



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 28, 2024 – 01:26 AM EDT

PDB ID : 2G5T
Title : Crystal structure of human dipeptidyl peptidase IV (DPPIV) complexed with cyanopyrrolidine (C5-pro-pro) inhibitor 2lag
Authors : Longenecker, K.L.; Fry, E.H.; Lake, M.R.; Solomon, L.R.; Pei, Z.; Li, X.
Deposited on : 2006-02-23
Resolution : 2.30 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

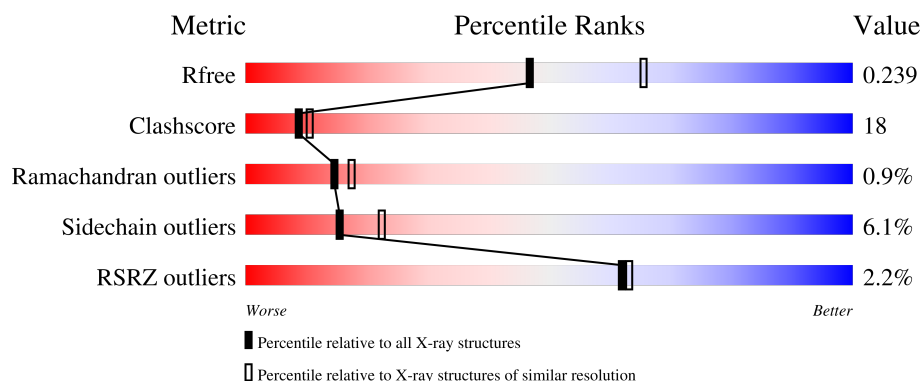
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

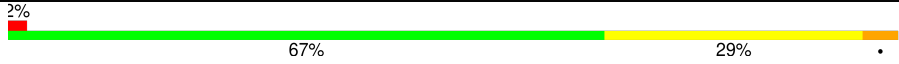

The reported resolution of this entry is 2.30 Å.

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}	164625	5963 (2.30-2.30)
Clashscore	180529	6698 (2.30-2.30)
Ramachandran outliers	177936	6640 (2.30-2.30)
Sidechain outliers	177891	6640 (2.30-2.30)
RSRZ outliers	164620	5963 (2.30-2.30)

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	726	
1	B	726	

2 Entry composition [i](#)

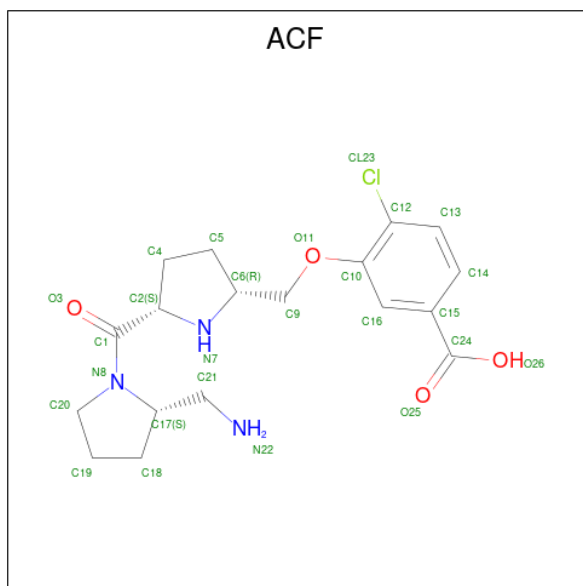
There are 3 unique types of molecules in this entry. The entry contains 13345 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Dipeptidyl peptidase 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	726	Total	C	N	O	S	0	0	0
			5949	3816	980	1127	26			
1	B	726	Total	C	N	O	S	0	0	0
			5949	3816	980	1127	26			

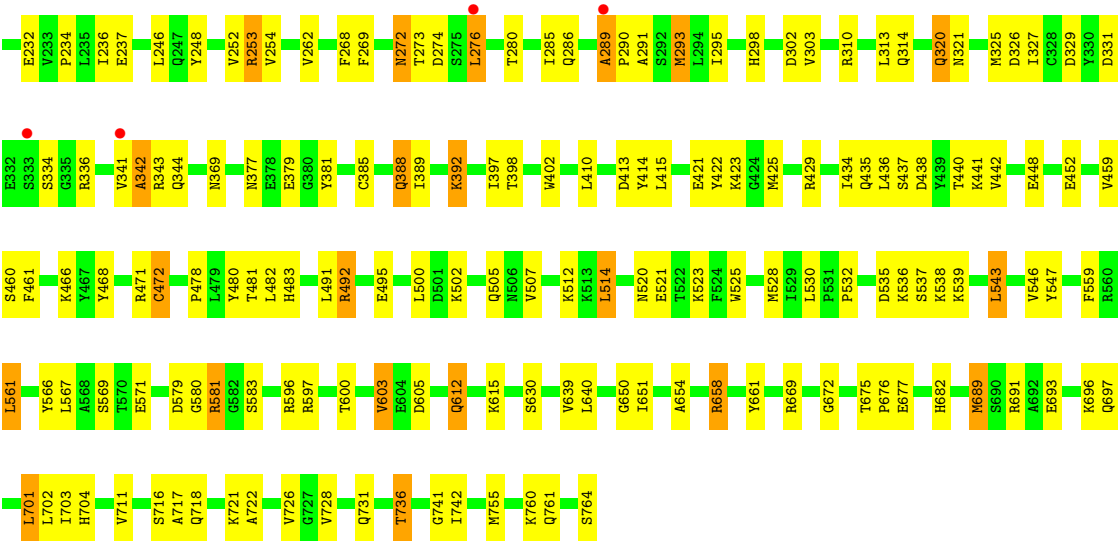
- Molecule 2 is 3-{{(2R,5S)-5-{{(2S)-2-(AMINOMETHYL)PYRROLIDIN-1-YL}CARBONYL}PYRROLIDIN-2-YL}METHOXY}-4-CHLOROBENZOIC ACID (three-letter code: ACF) (formula: C₁₈H₂₄ClN₃O₄).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	0	0
			26	18	1	3	4		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	738	Total 738	O 738	0	0
3	B	683	Total 683	O 683	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	65.73Å 126.79Å 112.29Å 90.00° 99.49° 90.00°	Depositor
Resolution (Å)	50.00 – 2.30 50.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	93.9 (50.00-2.30) 93.9 (50.00-2.30)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.27 (at 2.29Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.190 , 0.243 0.187 , 0.239	Depositor DCC
R_{free} test set	3734 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	29.0	Xtriage
Anisotropy	0.154	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 51.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13345	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.04% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.37	1/6120 (0.0%)	0.64	1/8321 (0.0%)
1	B	0.34	0/6120	0.63	2/8321 (0.0%)
All	All	0.36	1/12240 (0.0%)	0.63	3/16642 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	630	SER	C-O	9.54	1.41	1.23

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	388	GLN	N-CA-C	-5.83	95.25	111.00
1	B	90	LEU	CA-CB-CG	5.20	127.26	115.30
1	A	300	LEU	N-CA-C	-5.01	97.47	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	5949	0	5666	219	0
1	B	5949	0	5667	213	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	26	0	21	1	0
3	A	738	0	0	47	0
3	B	683	0	0	42	0
All	All	13345	0	11354	428	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 18.

All (428) 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:114:ILE:HD11	1:B:137:LEU:HD21	1.41	1.03
1:B:289:ALA:HB1	1:B:290:PRO:HA	1.43	1.00
1:B:442:VAL:HB	3:B:1074:HOH:O	1.61	0.99
1:A:172:ILE:H	1:A:186:THR:HG22	1.30	0.96
1:B:193:ILE:HG22	1:B:194:ILE:HD12	1.47	0.94
1:B:72:GLN:HE21	1:B:72:GLN:N	1.65	0.92
1:B:172:ILE:H	1:B:186:THR:HG22	1.35	0.92
1:A:276:LEU:H	1:A:276:LEU:HD23	1.41	0.86
1:A:736:THR:HG21	1:B:717:ALA:O	1.76	0.85
1:B:289:ALA:HB1	1:B:290:PRO:CA	2.06	0.85
1:A:717:ALA:O	1:B:736:THR:HG21	1.79	0.83
1:A:289:ALA:HB1	1:A:290:PRO:HA	1.62	0.81
1:A:272:ASN:ND2	1:A:274:ASP:H	1.77	0.81
1:A:114:ILE:HD11	1:A:137:LEU:HD21	1.62	0.81
1:A:640:LEU:HD11	1:A:650:GLY:HA3	1.62	0.80
1:A:69:LEU:HD13	1:A:107:ILE:HD12	1.62	0.80
1:A:71:LYS:NZ	1:A:105:TYR:HB2	1.97	0.79
1:A:289:ALA:HB1	1:A:290:PRO:CA	2.13	0.79
1:B:435:GLN:HE22	1:B:441:LYS:NZ	1.81	0.78
1:A:388:GLN:HB2	1:A:391:LYS:HB2	1.67	0.77
1:A:153:GLN:HE22	1:A:170:ASN:ND2	1.83	0.76
1:A:391:LYS:HG3	3:A:844:HOH:O	1.85	0.76
1:B:343:ARG:HA	1:B:389:ILE:O	1.86	0.76
1:A:71:LYS:HZ3	1:A:105:TYR:HB2	1.48	0.75
1:A:272:ASN:HD22	1:A:274:ASP:H	1.31	0.75
1:B:51:ASN:HB2	3:B:1235:HOH:O	1.84	0.75
1:B:72:GLN:HB2	3:B:1399:HOH:O	1.87	0.75
1:A:320:GLN:OE1	1:A:669:ARG:HD3	1.88	0.73
1:B:672:GLY:HA2	3:B:1415:HOH:O	1.88	0.73
1:A:276:LEU:H	1:A:276:LEU:CD2	2.02	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:310:ARG:HH12	1:A:343:ARG:NH1	1.86	0.73
1:A:52:THR:HG22	3:A:1277:HOH:O	1.89	0.72
1:A:69:LEU:CD1	1:A:107:ILE:HD12	2.20	0.71
1:B:505:GLN:HB3	3:B:1041:HOH:O	1.89	0.71
1:A:172:ILE:H	1:A:186:THR:CG2	2.04	0.70
1:A:176:ILE:HG12	3:A:1465:HOH:O	1.90	0.70
1:A:289:ALA:HB2	3:A:1119:HOH:O	1.91	0.70
1:A:388:GLN:CB	1:A:391:LYS:HB2	2.23	0.69
1:B:579:ASP:HB3	1:B:583:SER:OG	1.93	0.69
1:B:106:SER:HB3	1:B:115:LEU:HB3	1.73	0.69
1:B:320:GLN:OE1	1:B:669:ARG:HD3	1.93	0.69
1:B:410:LEU:HD13	1:B:415:LEU:HD23	1.75	0.68
1:A:516:PHE:CE2	1:A:523:LYS:HD2	2.28	0.68
1:B:175:LYS:HG2	1:B:182:SER:HB3	1.73	0.68
1:A:114:ILE:CD1	1:A:137:LEU:HD21	2.24	0.68
1:A:410:LEU:HD13	1:A:415:LEU:HD23	1.76	0.67
1:B:172:ILE:H	1:B:186:THR:CG2	2.04	0.67
1:A:47:ASP:HA	1:A:52:THR:HG23	1.76	0.67
1:B:72:GLN:HE21	1:B:72:GLN:H	1.42	0.67
1:B:153:GLN:HE22	1:B:170:ASN:ND2	1.92	0.67
1:B:55:LEU:HD21	1:B:559:PHE:HE2	1.60	0.67
1:B:76:ILE:HD12	1:B:90:LEU:HD11	1.78	0.66
1:B:184:ARG:HD2	1:B:187:TRP:CE2	2.30	0.66
1:B:71:LYS:HG2	1:B:76:ILE:HG12	1.78	0.65
1:B:392:LYS:HD3	3:B:1049:HOH:O	1.96	0.65
1:B:280:THR:HB	3:B:1352:HOH:O	1.96	0.65
1:B:321:ASN:ND2	3:B:1116:HOH:O	2.27	0.65
1:B:437:SER:HB2	3:B:1339:HOH:O	1.95	0.65
1:B:438:ASP:OD1	1:B:440:THR:HB	1.96	0.65
1:B:61:ARG:HB3	1:B:61:ARG:CZ	2.27	0.64
1:B:658:ARG:HG2	1:B:661:TYR:CE2	2.32	0.64
1:A:76:ILE:HD12	1:A:90:LEU:HD11	1.80	0.64
1:B:392:LYS:HG2	3:B:1037:HOH:O	1.97	0.64
1:A:272:ASN:HD22	1:A:272:ASN:C	2.01	0.64
1:A:183:TYR:HE1	1:A:277:SER:O	1.82	0.63
1:B:272:ASN:HD22	1:B:274:ASP:H	1.47	0.63
1:B:76:ILE:HB	1:B:90:LEU:CD1	2.29	0.62
1:A:693:GLU:OE1	1:A:696:LYS:HE2	1.99	0.62
1:A:286:GLN:NE2	1:A:288:THR:HG22	2.14	0.62
1:A:184:ARG:HD2	1:A:187:TRP:CE2	2.35	0.62
1:A:171:ASP:OD1	1:A:186:THR:HG23	1.98	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:718:GLN:HE22	1:B:721:LYS:NZ	1.98	0.61
1:B:72:GLN:N	1:B:72:GLN:NE2	2.45	0.61
1:B:184:ARG:HD3	1:B:186:THR:O	2.01	0.61
1:B:272:ASN:ND2	1:B:274:ASP:H	1.99	0.61
1:B:377:ASN:HB2	1:B:381:TYR:O	2.01	0.61
1:A:528:MET:CE	1:A:574:ILE:HG21	2.31	0.61
1:A:438:ASP:OD1	1:A:440:THR:HB	2.01	0.60
1:A:90:LEU:O	1:A:90:LEU:HD13	2.01	0.60
1:A:597:ARG:HH12	1:A:679:ASN:HD21	1.49	0.60
1:A:608:GLU:HG2	3:A:1485:HOH:O	2.00	0.60
1:A:325:MET:HE2	1:A:327:ILE:HD11	1.82	0.60
1:B:89:PHE:HD1	1:B:90:LEU:HD12	1.65	0.60
1:B:125:ARG:HG2	1:B:126:HIS:CE1	2.35	0.60
1:B:512:LYS:HD3	3:B:822:HOH:O	2.02	0.60
1:A:51:ASN:OD1	1:A:54:ARG:HD3	2.01	0.60
1:B:377:ASN:HB2	1:B:381:TYR:H	1.67	0.60
1:A:177:GLU:HB2	1:A:180:LEU:HD13	1.83	0.60
1:A:203:TYR:HA	1:A:207:VAL:HG13	1.84	0.60
1:B:272:ASN:HD22	1:B:272:ASN:C	2.04	0.59
1:B:538:LYS:HE2	3:B:1396:HOH:O	2.02	0.59
1:B:731:GLN:HG2	3:B:1042:HOH:O	2.01	0.59
1:B:651:ILE:CD1	1:B:755:MET:HE2	2.32	0.59
1:B:310:ARG:HH22	1:B:369:ASN:ND2	2.00	0.59
1:A:177:GLU:HB2	1:A:180:LEU:HD22	1.84	0.59
1:B:289:ALA:CB	1:B:290:PRO:HA	2.26	0.59
1:A:614:SER:HA	1:A:619:VAL:HB	1.83	0.59
1:A:170:ASN:N	1:A:170:ASN:HD22	1.99	0.59
1:A:618:PHE:HB2	3:A:1514:HOH:O	2.02	0.59
1:B:697:GLN:HG3	3:B:852:HOH:O	2.02	0.58
1:A:579:ASP:HB3	1:A:583:SER:OG	2.01	0.58
1:A:214:LEU:O	1:A:214:LEU:HD12	2.03	0.58
1:B:229:ASN:ND2	3:B:869:HOH:O	2.36	0.58
1:A:103:ASN:HB3	3:A:1186:HOH:O	2.03	0.58
1:B:538:LYS:HD3	3:B:1434:HOH:O	2.04	0.58
1:A:184:ARG:HD2	1:A:187:TRP:CD2	2.39	0.58
1:A:514:LEU:HD12	1:A:557:THR:HG22	1.85	0.57
1:A:327:ILE:HB	1:A:343:ARG:HG2	1.86	0.57
1:B:676:PRO:HD2	1:B:677:GLU:OE2	2.05	0.57
1:B:105:TYR:HB2	3:B:1318:HOH:O	2.05	0.57
1:A:481:THR:OG1	1:A:483:HIS:HE1	1.87	0.57
1:A:114:ILE:HG13	1:A:137:LEU:HD11	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:658:ARG:HG2	1:A:661:TYR:CE2	2.40	0.57
1:A:76:ILE:HB	1:A:90:LEU:CD1	2.34	0.57
1:B:693:GLU:HB2	3:B:1135:HOH:O	2.04	0.57
1:B:193:ILE:HG22	1:B:194:ILE:CD1	2.29	0.56
1:B:693:GLU:OE1	1:B:696:LYS:HE3	2.04	0.56
1:B:502:LYS:HA	1:B:505:GLN:HE21	1.71	0.56
1:B:502:LYS:O	1:B:505:GLN:HG2	2.04	0.56
1:A:106:SER:HB3	1:A:115:LEU:HB3	1.86	0.56
1:A:429:ARG:NE	3:A:964:HOH:O	2.25	0.56
1:B:276:LEU:HD23	1:B:276:LEU:O	2.06	0.56
1:B:55:LEU:HD21	1:B:559:PHE:CE2	2.40	0.56
1:B:103:ASN:HB2	3:B:886:HOH:O	2.03	0.56
1:B:140:ARG:HH11	1:B:140:ARG:HG2	1.70	0.56
1:A:51:ASN:HB2	3:A:1026:HOH:O	2.04	0.56
1:A:377:ASN:HB2	1:A:381:TYR:O	2.06	0.56
1:B:57:LEU:HD23	3:B:994:HOH:O	2.04	0.56
1:B:481:THR:OG1	1:B:483:HIS:HE1	1.89	0.56
1:A:341:VAL:HG22	1:A:341:VAL:O	2.06	0.55
1:B:435:GLN:NE2	1:B:441:LYS:HD3	2.22	0.55
1:B:691:ARG:NE	3:B:773:HOH:O	2.27	0.55
1:A:704:HIS:HD2	1:A:716:SER:OG	1.89	0.55
1:A:184:ARG:HD3	1:A:186:THR:O	2.06	0.55
1:B:61:ARG:HB3	1:B:61:ARG:NH1	2.20	0.55
1:A:229:ASN:ND2	3:A:852:HOH:O	2.40	0.55
1:A:684:ARG:HG3	3:A:1534:HOH:O	2.07	0.55
1:B:184:ARG:HD2	1:B:187:TRP:CD2	2.42	0.55
1:A:528:MET:HE2	1:A:574:ILE:HG21	1.88	0.55
1:B:289:ALA:HB2	3:B:1115:HOH:O	2.07	0.55
1:B:435:GLN:HE22	1:B:441:LYS:HZ3	1.54	0.55
1:A:71:LYS:HZ3	1:A:105:TYR:HD1	1.54	0.55
1:A:272:ASN:HD21	1:A:274:ASP:HB2	1.72	0.54
1:A:704:HIS:HE1	1:A:711:VAL:O	1.91	0.54
1:B:413:ASP:HB2	3:B:1152:HOH:O	2.07	0.54
1:B:452:GLU:HB3	3:B:1137:HOH:O	2.07	0.54
1:B:74:ASN:C	1:B:92:ASN:HB3	2.28	0.54
1:B:471:ARG:HG2	1:B:480:TYR:CD2	2.43	0.54
1:B:414:TYR:HA	1:B:436:LEU:HD13	1.89	0.54
1:B:726:VAL:HG12	1:B:728:VAL:HG23	1.89	0.54
1:A:98:PHE:CE2	1:A:100:HIS:HB2	2.42	0.54
1:B:377:ASN:HB3	1:B:379:GLU:H	1.73	0.54
1:B:600:THR:O	1:B:603:VAL:HG13	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:762:CYS:HB2	3:A:1122:HOH:O	2.06	0.53
1:A:471:ARG:HB3	3:A:1383:HOH:O	2.09	0.53
1:A:243:ASP:HB3	3:A:1049:HOH:O	2.07	0.53
1:B:97:GLU:HB2	3:B:1067:HOH:O	2.07	0.53
1:B:289:ALA:HB2	3:B:904:HOH:O	2.09	0.53
1:B:651:ILE:HD12	1:B:755:MET:HE2	1.90	0.53
1:A:234:PRO:HB2	1:B:248:TYR:CZ	2.43	0.53
1:B:112:GLN:HG2	1:B:138:ASN:HD21	1.73	0.53
1:B:203:TYR:HA	1:B:207:VAL:CG1	2.39	0.53
1:A:276:LEU:CD2	1:A:276:LEU:N	2.69	0.53
1:A:310:ARG:NH1	1:A:329:ASP:OD1	2.42	0.53
1:A:71:LYS:HG2	1:A:76:ILE:HG12	1.91	0.53
1:A:276:LEU:HD23	3:A:1080:HOH:O	2.09	0.53
1:A:581:ARG:HB2	1:A:605:ASP:OD2	2.08	0.53
1:B:331:ASP:HB3	1:B:334:SER:HB3	1.91	0.53
1:A:487:ASN:OD1	1:A:489:LYS:HE2	2.09	0.52
1:A:51:ASN:HB2	3:A:883:HOH:O	2.08	0.52
1:A:379:GLU:HB2	3:A:842:HOH:O	2.09	0.52
1:A:348:MET:HG3	3:A:900:HOH:O	2.08	0.52
1:A:52:THR:HB	3:A:1079:HOH:O	2.08	0.52
1:B:535:ASP:OD1	1:B:537:SER:HB3	2.10	0.52
1:B:78:VAL:HG12	1:B:87:SER:O	2.09	0.52
1:A:65:ASP:OD2	1:A:466:LYS:HB2	2.10	0.52
1:B:502:LYS:HD2	1:B:505:GLN:NE2	2.25	0.52
1:A:626:ILE:O	1:A:650:GLY:HA2	2.10	0.52
1:B:214:LEU:HD12	1:B:214:LEU:O	2.10	0.52
1:A:47:ASP:HA	1:A:52:THR:CG2	2.40	0.51
1:B:410:LEU:HD13	1:B:415:LEU:CD2	2.40	0.51
1:B:543:LEU:HD12	1:B:567:LEU:HD13	1.92	0.51
1:A:115:LEU:HD21	1:A:155:VAL:HG11	1.93	0.51
1:A:289:ALA:HB1	1:A:290:PRO:C	2.31	0.51
1:A:321:ASN:ND2	3:A:951:HOH:O	2.43	0.51
1:B:435:GLN:HE22	1:B:441:LYS:HZ2	1.58	0.51
1:A:310:ARG:HH12	1:A:343:ARG:HH11	1.58	0.51
1:A:471:ARG:HG3	3:A:1099:HOH:O	2.10	0.51
1:A:528:MET:HE2	1:A:574:ILE:CG2	2.41	0.51
1:B:459:VAL:HG22	1:B:460:SER:N	2.25	0.51
1:A:289:ALA:CB	1:A:290:PRO:CA	2.87	0.51
1:A:651:ILE:CD1	1:A:755:MET:HE2	2.41	0.51
1:A:615:LYS:HG3	3:A:955:HOH:O	2.11	0.51
1:A:65:ASP:CG	1:A:464:GLU:HB2	2.31	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:57:LEU:HD21	3:B:1084:HOH:O	2.11	0.50
1:A:293:MET:HG3	1:A:298:HIS:CB	2.41	0.50
1:A:520:ASN:HA	3:A:1108:HOH:O	2.11	0.50
1:A:331:ASP:HB3	1:A:334:SER:HB2	1.94	0.50
1:A:487:ASN:HB2	1:A:489:LYS:HG3	1.93	0.50
1:B:170:ASN:N	1:B:170:ASN:HD22	2.10	0.50
1:B:741:GLY:O	1:B:742:ILE:C	2.50	0.50
1:A:56:LYS:HD2	3:A:826:HOH:O	2.12	0.50
1:A:483:HIS:HD2	3:A:954:HOH:O	1.94	0.50
1:B:285:ILE:HD12	1:B:285:ILE:N	2.26	0.50
1:B:580:GLY:O	1:B:583:SER:HB2	2.11	0.50
1:A:272:ASN:HD22	1:A:273:THR:N	2.09	0.50
1:A:519:LEU:HD13	3:A:1470:HOH:O	2.12	0.49
1:B:693:GLU:HA	1:B:726:VAL:HG11	1.94	0.49
1:B:175:LYS:CG	1:B:182:SER:HB3	2.42	0.49
1:A:630:SER:HA	1:A:654:ALA:O	2.11	0.49
1:B:435:GLN:CD	1:B:441:LYS:HD3	2.33	0.49
1:B:718:GLN:HE22	1:B:721:LYS:HZ1	1.60	0.49
1:A:147:ARG:HD2	3:A:1435:HOH:O	2.12	0.49
1:A:177:GLU:CB	1:A:180:LEU:HD13	2.42	0.49
1:A:333:SER:HB2	3:A:1292:HOH:O	2.11	0.49
1:B:65:ASP:OD2	1:B:466:LYS:HB2	2.12	0.49
1:B:147:ARG:HD3	3:B:1386:HOH:O	2.12	0.49
1:B:197:GLY:C	1:B:213:ALA:HB3	2.33	0.49
1:A:651:ILE:HD13	1:A:755:MET:HE2	1.94	0.49
1:B:171:ASP:OD1	1:B:186:THR:HG23	2.12	0.49
1:B:696:LYS:HG3	1:B:728:VAL:HG22	1.95	0.48
1:A:150:ASN:ND2	3:A:914:HOH:O	2.40	0.48
1:A:193:ILE:HG22	1:A:194:ILE:HG13	1.95	0.48
1:A:310:ARG:NH1	1:A:343:ARG:NH1	2.58	0.48
1:A:372:TYR:OH	1:A:436:LEU:HG	2.13	0.48
1:A:415:LEU:HB2	1:A:436:LEU:HD11	1.95	0.48
1:B:341:VAL:HG13	1:B:341:VAL:O	2.14	0.48
1:A:512:LYS:HD2	3:A:917:HOH:O	2.12	0.48
1:B:232:GLU:HG2	3:B:1329:HOH:O	2.13	0.48
1:A:54:ARG:HG2	3:A:1038:HOH:O	2.14	0.48
1:A:472:CYS:O	1:A:478:PRO:HA	2.14	0.48
1:B:289:ALA:CB	1:B:290:PRO:CA	2.81	0.48
1:A:80:ASN:HB3	1:A:85:ASN:OD1	2.13	0.48
1:A:176:ILE:HD11	1:A:276:LEU:HD21	1.96	0.48
1:A:528:MET:HE3	1:A:574:ILE:HG21	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:630:SER:HA	1:B:654:ALA:O	2.14	0.48
1:A:236:ILE:CG2	1:A:254:VAL:HG13	2.44	0.48
1:B:397:ILE:HG13	1:B:398:THR:HG23	1.95	0.48
1:A:89:PHE:CE1	1:A:107:ILE:HD13	2.49	0.48
1:B:75:ASN:N	3:B:1399:HOH:O	2.45	0.48
1:B:701:LEU:HD22	1:B:703:ILE:HG13	1.96	0.48
1:A:248:TYR:CZ	1:B:234:PRO:HB2	2.49	0.47
1:A:277:SER:O	1:A:278:SER:HB3	2.13	0.47
1:A:562:ASN:HB2	3:A:965:HOH:O	2.14	0.47
1:B:150:ASN:O	1:B:151:ASN:HB2	2.14	0.47
1:B:268:PHE:CD2	1:B:313:LEU:HD21	2.49	0.47
1:B:291:ALA:O	1:B:295:ILE:HG23	2.13	0.47
1:B:56:LYS:HD3	1:B:495:GLU:OE1	2.14	0.47
1:B:158:SER:HB3	1:B:163:LYS:HB2	1.97	0.47
1:B:293:MET:HG3	1:B:298:HIS:CB	2.44	0.47
1:B:173:TYR:CE2	1:B:184:ARG:HG3	2.49	0.47
1:A:341:VAL:O	1:A:342:ALA:HB2	2.14	0.47
1:B:110:ASP:OD2	1:B:162:HIS:ND1	2.46	0.47
1:A:377:ASN:HB3	1:A:379:GLU:H	1.78	0.47
1:A:516:PHE:CD2	1:A:523:LYS:HD2	2.49	0.47
1:A:726:VAL:CG1	1:A:728:VAL:HG23	2.45	0.47
1:B:429:ARG:NE	3:B:812:HOH:O	2.26	0.47
1:B:471:ARG:HG2	1:B:480:TYR:HD2	1.80	0.47
1:B:472:CYS:O	1:B:478:PRO:HA	2.14	0.47
1:A:85:ASN:ND2	3:A:825:HOH:O	2.48	0.47
1:A:156:THR:HG21	1:A:214:LEU:HD11	1.95	0.47
1:B:269:PHE:CE2	1:B:286:GLN:HB2	2.49	0.47
1:B:689:MET:HB3	1:B:722:ALA:CB	2.44	0.47
1:B:764:SER:HB3	3:B:855:HOH:O	2.14	0.47
1:A:74:ASN:HB3	1:A:92:ASN:HB3	1.97	0.47
1:A:369:ASN:O	1:A:389:ILE:HG12	2.15	0.47
1:B:341:VAL:O	1:B:342:ALA:HB2	2.14	0.47
1:B:514:LEU:HD22	1:B:525:TRP:HE3	1.80	0.47
1:A:77:LEU:HD23	1:A:88:VAL:HA	1.97	0.47
1:A:377:ASN:HB2	1:A:381:TYR:H	1.79	0.47
1:B:237:GLU:HA	1:B:252:VAL:O	2.15	0.47
1:A:114:ILE:CG1	1:A:137:LEU:HD11	2.45	0.47
1:B:92:ASN:HD22	1:B:93:SER:N	2.12	0.47
1:B:491:LEU:O	1:B:492:ARG:HB3	2.15	0.46
1:A:281:ASN:ND2	3:A:861:HOH:O	2.46	0.46
1:A:689:MET:HB3	1:A:722:ALA:HB2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:435:GLN:NE2	1:A:441:LYS:HD2	2.30	0.46
1:A:658:ARG:HB2	1:A:687:THR:HG22	1.97	0.46
1:B:236:ILE:O	1:B:253:ARG:HA	2.14	0.46
1:A:72:GLN:HB3	3:A:870:HOH:O	2.16	0.46
1:A:110:ASP:OD1	1:A:161:GLY:HA2	2.16	0.46
1:A:224:ALA:HB1	1:A:268:PHE:CZ	2.50	0.46
1:B:325:MET:HE1	1:B:327:ILE:HD11	1.97	0.46
1:B:704:HIS:CE1	1:B:711:VAL:O	2.68	0.46
1:A:183:TYR:CE1	1:A:277:SER:O	2.66	0.46
1:A:74:ASN:HB3	1:A:92:ASN:CB	2.45	0.46
1:A:384:ILE:HG13	1:A:404:VAL:HG21	1.98	0.46
1:A:594:ILE:HG22	1:A:601:PHE:HB2	1.97	0.46
1:B:74:ASN:HB2	3:B:769:HOH:O	2.15	0.46
1:B:83:TYR:HB2	1:B:85:ASN:OD1	2.16	0.46
1:A:397:ILE:HG13	1:A:398:THR:HG23	1.96	0.46
1:A:402:TRP:CD2	1:A:421:GLU:HB2	2.50	0.46
1:B:471:ARG:NH1	3:B:1234:HOH:O	2.48	0.46
1:B:39:SER:O	1:B:40:ARG:HB2	2.16	0.46
1:B:126:HIS:HE1	3:B:807:HOH:O	1.98	0.46
1:B:612:GLN:HE21	1:B:612:GLN:HB3	1.54	0.46
1:B:651:ILE:HG23	1:B:701:LEU:HB3	1.98	0.46
1:B:90:LEU:HD13	1:B:90:LEU:O	2.15	0.45
1:B:310:ARG:NH2	1:B:369:ASN:ND2	2.64	0.45
1:B:654:ALA:HA	1:B:704:HIS:CD2	2.51	0.45
1:A:153:GLN:HE22	1:A:170:ASN:HD21	1.60	0.45
1:A:350:THR:HG23	3:A:900:HOH:O	2.17	0.45
1:A:666:TYR:CE2	2:A:800:ACF:H41	2.51	0.45
1:B:392:LYS:HG2	1:B:392:LYS:H	1.54	0.45
1:A:388:GLN:HB3	1:A:391:LYS:HB2	1.99	0.45
1:A:471:ARG:NE	3:A:1099:HOH:O	2.50	0.45
1:B:377:ASN:HB2	1:B:381:TYR:N	2.29	0.45
1:A:310:ARG:NH1	1:A:343:ARG:HH11	2.15	0.45
1:A:513:LYS:O	1:A:527:GLN:HA	2.17	0.45
1:A:693:GLU:HG2	3:A:1422:HOH:O	2.17	0.45
1:B:89:PHE:CE1	1:B:107:ILE:HD13	2.52	0.45
1:B:146:GLU:HG3	1:B:181:PRO:HG3	1.99	0.45
1:B:461:PHE:CD2	1:B:468:TYR:HB3	2.52	0.45
1:A:340:LEU:O	1:A:342:ALA:N	2.51	0.44
1:A:596:ARG:O	1:A:597:ARG:NH1	2.49	0.44
1:B:651:ILE:HD13	1:B:755:MET:HE2	1.98	0.44
1:A:74:ASN:C	1:A:92:ASN:HB3	2.37	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:177:GLU:HB2	1:B:180:LEU:HD13	1.99	0.44
1:B:203:TYR:HA	1:B:207:VAL:HG13	1.99	0.44
1:B:596:ARG:O	1:B:597:ARG:NH1	2.46	0.44
1:A:41:LYS:HB2	3:A:1120:HOH:O	2.17	0.44
1:B:402:TRP:CD2	1:B:421:GLU:HB2	2.53	0.44
1:A:74:ASN:HB2	3:A:870:HOH:O	2.18	0.44
1:A:540:TYR:HE1	3:A:1514:HOH:O	1.99	0.44
1:A:612:GLN:HE21	1:A:612:GLN:HB3	1.57	0.44
1:A:104:ASP:OD1	1:A:105:TYR:N	2.48	0.44
1:B:310:ARG:NH2	1:B:369:ASN:HD22	2.15	0.44
1:A:229:ASN:ND2	3:A:819:HOH:O	2.41	0.44
1:B:153:GLN:HE22	1:B:170:ASN:HD22	1.66	0.44
1:A:751:ILE:HG23	1:A:752:TYR:N	2.33	0.44
1:B:483:HIS:HD2	3:B:1231:HOH:O	2.00	0.44
1:A:302:ASP:HB3	1:A:314:GLN:HB2	1.99	0.43
1:B:539:LYS:HD3	3:B:937:HOH:O	2.17	0.43
1:A:704:HIS:CE1	1:A:711:VAL:O	2.70	0.43
1:A:72:GLN:HE22	1:A:77:LEU:HD12	1.83	0.43
1:A:186:THR:HG21	1:A:196:ASN:CB	2.48	0.43
1:A:190:LYS:HE3	1:A:193:ILE:HG13	2.00	0.43
1:B:112:GLN:O	1:B:137:LEU:HB2	2.18	0.43
1:B:262:VAL:HG23	3:B:929:HOH:O	2.19	0.43
1:B:689:MET:HB3	1:B:722:ALA:HB2	2.00	0.43
1:B:325:MET:O	1:B:344:GLN:HA	2.19	0.43
1:A:115:LEU:HD21	1:A:155:VAL:CG1	2.48	0.43
1:A:154:TRP:CE2	1:A:212:SER:HB2	2.54	0.43
1:B:546:VAL:HG22	1:B:547:TYR:N	2.33	0.43
1:B:415:LEU:HB3	1:B:434:ILE:CG2	2.48	0.43
1:A:614:SER:HB3	1:A:624:ILE:HD11	1.99	0.43
1:B:344:GLN:NE2	3:B:969:HOH:O	2.51	0.43
1:A:124:TRP:HB2	1:A:204:GLU:OE2	2.19	0.43
1:A:90:LEU:C	1:A:90:LEU:HD22	2.39	0.43
1:A:194:ILE:HD11	3:A:1460:HOH:O	2.19	0.43
1:A:242:SER:HB3	1:A:246:LEU:HD12	2.00	0.43
1:B:93:SER:O	1:B:95:PHE:N	2.51	0.43
1:B:276:LEU:CD2	1:B:276:LEU:H	2.32	0.43
1:A:49:LEU:HD22	1:A:749:GLN:HA	2.00	0.42
1:A:207:VAL:HG22	1:A:208:PHE:N	2.34	0.42
1:A:453:ARG:HG3	1:A:476:GLY:HA3	2.01	0.42
1:A:741:GLY:O	1:A:742:ILE:C	2.56	0.42
1:B:597:ARG:HA	1:B:682:HIS:CD2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:TYR:HB2	3:A:901:HOH:O	2.18	0.42
1:B:41:LYS:O	1:B:507:VAL:HG23	2.19	0.42
1:B:290:PRO:HG3	1:B:326:ASP:OD2	2.18	0.42
1:B:55:LEU:HD23	1:B:500:LEU:CD2	2.49	0.42
1:B:658:ARG:HD2	3:B:1277:HOH:O	2.19	0.42
1:B:325:MET:HE2	1:B:327:ILE:HG12	2.01	0.42
1:B:514:LEU:HD22	1:B:525:TRP:CE3	2.54	0.42
1:A:510:PRO:HD3	1:A:569:SER:HB2	2.02	0.42
1:B:93:SER:HA	1:B:96:ASP:OD2	2.19	0.42
1:A:310:ARG:HG3	1:A:329:ASP:OD1	2.20	0.42
1:A:459:VAL:HG22	1:A:460:SER:N	2.34	0.42
1:A:542:LEU:HD23	1:A:542:LEU:C	2.39	0.42
1:B:675:THR:HB	1:B:677:GLU:OE2	2.19	0.42
1:A:60:LEU:C	1:A:60:LEU:HD12	2.40	0.42
1:A:71:LYS:HE2	1:A:76:ILE:CD1	2.50	0.42
1:B:615:LYS:HE2	3:B:1361:HOH:O	2.20	0.42
1:A:136:ASP:CG	1:A:139:LYS:HG2	2.40	0.42
1:A:418:ILE:HD13	1:A:431:LEU:HA	2.02	0.42
1:A:654:ALA:HA	1:A:704:HIS:CD2	2.55	0.42
1:B:71:LYS:CG	1:B:76:ILE:HG12	2.46	0.42
1:B:466:LYS:HB2	3:B:954:HOH:O	2.20	0.42
1:B:704:HIS:HD2	1:B:716:SER:OG	2.02	0.42
1:A:661:TYR:OH	1:A:718:GLN:HG3	2.20	0.42
1:A:677:GLU:H	1:A:677:GLU:CD	2.23	0.42
1:B:156:THR:HG21	1:B:214:LEU:HD11	2.01	0.42
1:B:415:LEU:HD13	1:B:415:LEU:C	2.40	0.42
1:B:559:PHE:CZ	1:B:561:LEU:HD13	2.55	0.42
1:B:640:LEU:HD11	1:B:650:GLY:HA3	2.02	0.42
1:A:81:ALA:O	1:A:492:ARG:NH2	2.48	0.41
1:A:159:PRO:HD3	1:A:216:TRP:HB3	2.02	0.41
1:A:630:SER:HB2	1:A:740:HIS:NE2	2.35	0.41
1:B:140:ARG:HG2	1:B:140:ARG:NH1	2.35	0.41
1:A:285:ILE:HG21	1:A:337:TRP:HD1	1.85	0.41
1:A:54:ARG:HD2	3:A:1177:HOH:O	2.20	0.41
1:A:89:PHE:CZ	1:A:107:ILE:HD13	2.55	0.41
1:A:236:ILE:O	1:A:253:ARG:HA	2.19	0.41
1:A:272:ASN:ND2	1:A:272:ASN:C	2.73	0.41
1:B:216:TRP:CZ3	1:B:273:THR:HG21	2.56	0.41
1:A:71:LYS:HZ1	1:A:105:TYR:HB2	1.78	0.41
1:B:60:LEU:C	1:B:60:LEU:HD12	2.41	0.41
1:B:109:PRO:HG2	1:B:158:SER:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:422:TYR:CE2	1:B:423:LYS:HD3	2.55	0.41
1:A:114:ILE:HG13	1:A:137:LEU:CD1	2.51	0.41
1:A:289:ALA:CB	1:A:290:PRO:HA	2.43	0.41
1:B:144:THR:HG22	1:B:147:ARG:NH2	2.35	0.41
1:B:193:ILE:CG2	1:B:194:ILE:HD12	2.34	0.41
1:B:302:ASP:HB3	1:B:314:GLN:HB2	2.03	0.41
1:A:391:LYS:HD3	3:A:987:HOH:O	2.20	0.41
1:A:520:ASN:O	1:A:521:GLU:HB2	2.21	0.41
1:B:152:THR:HG21	1:B:155:VAL:CG2	2.51	0.41
1:B:603:VAL:HG23	1:B:639:VAL:CG2	2.50	0.41
1:A:159:PRO:HD3	1:A:216:TRP:CB	2.51	0.41
1:A:486:VAL:HG13	1:A:487:ASN:N	2.36	0.41
1:B:276:LEU:H	1:B:276:LEU:HD22	1.85	0.41
1:A:293:MET:HG2	1:A:315:TRP:HB3	2.03	0.41
1:B:310:ARG:HD3	1:B:329:ASP:OD1	2.21	0.41
1:B:532:PRO:HD3	1:B:569:SER:HA	2.03	0.41
1:B:718:GLN:HE21	1:B:718:GLN:HA	1.86	0.41
1:B:520:ASN:O	1:B:521:GLU:HB2	2.20	0.41
1:B:528:MET:HE1	1:B:530:LEU:HD21	2.02	0.41
1:A:458:SER:OG	1:A:471:ARG:HB2	2.21	0.40
1:A:538:LYS:HE3	3:A:1233:HOH:O	2.21	0.40
1:B:154:TRP:O	1:B:166:TYR:HA	2.21	0.40
1:B:168:TRP:O	1:B:169:ASN:HB2	2.20	0.40
1:B:571:GLU:CD	1:B:760:LYS:HD3	2.41	0.40
1:B:581:ARG:NE	1:B:605:ASP:OD2	2.50	0.40
1:B:726:VAL:O	1:B:726:VAL:CG1	2.70	0.40
1:A:290:PRO:HD3	1:A:315:TRP:CD1	2.57	0.40
1:A:392:LYS:HG3	1:A:393:ASP:N	2.37	0.40
1:B:237:GLU:HG2	1:B:253:ARG:HB3	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	724/726 (100%)	677 (94%)	39 (5%)	8 (1%)	12	13
1	B	724/726 (100%)	674 (93%)	45 (6%)	5 (1%)	19	23
All	All	1448/1452 (100%)	1351 (93%)	84 (6%)	13 (1%)	14	17

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	278	SER
1	A	342	ALA
1	B	94	THR
1	B	342	ALA
1	A	40	ARG
1	A	289	ALA
1	A	320	GLN
1	A	520	ASN
1	B	289	ALA
1	A	277	SER
1	B	320	GLN
1	A	341	VAL
1	B	140	ARG

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	651/651 (100%)	610 (94%)	41 (6%)	15	21
1	B	651/651 (100%)	613 (94%)	38 (6%)	17	24
All	All	1302/1302 (100%)	1223 (94%)	79 (6%)	15	22

All (79) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	LYS
1	A	51	ASN
1	A	61	ARG

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Mol	Chain	Res	Type
1	A	72	GLN
1	A	90	LEU
1	A	145	GLU
1	A	170	ASN
1	A	207	VAL
1	A	230	ASP
1	A	246	LEU
1	A	253	ARG
1	A	254	VAL
1	A	272	ASN
1	A	276	LEU
1	A	303	VAL
1	A	341	VAL
1	A	373	LYS
1	A	385	CYS
1	A	390	ASP
1	A	436	LEU
1	A	440	THR
1	A	442	VAL
1	A	448	GLU
1	A	472	CYS
1	A	482	LEU
1	A	507	VAL
1	A	514	LEU
1	A	536	LYS
1	A	543	LEU
1	A	561	LEU
1	A	581	ARG
1	A	603	VAL
1	A	658	ARG
1	A	673	LEU
1	A	679	ASN
1	A	689	MET
1	A	701	LEU
1	A	702	LEU
1	A	726	VAL
1	A	736	THR
1	A	761	GLN
1	B	51	ASN
1	B	72	GLN
1	B	90	LEU
1	B	92	ASN

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Mol	Chain	Res	Type
1	B	125	ARG
1	B	141	GLN
1	B	207	VAL
1	B	246	LEU
1	B	253	ARG
1	B	254	VAL
1	B	272	ASN
1	B	276	LEU
1	B	293	MET
1	B	303	VAL
1	B	336	ARG
1	B	385	CYS
1	B	388	GLN
1	B	392	LYS
1	B	425	MET
1	B	448	GLU
1	B	472	CYS
1	B	482	LEU
1	B	492	ARG
1	B	514	LEU
1	B	523	LYS
1	B	536	LYS
1	B	543	LEU
1	B	561	LEU
1	B	566	TYR
1	B	581	ARG
1	B	603	VAL
1	B	612	GLN
1	B	658	ARG
1	B	689	MET
1	B	701	LEU
1	B	702	LEU
1	B	736	THR
1	B	761	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	GLN
1	A	126	HIS
1	A	141	GLN
1	A	169	ASN

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Mol	Chain	Res	Type
1	A	170	ASN
1	A	247	GLN
1	A	272	ASN
1	A	286	GLN
1	A	314	GLN
1	A	369	ASN
1	A	435	GLN
1	A	483	HIS
1	A	505	GLN
1	A	508	GLN
1	A	533	HIS
1	A	572	ASN
1	A	612	GLN
1	A	679	ASN
1	A	694	ASN
1	A	704	HIS
1	A	718	GLN
1	A	761	GLN
1	B	51	ASN
1	B	72	GLN
1	B	126	HIS
1	B	138	ASN
1	B	141	GLN
1	B	170	ASN
1	B	247	GLN
1	B	272	ASN
1	B	314	GLN
1	B	344	GLN
1	B	345	HIS
1	B	369	ASN
1	B	377	ASN
1	B	435	GLN
1	B	483	HIS
1	B	505	GLN
1	B	533	HIS
1	B	606	GLN
1	B	612	GLN
1	B	679	ASN
1	B	694	ASN
1	B	704	HIS
1	B	718	GLN
1	B	731	GLN

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 ⓘ

1 ligand is 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	ACF	A	800	1	28,28,28	1.50	6 (21%)	35,39,39	0.85	2 (5%)

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	ACF	A	800	1	-	3/19/38/38	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	800	ACF	C1-N8	3.23	1.41	1.34
2	A	800	ACF	C21-N22	-3.00	1.33	1.48
2	A	800	ACF	C16-C10	2.56	1.43	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	800	ACF	O26-C24	-2.55	1.22	1.30
2	A	800	ACF	C2-C1	2.16	1.57	1.53
2	A	800	ACF	C14-C15	2.15	1.42	1.39

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	800	ACF	C18-C17-C21	-2.16	104.10	112.17
2	A	800	ACF	C21-C17-N8	2.11	117.92	110.64

There are no chirality outliers.

All (3) torsion outliers are listed below:

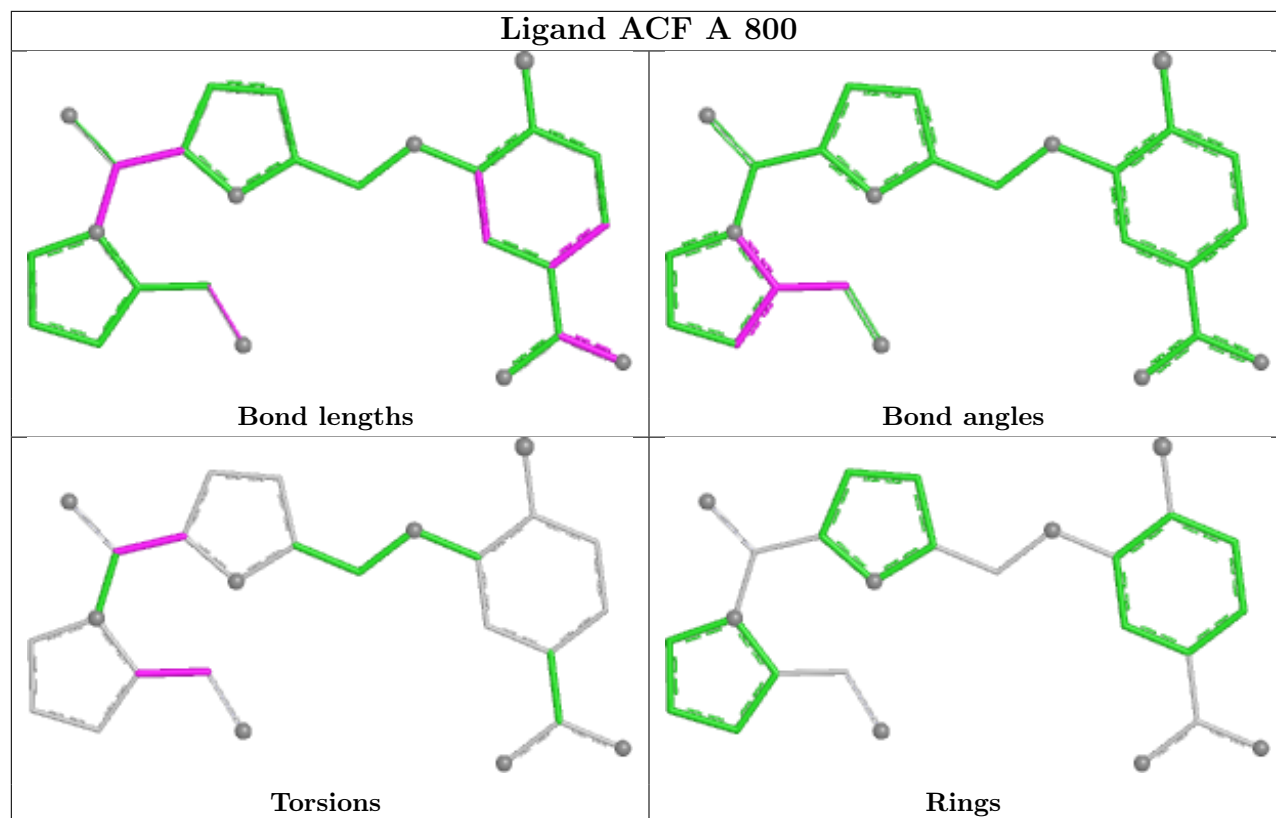
Mol	Chain	Res	Type	Atoms
2	A	800	ACF	N8-C17-C21-N22
2	A	800	ACF	O3-C1-C2-C4
2	A	800	ACF	N8-C1-C2-C4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	800	ACF	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	726/726 (100%)	-0.17	18 (2%) 58 59	12, 27, 52, 71	0
1	B	726/726 (100%)	-0.13	14 (1%) 66 67	16, 30, 55, 72	0
All	All	1452/1452 (100%)	-0.15	32 (2%) 62 63	12, 29, 54, 72	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	39	SER	6.2
1	A	277	SER	3.8
1	B	105	TYR	3.7
1	A	40	ARG	3.7
1	A	71	LYS	3.1
1	B	71	LYS	3.1
1	A	289	ALA	3.0
1	A	90	LEU	2.9
1	B	341	VAL	2.9
1	B	90	LEU	2.7
1	A	487	ASN	2.6
1	A	334	SER	2.6
1	B	289	ALA	2.6
1	B	276	LEU	2.6
1	B	72	GLN	2.5
1	B	39	SER	2.5
1	A	103	ASN	2.4
1	A	764	SER	2.4
1	A	615	LYS	2.4
1	A	110	ASP	2.4
1	B	73	GLU	2.3
1	B	66	HIS	2.3
1	B	141	GLN	2.3
1	A	341	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	342	ALA	2.3
1	B	110	ASP	2.3
1	A	105	TYR	2.2
1	A	96	ASP	2.2
1	A	321	ASN	2.1
1	B	333	SER	2.1
1	A	140	ARG	2.1
1	B	142	LEU	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](#)

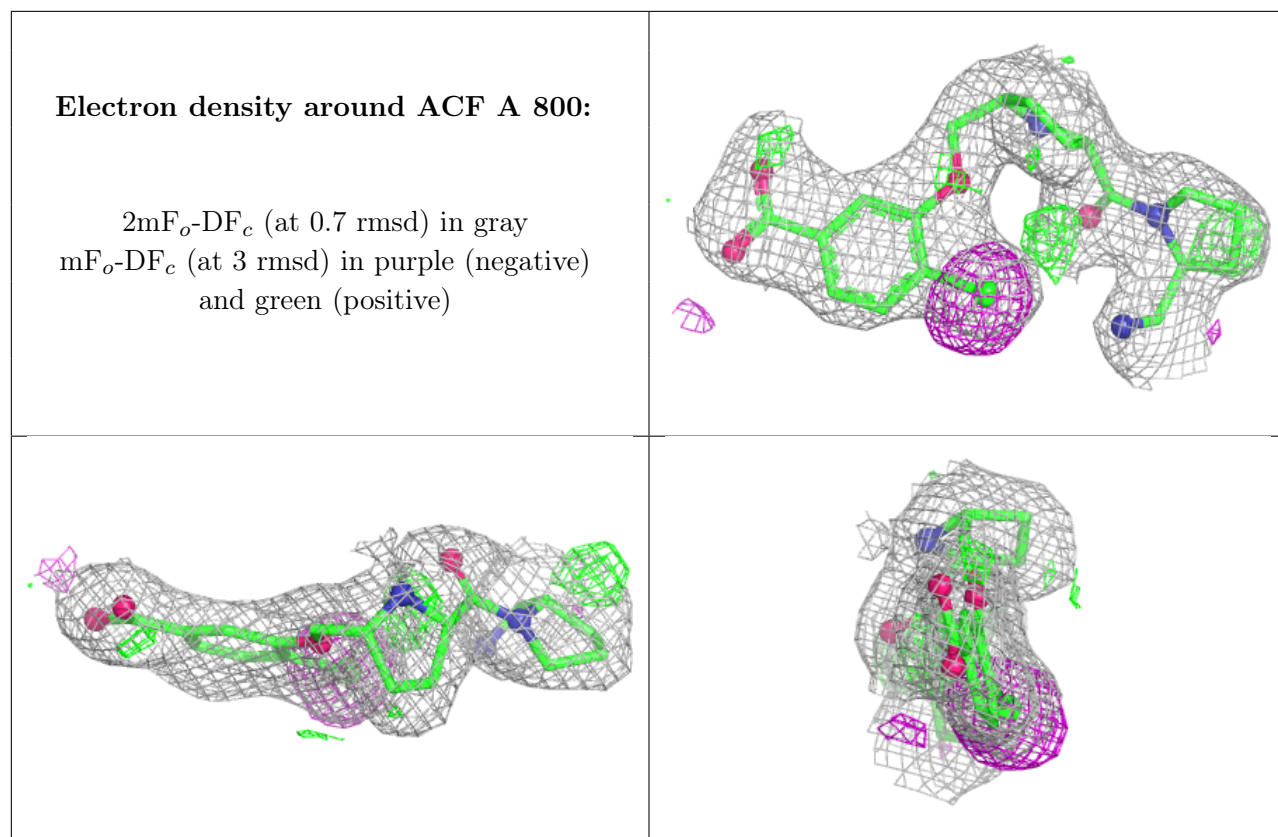
There are no monosaccharides in this entry.

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(\AA^2)	Q<0.9
2	ACF	A	800	26/26	0.84	0.12	11,23,28,32	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.