SFC_sf_res_high	best resolution of available diffraction data
PDB_Resolution	reported nominal resolution
SFC_rfact_all_refl	Rfactor using all available reflections
SFC_correlation	Reflection correlation coefficient using all reflections
SFC_rfact_2sigma	Rfactor using reflections with S/N >= 2
SFC_correlation_2sigma	Reflection correlation coefficient using reflections with S/N >= 2
PDB_RWork	reported Rwork
SFC_rwork_recomp	recomputed Rwork
SFC_rwork_recomp_diff	difference between reported and recalculated Rwork
PDB_RFree	reported Rfree
SFC_rfree_recomp	recomputed Rfree
SFC_rfree_recomp_diff	difference between reported and recalculated Rfree
PDB_Rdiff	difference between reported Rfree and Rwork
SFC_rdiff_recomp	difference between recomputed Rfree and Rwork
SFC_rdiff_recomp_diff	difference between recomputed and reported Rdiff
PDB_Rfrac	fractional difference between reported Rfree and Rwork
SFC_rfrac_recomp	fractional difference between recomputed Rfree and Rwork
SFC_rfrac_recomp_diff	difference between reported and recomputed Rfrac
B_mean_u_all	mean u for all atoms
B_mean_u_amino	mean u for amino acid atoms
B_mean_u_main	mean u for main chain atoms
B_mean_u_side	mean u for side chain atoms
B_mean_u_water	mean u for water atoms
B_stdev_u_all	stdev of u for all atoms
B_stdev_u_amino	stdev of u for amino acid atoms
B_stdev_u_main	stdev of u for main chain atoms
B_stdev_u_side	stdev of u for side chain atoms
B_stdev_u_water	stdev of u for water atoms
B_CV_u_all	stdev(u)/mean(u) for all atoms
B_CV_u_amino	stdev(u)/mean(u) for amino acid atoms
B_CV_u_main	stdev(u)/mean(u) for main chain atoms
B_CV_u_side	stdev(u)/mean(u) for side chain atoms
B_CV_u_water	stdev(u)/mean(u) for water atoms
B_frac_delta_u	fractional difference between mean u and E[mean u | optical]
B_frac_delta_u_pos	fractional difference between mean u and E[mean u | optical] (positive values or zero)
B_frac_delta_u_neg	fractional difference between mean u and E[mean u | optical] (negative values or zero)
B_frac_delta_u_abs	fractional difference between mean u and E[mean u | optical] (absolute value)
B_ratio_u_means	ratio of mean u for main chain and side chain atoms
B_ratio_u_stdevs	ratio of stdev of u for main chain and side chain atoms
WC_per_buried_B	percentage of buried atoms with B < 5 Ang^2
WC_avg_B_bond_diff	average difference between B-factors of bonded atoms
WC_rms_B_bond_diff	rms deviation of B-factors of bonded atoms
WC_rms_B_z	rms z-score for B-factors
SFC_B_mean	mean B-factor
SFC_B_stddev	stdev of B-factors
SFC_B_Wilson	Wilson B-factor
SFC_Boveral	unknown B-factor
SFC_B_Patterson	Patterson B-factor
SFC_B_Patterson_diff	difference between Patterson B-factors for observed and calculated reflections
PDB_ratio_water_amino	ratio of water atoms to amino acid atoms
PDB_ratio_hydrogen_amino	ratio of hydrogens to amino acid atoms
SFC_ratio_atoms_water_total	ratio of water atoms to total number of atoms

ProSA_fracdelta_en_combined	fractional difference between combined ProSA energy score and E[score | residue count]
ProSA_fracdelta_en_surface	fractional difference between surface ProSA energy score and E[score | residue count]
ProSA_fracdelta_en_pair	fractional difference between pairwise ProSA energy score and E[score | residue count]
ProSA_fracdelta_z_combined	fractional difference between combined ProSA z-score and E[score | residue count]
ProSA_fracdelta_z_surface	fractional difference between surface ProSA z-score and E[score | residue count]
ProSA_fracdelta_z_pair	fractional difference between pairwise ProSA z-score and E[score | residue count]
V3D_fracdelta_quality	fractional difference between Verify3D score and E[score | residue count]
Errat_qual_rem	100 - Errat quality score
WC_in_out_z	inside-outside z-score
WC_pack_avg	average packing score
MP_molprobity_score	MolProbity score
MP_rama_outliers	percentage of outlying Ramachandran angle pairs, according to MolProbity
MP_rama_unfavored	percentage of unfavored Ramachandran angle pairs, according to MolProbity
PC_per_rama_labelled	percentage of Ramachandran angle pairs labelled by ProCheck
PC_per_rama_disfavored	percentage of Ramachandran angle pairs outisde of the favored region, acording to ProCheck
PC_per_rama_ungenerous	percentage of Ramachandran angle pairs outside of the generously allowed region, acording to ProCheck
PC_per_rama_disallow	percentage of Ramachandran angle pairs outside in the disallowed region, according to ProCheck
WC_rama_z	Ramachandran z-score from WhatCheck
WC_back_z	Backbine z-score from WhatCheck
TAP_remainder	1 - TAP score
MP_rotamers	Percentage of rotamer outliers, according MolProbity
PC_per_rota_labelled	Percentage of rotamers labelled by ProCheck
PC_stdv_chi1gminus	stdev of chi1 gauche minus
PC_stdv_chi1trans	stdev of chi1 gauche trans
PC_stdv_chi1gplus	stdev of chi1 gauche plus
PC_stdv_chi1pooled	pooled stdev of all chi1
PC_stdv_chi2trans	stdev of chi2 trans
WC_rota_z	rotamer z-score from WhatCheck
WC_Vm_obs	Matthews coefficient calculated from observed atoms by WhatCheck
SFC_vol_not_model	percentage of unit cell volume not occupied by model
SFC_matthews	Matthews coefficient calculated by SFCheck
SFC_solv_content	percentage of unit cell volume occupied by solvent, according to SFCheck
PC_per_planar_outside	percentage of planar group outliers
WC_planar_z	planar groups z-score from WhatCheck
PC_stdv_omega	stdev of the omega torsion angle, according to ProCheck
WC_omega_stdev	stdev of the omega torsion angle, according to WhatCheck
PC_stdv_zeta	stdev of the zeta improper torsion angle
WC_rms_improper_z	rms deviation of the zeta improper torsion angle
WC_chiral_dev	WhatCheck chirality deviation score
PC_per_mcbl_outside	percentage of main chain bond length outliers
WC_rms_BL_dev	rms bond length deviation
WC_rms_BL_z	rms bond length deviation z-score
PC_per_mcba_outside	percentage of main chain bond angle outliers
WC_rms_BA_dev	rms bond angle deviation
WC_rms_BA_z	rms bond angle deviation z-score
MP_cbetadev	C-beta deviation count, according to MolProbity
PC_max_dev	max deviation (of what?!), according to ProCheck
PC_bond_ratio	bond ratio (?), according to ProCheck
WC_rms_tau_z	rms tau deviation z-score
PC_per_bad	bad contacts per 100 residues, according to ProCheck
MP_clashscore	MolProbity clash score

WC_bump_total	total bump value
WC_bump_per_res	total bump value per residue
WC_bump_num	total number of bumps
WC_bump_squared	total squared bump value
WC_bump_mildest	total number of bumps in the mildest bin
WC_bump_second	total number of bumps in the second bin
WC_bump_middle	total number of bumps in the third bin
WC_bump_fourth	total number of bumps in the fourth bin
WC_bump_worst	total number of bumps in the worst bin
PC_stdv_hbond	stdev of main chain h-bond energy
WC_per_donors_buried	fraction of donors buried
WC_per_acceptors_buried	fraction of acceptors buried
WC_per_acceptors_no_H	fraction acceptors with no H-bond
WC_per_acceptors_ess_no_H	fraction of acceptors with essentially no H-bond
WC_per_acceptors_vpoor_H	fraction of acceptors with very poor H-bond
WC_per_acceptors_poor_H	fraction of acceptors with poor H-bond
WC_per_donors_no_H	fraction donors with no H-bond
WC_per_donors_ess_no_H	fraction of donors with essentially no H-bond
WC_per_donors_vpoor_H	fraction of donors with very poor H-bond
WC_per_donors_poor_H	fraction of donors with poor H-bond
SFC_min_est_error	minimal estimated error, according to SFCheck
SFC_max_est_error	maximal estimated error, according to SFCheck
SFC_diff_est_error	difference between maximal and minimal estimated error
SFC_DPI	Cruickshank DPI
SFC_Luzzati	Luzzati score
SFC_displacement_stdev	stdev of displacement of atoms from electron density, estimated from the difference (Fobs - Fcal) map
SFC_Dens_mean	mean density within a certain radius of atoms
SFC_Dens_stdev	stdev of density within a certain radius of atoms
SFC_Dens_CV	stdev(Dens)/mean(Dens)
SFC_real_space_corr	real space correlation coefficient
SFC_rstand_I	sigma(I)/<I>
SFC_rstand_F	sigma(F)/<F>
SFC_frac_refl_unacc	fraction of reflections that are unacceptable
SFC_frac_refl_1sigma	fraction of reflections with S/N >= 1
SFC_frac_refl_3sigma	fraction of reflection with S/N >= 3
SFC_completeness	percent complete
SFC_ani_ratio_1	ratio of first and second diffraction eigenvalues
SFC_ani_ratio_2	ratio of first and third diffraction eigenvalues
SFC_ani_ratio_3	ratio of first and third diffraction eigenvalues
SFC_Padd	something related to Patterson scaling?
SFC_scale	Patterson scale factor
SFC_Ks	solvent correction Ks
SFC_Bs	solvent correction Bs