:HG3	1:A:378:LYS:HZ2	1.77	0.50
1:A:605:THR:O	1:A:608:SER:HB2	2.12	0.50
1:B:368:GLU:HA	1:B:369:PRO:C	2.35	0.50
1:B:545:LYS:O	1:B:557:PHE:HA	2.12	0.49
1:B:637:HIS:H	1:B:637:HIS:CD2	2.30	0.49
1:A:302:GLN:CD	1:A:358:ASN:HD22	2.20	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:VAL:HG12	1:A:240:TYR:CE2	2.48	0.49
1:A:291:LEU:CD1	1:A:296:ILE:HG22	2.41	0.49
1:B:398:GLN:HB3	1:B:731:ARG:NH1	2.27	0.49
1:A:10:ALA:O	1:A:289:ARG:NH2	2.41	0.49
1:A:399:TYR:CG	1:A:689:MET:HE1	2.48	0.49
1:B:199:GLN:HG2	1:B:516:ARG:HB2	1.93	0.49
1:B:40:GLU:HB3	1:B:43:LEU:HD12	1.95	0.49
1:B:360:LEU:HD12	1:B:365:PRO:HA	1.94	0.49
1:A:398:GLN:HB3	1:A:731:ARG:NH1	2.27	0.49
1:B:97:VAL:HG12	1:B:240:TYR:CE2	2.48	0.49
1:B:341:MET:HG3	1:B:378:LYS:HZ2	1.77	0.49
1:B:600:THR:HG22	1:B:601:GLN:N	2.27	0.49
1:B:186:LEU:HD13	1:B:187:TYR:CZ	2.48	0.49
1:B:399:TYR:CG	1:B:689:MET:HE1	2.47	0.49
1:A:119:GLU:HG2	1:A:129:LEU:HD12	1.95	0.48
1:A:470:LEU:HD13	1:A:546:PRO:CG	2.42	0.48
1:B:312:LEU:CB	1:B:369:PRO:HG3	2.43	0.48
1:A:600:THR:HG22	1:A:601:GLN:N	2.29	0.48
1:B:302:GLN:CD	1:B:358:ASN:HD22	2.20	0.48
1:B:540:LYS:O	1:B:540:LYS:HG2	2.12	0.48
1:B:92:GLN:NE2	1:B:92:GLN:N	2.58	0.48
1:A:350:THR:O	1:A:353:SER:HB2	2.13	0.48
1:A:388:ALA:O	1:A:392:ILE:HG13	2.13	0.48
1:A:637:HIS:CD2	1:A:637:HIS:H	2.29	0.48
1:B:291:LEU:HD12	1:B:296:ILE:O	2.14	0.48
1:B:637:HIS:HE1	1:B:749:ASP:OD1	1.96	0.48
1:A:4:ASN:CG	1:A:5:GLU:H	2.22	0.48
1:A:302:GLN:OE1	1:A:355:ARG:HA	2.14	0.48
1:B:743:THR:OG1	1:B:746:GLN:HG3	2.13	0.48
1:A:641:GLN:HG2	3:A:969:HOH:O	2.12	0.48
1:B:328:SER:HB3	1:B:746:GLN:NE2	2.29	0.48
1:B:388:ALA:O	1:B:392:ILE:HG13	2.13	0.48
1:A:127:ARG:HG3	1:A:127:ARG:HH11	1.79	0.48
1:A:401:ASN:ND2	1:A:404:LEU:HB2	2.29	0.48
1:A:637:HIS:HE1	1:A:749:ASP:OD1	1.97	0.48
1:A:97:VAL:HG12	1:A:98:GLY:N	2.29	0.48
1:A:92:GLN:H	1:A:92:GLN:HE21	1.58	0.47
1:B:556:ASP:C	1:B:557:PHE:CD1	2.92	0.47
1:A:291:LEU:HD12	1:A:296:ILE:O	2.14	0.47
1:A:6:LYS:O	1:A:7:LEU:C	2.58	0.47
1:B:467:GLY:O	1:B:548:ARG:NH2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:302:GLN:CG	3:A:899:HOH:O	2.63	0.47
1:A:486:LEU:HD12	1:A:584:PHE:CE1	2.49	0.47
1:B:97:VAL:HG12	1:B:98:GLY:N	2.29	0.47
1:B:165:LEU:HD23	1:B:165:LEU:HA	1.78	0.47
1:B:302:GLN:OE1	1:B:355:ARG:HA	2.15	0.47
1:B:486:LEU:HD12	1:B:584:PHE:CE1	2.50	0.47
1:A:151:VAL:HB	1:A:496:ILE:HD13	1.95	0.47
1:A:199:GLN:HG2	1:A:516:ARG:HB2	1.97	0.47
1:B:332:ILE:HG23	1:B:368:GLU:HG3	1.97	0.47
1:A:270:ASN:O	1:A:271:GLY:C	2.57	0.47
1:B:302:GLN:HG2	3:B:967:HOH:O	2.14	0.46
1:B:704:HIS:CG	1:B:705:LEU:N	2.83	0.46
1:A:186:LEU:HD13	1:A:187:TYR:CZ	2.50	0.46
1:A:743:THR:OG1	1:A:746:GLN:HG3	2.15	0.46
1:B:270:ASN:O	1:B:271:GLY:C	2.58	0.46
1:A:333:TRP:HE1	1:A:735:TYR:HB3	1.80	0.46
1:B:159:CYS:HB3	1:B:165:LEU:HB2	1.97	0.46
1:B:333:TRP:HE1	1:B:735:TYR:HB3	1.80	0.46
1:B:176:ARG:HD2	1:B:430:GLN:NE2	2.31	0.46
1:B:270:ASN:HD22	1:B:270:ASN:HA	1.53	0.46
1:B:372:THR:HG21	1:B:400:GLU:HG3	1.98	0.46
1:A:409:PHE:CE2	1:A:422:PRO:HB2	2.49	0.46
1:B:88:TYR:CE2	1:B:97:VAL:HG11	2.51	0.46
1:B:409:PHE:CE2	1:B:422:PRO:HB2	2.50	0.46
1:A:153:THR:CG2	1:B:204:GLN:HG3	2.46	0.45
1:A:420:VAL:CG2	1:A:662:GLY:HA3	2.46	0.45
1:B:80:THR:HG22	1:B:82:THR:N	2.24	0.45
1:A:148:VAL:HA	1:A:496:ILE:HD11	1.97	0.45
1:A:312:LEU:CB	1:A:369:PRO:HG3	2.47	0.45
1:A:603:VAL:HG11	1:A:633:ALA:HB2	1.98	0.45
1:A:332:ILE:HG23	1:A:368:GLU:OE2	2.16	0.45
1:B:132:MET:HE2	1:B:136:ILE:CG1	2.45	0.45
1:B:386:PHE:O	1:B:390:VAL:HG23	2.17	0.45
1:A:40:GLU:HB3	1:A:43:LEU:HD12	1.98	0.45
1:A:97:VAL:HG12	1:A:240:TYR:CD2	2.52	0.45
1:A:270:ASN:HD22	1:A:270:ASN:HA	1.53	0.45
1:B:578:VAL:HG13	1:B:655:PRO:HD3	1.98	0.45
1:B:677:ASP:O	1:B:681:ARG:HG3	2.16	0.45
1:A:367:PRO:HG2	1:A:738:ARG:HG3	1.99	0.45
1:A:401:ASN:HB2	1:A:693:PHE:CD1	2.52	0.45
1:B:600:THR:CG2	1:B:601:GLN:N	2.79	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:602:SER:HB3	1:B:661:ASP:CB	2.28	0.45
1:B:420:VAL:O	1:B:422:PRO:HD3	2.16	0.45
1:B:453:LYS:HB3	1:B:454:LEU:HD22	1.98	0.45
1:A:332:ILE:HG21	3:A:791:HOH:O	2.16	0.45
1:B:127:ARG:HG3	1:B:127:ARG:NH1	2.31	0.45
1:A:81:ILE:HG13	3:A:963:HOH:O	2.17	0.45
1:A:182:ARG:NH2	1:A:425:VAL:CG2	2.74	0.45
1:B:151:VAL:O	1:B:151:VAL:HG12	2.16	0.45
1:B:367:PRO:HG2	1:B:738:ARG:HG3	1.99	0.45
1:B:431:PHE:HB3	1:B:498:HIS:CD2	2.51	0.45
1:B:569:ASN:O	1:B:571:PRO:HD3	2.17	0.45
1:B:637:HIS:CE1	1:B:749:ASP:OD1	2.70	0.45
1:A:359:THR:CA	1:A:362:THR:HG22	2.37	0.45
1:A:704:HIS:CG	1:A:705:LEU:N	2.85	0.45
1:B:332:ILE:HG23	1:B:368:GLU:CG	2.47	0.44
1:B:706:ASN:HB3	1:B:731:ARG:HB3	1.99	0.44
1:A:466:LYS:O	1:A:467:GLY:C	2.60	0.44
1:A:603:VAL:CG1	1:A:633:ALA:HB2	2.46	0.44
1:B:60:GLY:O	1:B:64:GLU:HG3	2.17	0.44
1:B:445:ALA:HA	1:B:482:PHE:CE1	2.53	0.44
1:B:603:VAL:HG11	1:B:633:ALA:HB2	2.00	0.44
1:B:79:SER:HB3	1:B:110:ILE:HD13	1.99	0.44
1:B:309:VAL:HG21	1:B:359:THR:HG21	2.00	0.44
1:B:420:VAL:CG2	1:B:662:GLY:HA3	2.47	0.44
1:A:372:THR:HG21	1:A:400:GLU:HG3	2.00	0.44
1:B:545:LYS:HD2	1:B:558:GLU:OE1	2.16	0.44
1:B:706:ASN:HD21	1:B:734:GLY:CA	2.30	0.44
1:A:344:ASP:OD2	1:A:346:ARG:HD3	2.18	0.44
1:B:97:VAL:HG12	1:B:240:TYR:CD2	2.52	0.44
1:B:101:THR:OG1	1:B:102:GLU:N	2.51	0.44
1:A:420:VAL:O	1:A:422:PRO:HD3	2.18	0.44
1:B:132:MET:HE3	1:B:135:LYS:HB3	2.00	0.44
1:B:329:GLY:HA3	1:B:737:VAL:HG22	1.99	0.44
1:B:442:MET:N	1:B:479:MET:HE1	2.33	0.44
1:B:357:LEU:HD12	1:B:357:LEU:N	2.31	0.44
1:B:442:MET:HA	1:B:479:MET:CE	2.48	0.44
1:A:33:TYR:CE2	1:A:35:PRO:HG3	2.53	0.43
1:A:88:TYR:CE2	1:A:97:VAL:HG11	2.52	0.43
1:A:547:ILE:HD11	1:A:558:GLU:HG3	1.99	0.43
1:B:3:LEU:O	1:B:4:ASN:C	2.61	0.43
1:B:367:PRO:HA	1:B:736:ALA:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:132:MET:HE3	1:A:135:LYS:HB3	2.00	0.43
1:A:600:THR:CG2	1:A:601:GLN:N	2.81	0.43
1:B:507:GLU:HB3	1:B:510:LEU:HD13	2.00	0.43
1:B:236:MET:HE1	1:B:260:PHE:O	2.18	0.43
1:B:332:ILE:HG23	1:B:368:GLU:OE2	2.18	0.43
1:B:350:THR:O	1:B:353:SER:HB2	2.18	0.43
1:A:127:ARG:HG3	1:A:127:ARG:NH1	2.33	0.43
1:A:465:ILE:CD1	1:A:475:VAL:HG22	2.49	0.43
1:B:148:VAL:HA	1:B:496:ILE:HD11	2.00	0.43
1:B:182:ARG:NH2	1:B:425:VAL:CG2	2.76	0.43
1:A:236:MET:HE1	1:A:260:PHE:O	2.19	0.43
1:A:637:HIS:CE1	1:A:749:ASP:OD1	2.71	0.43
1:B:101:THR:CG2	1:B:106:LYS:HB3	2.41	0.43
1:B:177:ILE:HG12	1:B:429:MET:HE3	1.99	0.43
1:B:603:VAL:CG1	1:B:633:ALA:HB2	2.49	0.43
1:B:401:ASN:HB2	1:B:693:PHE:CD1	2.53	0.43
1:A:547:ILE:HD11	1:A:558:GLU:CG	2.48	0.43
1:A:706:ASN:HD21	1:A:734:GLY:CA	2.32	0.43
1:B:472:TYR:CE2	1:B:476:MET:HE2	2.53	0.43
1:A:4:ASN:CG	1:A:5:GLU:N	2.77	0.43
1:A:6:LYS:NZ	1:A:247:PRO:O	2.52	0.43
1:B:151:VAL:HB	1:B:496:ILE:HD13	2.00	0.43
1:B:628:PRO:HG3	3:B:826:HOH:O	2.19	0.43
1:A:251:ALA:HA	1:A:286:TYR:HB3	2.01	0.43
1:A:540:LYS:O	1:A:540:LYS:HG2	2.18	0.43
1:B:196:LYS:HD3	1:B:196:LYS:HA	1.81	0.43
1:B:451:ASP:C	1:B:453:LYS:H	2.27	0.43
1:B:571:PRO:O	1:B:575:ASP:HB2	2.19	0.43
1:A:60:GLY:O	1:A:64:GLU:HG3	2.19	0.42
1:A:86:ALA:HA	1:A:240:TYR:CZ	2.54	0.42
1:A:332:ILE:HG23	1:A:368:GLU:HG3	2.01	0.42
1:B:359:THR:CA	1:B:362:THR:HG22	2.38	0.42
1:B:669:ILE:O	1:B:709:VAL:HA	2.19	0.42
1:A:79:SER:HB3	1:A:110:ILE:HD13	2.02	0.42
1:A:329:GLY:HA3	1:A:737:VAL:HG22	2.02	0.42
1:B:364:GLY:HA3	1:B:727:GLN:NE2	2.32	0.42
1:A:330:ASP:N	1:A:331:PRO:CD	2.82	0.42
1:B:162:SER:OG	1:B:164:VAL:HG12	2.19	0.42
1:B:251:ALA:HA	1:B:286:TYR:HB3	2.02	0.42
1:A:101:THR:OG1	1:A:102:GLU:N	2.52	0.42
1:B:86:ALA:HA	1:B:240:TYR:CZ	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:510:LEU:HD12	1:A:510:LEU:N	2.35	0.42
1:B:302:GLN:CG	3:B:967:HOH:O	2.67	0.42
1:B:438:LEU:HD23	1:B:438:LEU:HA	1.82	0.42
1:A:4:ASN:HD22	1:A:6:LYS:N	2.07	0.42
1:A:66:ARG:HH11	1:A:66:ARG:HG2	1.84	0.42
1:B:160:ARG:HA	1:B:165:LEU:O	2.19	0.42
1:A:357:LEU:N	1:A:357:LEU:HD12	2.35	0.42
1:B:89:ILE:CD1	1:B:310:MET:HE3	2.50	0.42
1:B:543:LYS:CB	1:B:560:GLU:HB3	2.43	0.42
1:B:549:ASP:O	1:B:551:ASP:N	2.52	0.42
1:A:526:ILE:HD11	1:A:584:PHE:CE2	2.55	0.42
1:A:1:SER:C	1:A:3:LEU:H	2.28	0.41
1:A:19:TRP:HD1	1:A:27:ASP:OD2	2.03	0.41
1:A:151:VAL:O	1:A:151:VAL:HG12	2.18	0.41
1:A:215:GLN:CD	1:A:215:GLN:N	2.77	0.41
1:B:79:SER:HB2	1:B:108:ALA:HB1	2.02	0.41
1:A:165:LEU:HD11	1:A:490:TYR:HA	2.01	0.41
1:B:332:ILE:HD12	1:B:332:ILE:O	2.20	0.41
1:B:478:ARG:O	1:B:479:MET:C	2.63	0.41
1:B:330:ASP:N	1:B:331:PRO:CD	2.83	0.41
1:B:706:ASN:OD1	1:B:731:ARG:HD3	2.21	0.41
1:A:332:ILE:HG23	1:A:368:GLU:CG	2.50	0.41
1:A:367:PRO:HA	1:A:736:ALA:HB3	2.02	0.41
1:B:510:LEU:N	1:B:510:LEU:HD12	2.35	0.41
1:A:693:PHE:O	1:A:694:HIS:C	2.62	0.41
1:B:565:GLN:C	1:B:573:VAL:HG21	2.45	0.41
1:A:364:GLY:HA3	1:A:727:GLN:NE2	2.30	0.41
1:B:706:ASN:HD21	1:B:734:GLY:HA2	1.85	0.41
1:A:181:TYR:O	1:A:184:VAL:HG13	2.21	0.41
1:A:309:VAL:HG21	1:A:359:THR:HG21	2.03	0.41
1:A:507:GLU:HB3	1:A:510:LEU:HD13	2.03	0.41
1:B:348:LEU:HD13	1:B:348:LEU:HA	1.95	0.41
1:B:549:ASP:C	1:B:551:ASP:H	2.28	0.41
1:A:79:SER:HB2	1:A:108:ALA:HB1	2.02	0.41
1:B:19:TRP:HD1	1:B:27:ASP:OD2	2.03	0.41
1:B:526:ILE:HD13	1:B:526:ILE:HA	1.84	0.41
1:A:148:VAL:HA	1:A:496:ILE:CD1	2.50	0.41
1:A:446:ILE:HG12	1:A:465:ILE:HD12	2.02	0.41
1:A:636:MET:O	1:A:637:HIS:C	2.63	0.41
1:A:706:ASN:HB3	1:A:731:ARG:HB3	2.03	0.41
1:B:148:VAL:HA	1:B:496:ILE:CD1	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:441:THR:HG22	1:B:479:MET:CE	2.51	0.41
1:B:623:ARG:NH1	1:B:627:ALA:O	2.54	0.41
1:B:693:PHE:O	1:B:694:HIS:C	2.63	0.41
1:B:182:ARG:HH22	1:B:425:VAL:CG2	2.31	0.41
1:B:568:ASN:O	1:B:642:LYS:HD2	2.20	0.41
1:A:332:ILE:O	1:A:333:TRP:HB2	2.20	0.40
1:A:677:ASP:O	1:A:681:ARG:HG3	2.21	0.40
1:A:271:GLY:HA3	1:A:274:MET:SD	2.61	0.40
1:A:545:LYS:O	1:A:545:LYS:HG3	2.20	0.40
1:A:565:GLN:NE2	1:A:639:ARG:HD3	2.36	0.40
1:A:752:THR:O	1:A:752:THR:CG2	2.69	0.40
1:B:33:TYR:CE2	1:B:35:PRO:HG3	2.56	0.40
1:B:215:GLN:CD	1:B:215:GLN:N	2.78	0.40
1:B:295:LYS:O	1:B:296:ILE:HD12	2.22	0.40
1:B:438:LEU:HG	1:B:526:ILE:HD12	2.03	0.40
1:A:338:ILE:HG22	1:A:339:GLY:N	2.36	0.40
1:A:481:HIS:O	1:A:484:ASP:HB2	2.21	0.40
1:B:362:THR:CG2	1:B:363:MET:HG3	2.34	0.40
1:A:132:MET:HE2	1:A:136:ILE:CG1	2.46	0.40
1:B:711:ASN:HB3	1:B:713:GLU:OE1	2.22	0.40
1:A:97:VAL:CG1	1:A:240:TYR:CD2	3.04	0.40
1:B:394:THR:O	1:B:395:SER:HB2	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	757/759 (100%)	706 (93%)	44 (6%)	7 (1%)	14	30
1	B	757/759 (100%)	703 (93%)	46 (6%)	8 (1%)	11	25
All	All	1514/1518 (100%)	1409 (93%)	90 (6%)	15 (1%)	12	28

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	434	ALA
1	B	434	ALA
1	B	550	GLU
1	A	271	GLY
1	A	467	GLY
1	A	606	ILE
1	A	733	SER
1	B	271	GLY
1	B	452	GLU
1	B	606	ILE
1	B	733	SER
1	B	723	GLU
1	A	723	GLU
1	A	4	ASN
1	B	169	PRO

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	638/638 (100%)	597 (94%)	41 (6%)	16	35
1	B	638/638 (100%)	597 (94%)	41 (6%)	16	35
All	All	1276/1276 (100%)	1194 (94%)	82 (6%)	16	35

All (82) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	GLU
1	A	75	THR
1	A	80	THR
1	A	92	GLN
1	A	129	LEU
1	A	152	TYR
1	A	157	LEU
1	A	165	LEU

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Mol	Chain	Res	Type
1	A	184	VAL
1	A	186	LEU
1	A	194	LYS
1	A	249	THR
1	A	270	ASN
1	A	278	ARG
1	A	291	LEU
1	A	296	ILE
1	A	318	LEU
1	A	326	LEU
1	A	332	ILE
1	A	336	GLU
1	A	346	ARG
1	A	348	LEU
1	A	360	LEU
1	A	362	THR
1	A	371	MET
1	A	400	GLU
1	A	430	GLN
1	A	431	PHE
1	A	435	ARG
1	A	438	LEU
1	A	470	LEU
1	A	488	LYS
1	A	496	ILE
1	A	513	LEU
1	A	529	LEU
1	A	531	VAL
1	A	543	LYS
1	A	595	ARG
1	A	624	ARG
1	A	680	VAL
1	A	737	VAL
1	B	5	GLU
1	B	40	GLU
1	B	75	THR
1	B	80	THR
1	B	92	GLN
1	B	129	LEU
1	B	152	TYR
1	B	157	LEU
1	B	184	VAL

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Mol	Chain	Res	Type
1	B	186	LEU
1	B	194	LYS
1	B	249	THR
1	B	270	ASN
1	B	278	ARG
1	B	291	LEU
1	B	296	ILE
1	B	318	LEU
1	B	326	LEU
1	B	332	ILE
1	B	336	GLU
1	B	346	ARG
1	B	348	LEU
1	B	360	LEU
1	B	362	THR
1	B	371	MET
1	B	400	GLU
1	B	435	ARG
1	B	438	LEU
1	B	453	LYS
1	B	468	ASP
1	B	479	MET
1	B	488	LYS
1	B	496	ILE
1	B	513	LEU
1	B	529	LEU
1	B	531	VAL
1	B	543	LYS
1	B	595	ARG
1	B	624	ARG
1	B	680	VAL
1	B	737	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	4	ASN
1	A	21	ASN
1	A	92	GLN
1	A	144	HIS
1	A	270	ASN
1	A	358	ASN

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Mol	Chain	Res	Type
1	A	430	GLN
1	A	471	ASN
1	A	565	GLN
1	A	637	HIS
1	A	684	ASN
1	A	694	HIS
1	A	706	ASN
1	A	711	ASN
1	B	92	GLN
1	B	144	HIS
1	B	270	ASN
1	B	358	ASN
1	B	430	GLN
1	B	489	GLN
1	B	601	GLN
1	B	637	HIS
1	B	684	ASN
1	B	694	HIS
1	B	711	ASN
1	B	740	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond

length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	OXM	A	761	-	5,5,5	3.17	1 (20%)	2,6,6	1.17	0
2	OXM	B	762	-	5,5,5	3.36	2 (40%)	2,6,6	1.29	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OXM	A	761	-	-	4/4/4/4	-
2	OXM	B	762	-	-	1/4/4/4	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	762	OXM	C1-C2	-7.07	1.47	1.55
2	A	761	OXM	C1-C2	-6.77	1.47	1.55
2	B	762	OXM	O3-C2	-2.27	1.24	1.30

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	761	OXM	N1-C1-C2-O2
2	A	761	OXM	N1-C1-C2-O3
2	A	761	OXM	O1-C1-C2-O2
2	A	761	OXM	O1-C1-C2-O3
2	B	762	OXM	O1-C1-C2-O3

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	759/759 (100%)	-0.05	8 (1%) 78 74	27, 45, 65, 100	0
1	B	759/759 (100%)	0.09	6 (0%) 82 80	30, 48, 73, 96	0
All	All	1518/1518 (100%)	0.02	14 (0%) 81 78	27, 47, 70, 100	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	GLU	5.0
1	A	3	LEU	3.6
1	A	1	SER	3.4
1	A	378	LYS	2.7
1	B	270	ASN	2.7
1	B	553	LEU	2.6
1	B	3	LEU	2.5
1	A	702	GLY	2.2
1	A	6	LYS	2.2
1	B	2	GLU	2.1
1	B	467	GLY	2.1
1	A	433	GLY	2.1
1	B	561	GLY	2.1
1	A	92	GLN	2.1

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	OXM	A	761	6/6	0.94	0.08	41,43,44,45	0
2	OXM	B	762	6/6	0.96	0.07	42,43,44,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.